

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253:

5 TTAGTAGTCA TCGGTATTGG TGGTTCCTAC TTAGGTGCAC GTGCAGCAAT CGAmATGTTA 60
 ACGTCATCAT TTAGAAACAG CAATGAATAC CCTGAmATTG TATTTGTTGG TAATCACTTA 120
 TCATCAACAT ATACGAAAGA GTTAGTTGAT TATTTAGCAG ACAAAGATTT CTCTGTAAAC 180
 10 GTTATTTCTA AATCTGGTAC AACTACAGAA CCAGCAGTTG CATTAGATT GTTCAAACAA 240
 TTAGTTGAAG AAAGATACGG TAAAGAAGAA GCACAAAAAC GTATATTTGC AACACGGAT 300
 AAAGAAAAAG GngCTTTTAA ACAGTTGGCT ACAAACGAAG GTTATGAAAC GTTTATCGTA 360
 15 CCTGATGATG TAGGTGGAAG ATATTCTGTT TTAACAGCAG TAGGATTATT ACCAATTGCA 420
 ACAGCTGGAA TTAACATCGA AGCTATGATG ATTGGTGTG CA 462

(2) INFORMATION FOR SEQ ID NO: 1254:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254:

30 ACTCATAAGT GAATGGTTGA TTACCACTAG TTAAACTTC ATATACTATA GTTCTTTTTT 60
 TTATTTTGCA ATTAGTTATT TTCATTATAA ACTTCCTTTC AAACACTGCT GAAATAGACG 120
 TCTTTTTCAA ATAAGCATGA TTAATACTTC AATTCTTTAA TCCACATATA TTTAAAGTG 180
 35 AGGTAGTAGG TAATAAATAT AAGACTTAA GTTAAGATTG CTTTTTTCAT GTTTCATAAT 240
 TAAACCTCT GTAAATTTAA GGTAGTATT ATGAAATAAT GGATTGGTTT ATTCTTTAGT 300
 ACTAACTTCG TAGTAAATTA TATAGTTCGC TAAATTGTAT TTATCTACTA TATTTTGGGA 360
 40 ATAAACAATT TCCTTTTCTT TCTTCAGTAA ATTATAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 1255:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255:

nAATCTATGT ATGGGGGCAT CCAAAGATTT CATAGACTAC TTATTTGTTG ATGAAGCCGG 120
 ACAAGCAATC CTCAAGC 137

(2) INFORMATION FOR SEQ ID NO: 1256:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256:

TGAAATGTAG AAATTGAATT AGAAATGAAG ATTAAAAATC nACACGTATC GTTCAAGTGG 60
 TGCAGGTGGT CAGCCGTAAA CACAACTGAC TCTGCGTACG TATTACCATT TCCACTGGTG 120
 TCATTGCAAC ATCTTCTGA 139

(2) INFORMATION FOR SEQ ID NO: 1257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257:

TTACCAntTA TTtTAACACC ATGTTTtagAC CAATTTGATC TGACTAAATT AATCGCTGTT 60
 TGTACCTCCA AATTGTTACA ACGTACACCT TTAGTTTTTC TAAATTAATG TATATTCATC 120
 ACATCTTCTT CAGTTAAGGG TCAAAGTATA ATTGTGCGAA ATTGTGAAGT CGTTGTA 177

(2) INFORMATION FOR SEQ ID NO: 1258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258:

AAGACCAACC GAAATGAATA TCGACATGGA TTAAGCCTAT ATTCAGATGT AAACGGCGAT 60
 TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA ATATGCCCAA GAATGGGCTG 120
 TATCACTTAG GTGTATCAAA CTGACCAAAA ATTGGAAGGA CTTTAGGCCA AAAACCATGC 180

TTAATTTTTC

250

(2) INFORMATION FOR SEQ ID NO: 1259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259:

ACATTTCACGG GACATTTTCAT TACATCACCC TGCTTTATTT TGGATTATGG CCTAATTTAT 60
 ACTGATAAAT CTAGGAGGTG GAAAAAGAA TGCCCTGCAA TTTAATTnCA TTTAACCAAA 120
 TAATGAAACA ATAAAAACA TTATATCGTT ACTTATTAAG TAATTTGGCA 170

(2) INFORMATION FOR SEQ ID NO: 1260:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260:

TTTGTACTION GATACGTTGT ATTCAGGTG ATGACACTAG GAATTTGTAA TGATCAATTT 60
 CTCTAATTCT TTACAATTGA TAGAATTCTT CGATTTGTGG ATAGACATTC ATATCATTGT 120
 CTAATGATTT TTGGTGATTC ATAAATTGTG ACTAAGCTT GGATGCTTTA GGATTGTAGC 180
 TGAGACACAT GTTGCCTGAC TGNnGATTTA TCAATAATC TCAATCACGT GATCCnATCA 240
 CATTATCAG CTCACTAAAT CAAGATGATC GTCGTTTATG GGCGATTAAT GGCGTACCGC 300
 CAGTGTCGGC ACG 313

(2) INFORMATION FOR SEQ ID NO: 1261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261:

TAGCGATCAT TTAATCAAGG TTAGATTATT TAATGTCAGC ATTACGTTTG ACAATGAACT 60

GTTTGAGGTT ATCACAATGC CATTTAACAC TATGCGCACA TGGCTGAACT AATnAGCGAC 180
 GAGATGACTT CAAACCTTGA TTAGGT 206

(2) INFORMATION FOR SEQ ID NO: 1262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262:

AAGTGTGTAC ACGATAGCTA AACTCAAATA TCACAGAACA ACAAATGTCT TAGTACTTTG 60
 TGCCGGTGGT GGTACAAGTG GATTATTAGC CAATGCACTA ATAAAGCAGC TGAAGAATAT 120
 CATnTGCCAG TGAAAGCGGC ACTG 144

(2) INFORMATION FOR SEQ ID NO: 1263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263:

ATAACGACAC CTAATGCAAT TTGAATAAAG CAGTAGAATT TGTGGGAATC GATTATTGAT 60
 AACCGAAGTATA ATAATCACAG CAAAAATAAA ATTAAAAATG CTCTAATAGT GCCTACATnC 120
 TCCTCAAATT TT 132

(2) INFORMATION FOR SEQ ID NO: 1264:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264:

TATGTCAATT TCGTAGAATT GGTTTTAnGC GCTATTTAGA ATAGCCATCA GATAAAAATCA 60
 TTATTTAAAC GTATAATAGG TCAAAATATA GAGAGTTACT ATACAAATTT CTAACCTTCA 120
 CTTAAATAAA AATATATATA ATTAAAGTGG AGGAGAAGG 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265:

ATAGCTCAAG CAATCATTAT GTTTATAATG ATTGTATGGT TCTTTATAGA TGCTTTATTG 60
 ATTAATTAAT AAAAAGCTTA TTGCAAAATA TGTTTTTCGG TAACTGTAAT TTAGTGATT 120
 TATCATTAAAC AG 132

(2) INFORMATION FOR SEQ ID NO: 1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266:

CATGGATTTA TCTTAGCGAT TGGTCTAATT TTACCTTTAG GTGCACAAA TGTATTTATT 60
 TTTAACCAAG GAGCTAATCA ACCAAAATAT AGATATGTAT TGCCTGCAAT AATTACAGCC 120
 GGGTTGTCAG ACAGCTTACT TATTATTATT GCAGTGGTAG GAGTWTCTAT CATTATTATG 180
 TCTTTACCTG TACTTCAWGC AWTATTTTAT ATAGTTGGTT TAATTTTCTT GATGTATATG 240
 GCTTGGACCA TTTGGCATGA TAAACCCTCA ACAGATGGAG AAACTCAAAT TATGTCTCCA 300
 ATGAAACAAG TAAGTTTTGC TTTATCAGTT tCATTACTCA ATCCACATGC TATTTtAGAT 360
 ACAATTGGAt TAATTGGtAG TAGTGCTGCA TTATATAGTG GcNcGC 405

(2) INFORMATION FOR SEQ ID NO: 1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267:

TCTTTATATT GCAGTACAAA ATTGCGGTGG AGGTTTAAAC CAAGTAGACC GCACAAGATT 60
 TAGCGTCTGA AGGTATTACT GTGTAATGCA TTCGCACCTG GtTATCGTTC AAACACCAAT 120

(2) INFORMATION FOR SEQ ID NO: 1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268:

TTTGCCCAAG TGACGTAAAG TACCCAATGT CCATTGTGAC TTGTATCGCC ATCAACAGTA 60
 ATCATATTAA ATGTATGGTC AGTCGAAGAT TTTAATAATT GATGAAGTGT ATTCGATTCA 120
 ATCGATGCAT CGTGTATATAA AAGCAAGCAT GTAGCCAATT GGGAATCAAC CCGAnCTTGG 180
 CACACATGTA CGTTACACAT TAGAACnCAA GTGACCGACG GTAATCCTAC CCGCTCAACA 240
 CAAGCGC 247

(2) INFORMATION FOR SEQ ID NO: 1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269:

TCATTGTATA TGACGAGATT GGCTAGGCGG TGGCTGGACT GACGGAATCG ACACCCGGCT 60
 GGGGTTGGGA AAAGTACAAG ACGCAACATG CTATGATTTT CCTATGTGGT TATCGTCCGA 120
 TTTAAAGTGA GCAGCGCAGG GTCAGTCATC TCTCACAGnA CCTAAAAAGA ACAGTAAGCn 180
 CAACCTAAAG CAGTGGAAGT TAAAATCATC AAGGT 215

(2) INFORMATION FOR SEQ ID NO: 1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270:

ACAATAAAGA CTATTAAAAG AGATATAGGT TAGATATTAC ACTTTTAGAG CAAGACGGTA 60
 TAAATGCAAG TAAATTCGTG TATTTATCAA TACAGCAGGT nGAGTGAAAG GCCCAGCAG 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271:

CGTGGCACGT TAAGCGTTTA ACCATAGCAT TAAGATGATT GTCTAGCAGA GGCGATTTCG 60
 GGGCTCACTA CAGTGCATGA TGAACCTAAT GCTTCAAATG TAACATTAAA AATAAAAGCA 120
 ACGATGTCAC TTCTTACTTC TACATCTGCC ATnTTCGTGA TTTCGTATCT ATCCCGCATC 180
 TCATCTTGAA CGTACGAGCC TAATCGCCCh GCGCGATCCT GCC 223

(2) INFORMATION FOR SEQ ID NO: 1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272:

TAGTTACAAT ATCTGTCAAT TTCTGGAGAA CCACTAAAGC TATGCATAAT CCCGCCTACC 60
 TCTTCAGCAT GCTCCTCCAA TAAGATATCG GTACAGTCTT GAGnTGCTTC ACGGTTATGA 120

(2) INFORMATION FOR SEQ ID NO: 1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273:

TTGCGCGGCA GTAAATTCA AACTATTGGC GTCATTTTGC CTAGCTTAAC AAATCCGnTT 60
 TTCTCAGCAC TGATGCAAAG TATTCATGAC CATAAACCAT CTGATGTTGA TTTATGCTGG 120
 TTAACA 126

(2) INFORMATION FOR SEQ ID NO: 1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274:

5 GATTCTGAAG GATCAATACn ACATGTACAA TTTTGGCGTA GGTGCAAAGG CATCAGGTTT 60
 GCTTGCTAAT CTACATCGAA GCGGCTACCT AAATTAATGA GAAATCACAC TCAGTTAATG 120
 CATGTACTAG C 131

(2) INFORMATION FOR SEQ ID NO: 1275:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275:

20 TGGAGTATTA CCTCAAGTGA ATACAACATA CCTGTTGGAA GATTTTTCAA AACTTTAATT 60
 GGACCAAGTG ATGCCATTGA TGAGTTAAAT CCTAATAGAT TCAGGTTACC TCGGATGATT 120
 GATACTAATT TGGCCTGGCG CACGCTTTAG TAnTAGTGG 159

25

(2) INFORMATION FOR SEQ ID NO: 1276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276:

35

GAAGTAAATA ATATATAGAA TATAACAGGA AATAAAATAG ATAATATTAA TGTTGTTTTT 60
 TTACGCATTA TAACTTTAAA TTCGATTTTC AAGTAACTTA GTATCATAAT TAGATCCCCCT 120
 40 TTGCTTTTTA TTGnTGAAGT ATGAATCAAC AATGAGACT tTTTGtATTT CAATATCATC 180
 CAAATTAATA TGAAGTTGTT GAAGATATAA AATCGTATCA TTTACATTTG AAGTAATAAT 240
 TTTsATAGTG CCATTATGAT TTTyycTGAA TAACTAAATC ATCTTTATCT AGTTTTAACT 300
 45 TTCTTATATA TTCATCGGAT AACGTAATCT GAGATTGCTG ATTGGTTCTA ATATGTGACG 360
 TTGAATCATT AAGTATTATT TCTCCATTTT CAATGAGAAT AATTTTGTCT GACATACGTT 420
 CGACTTCTTC AATATAGTGC GATGTATAGA GTATCGTTCTG ATTATCTTCT TTTAAATTTT 480
 50 CAATAATTGA CCAAAAATAT TCTCTAATTT CTATATCCAT AGTCGATGTT GGTTCATCTA 540

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(2) INFORMATION FOR SEQ ID NO: 1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277:

CTAAANTAG GTAATAGTTA CCAAGTACCA TATCTGTGG ATGGTGTACT ACAGGTTTAC 60
 CATCTTTAGG TTCAAGATGT TTTGATGACT GCTAACATCA ACATTCTTGC TTCAGCTTGT 120
 GCCTCTTTTG A 131

(2) INFORMATION FOR SEQ ID NO: 1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278:

GTTTGCATA TTTTAGGCAG ACAACCTAAC TTTACAGAAA CAGGTATCTT TTCTGTTATG 60
 TGGAGTGAAC ATTGCTCTTA TAAACATTCT AAACCGTTTT TAAAGAATTT CCTACGCAGG 120
 TGCCATGGTT TGGGCTGGAG TCAGGTGCGT TGTGTATAGC TGATna 166

(2) INFORMATION FOR SEQ ID NO: 1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279:

CATAATTATG AAAATGATAT GATTTTTATT AGACCATTTA AAAAAGCATA ATTTAAATCG 60
 AAGGCAGGAC ATTGAAATAT GAAATTTTCA ACTTTAAGTG AAGAAGAATT TACCAACTAC 120
 ACCAAAAAGC ACTTCAAACA TTATACGCAG TCTATAGAAT TATATAATTA TAGAAATAAA 180
 ATAAATCATG AAGCACATAT TGTGGGAGTG AAGAATGATA AAAATGAAGT TATAGCTGCA 240
 TGTTTATTAA CAGAGGCACG AATTTTTTAAA TTCTACAAAT ATTTCTACTC TCATAGAGGT 300

ATTCATTAT AAAAATAGAG GAGTATTTAT TCTTGTGAT CCATATnTAA TAGAGAAT

418

(2) INFORMATION FOR SEQ ID NO: 1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280:

GACATATCAT AAATTACATG GTGATAAAAT TnTCGGCTAC GATACTAACG GATTCCCGAT 60
 TACCTGGTTT TATCCATTAG GTGAAAAGAA AGTTGAACGT AAGGCACCAA AATTAGAAAA 120
 ATAATTAAAT AAAACAGCTT AATGATGTAA TGAAATTAGT GAGTTAATCA CTGACTTCTA 180
 CGTCAITGAG CTGTTTTTTT GTGCTTTGTT ACAAAGCATT ATTGAATTTA TTTTACGTGT 240
 TCATATTTTG AAACATCAAA GCCGTCTTGT TTAGCTTTGT TGATAATGTC TTTGATTGAA 300
 TGTAGTCCTT TATCGGCGAA GTATGATCTT AAGTTGTCTT TTGTAGCTTG GTCAGCATTC 360
 TTATCTAATA ACACATCAAT ATAACCTAAT TCATGTTCTA AGAAGTTTGC ATCATCATGT 420
 AGTACGAGTC CATTTTGAGA ATAACTTT 449

(2) INFORMATION FOR SEQ ID NO: 1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281:

TATTTATATG TACTGATGAT GAAGTTTATT ATCTATCAAG TGGATCAAAT CCGAAATATA 60
 ATCAGTATAT GGGTGCATAT CATCTACAAT GGCATATGAT AAAATATGCA AAATCACATA 120
 ATATTAATAG GTATAATTTT TATGGAATAA CAGGCGTCTT TAGTAATGAG GCGGATGATT 180
 TTGGTGTTC ACAAATTTAA AAGGGTTTTA ATGCACATGT TGAAGAATTA ATTGGTGATT 240
 TCATCCAACC AGTAAAACCC ATTCCAATAT TAATnTGCCA AACCTnAAT 289

(2) INFORMATION FOR SEQ ID NO: 1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282:

5 ATTGAGGTCG AGGTGGCCCG GCTCCATGCA CCGCGACGCA ACGGGGGAGG CAGACAAGGT 60
 ATAGGGCGGC GCCTACAATC CATGCCAACC CGTTCCATGT GTCGCGCGAG GCGGCATAAA 120
 TCGCCGTGAC GATCAGCGGT CCAATGATCG AAGTTAGGCT GGTAAGAGCC GCGAGCGATC 180
 10 CTTGAAGCTG TCCCTGATGG TCGTCATCTA CCTGCCTGGA CAGCATGGCC TGCAACGCGG 240
 GCATCCCGAT GCCGCCGGA GCGAGAAGAA CTAATTGATA CAACACTTTC TCAACCTGAT 300
 CTTCTTTACC TTCTACATAG CGCGTGAGCA GAACCATCTT GATGgCACAG CTAAATAATG 360
 15 CaATgGGAAT GATGTATGAC ATTCGGGGTG CATAATTTCT CT 402

(2) INFORMATION FOR SEQ ID NO: 1283:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283:

25 TATTGACAAC CAGAGTACAA ACAGCAGCTA TATTATAGAC TTAGGTCTGA AGTGGTAGTG 60
 GCGGTGGACT ATTGTTGCGA CTGGACACCC GAGATATTGC TCAGCAAGAGC ATCATATACA 120
 30 GGAAGTATTA AAAGAGACTT GnCGAGTAAC AAATACTGAA GTAATAAGAT TAAAAGAGTG 180
 AGGTGTATAA TTATCCTCGT TCTTTTATAT TAGTATGATA GAGA 224

(2) INFORMATION FOR SEQ ID NO: 1284:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284:

45 CGTGGGAGAT TGTGCATATT GATTATGCAA GGAAGnACGC CATAAAAGTG GATGGCCAGA 60
 CATCATTAAT ATTATTGATA CCACATCAGA AGGTATTCAA AGTGAATCGG TGATAAGTGA 120
 ATCAATTAAG TCTGCCAAAG AAAAGA 146

(2) INFORMATION FOR SEQ ID NO: 1285:

(A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285:

10 ATTTGCGGTG ACTGGACTTG GATCCGCAAC TTGGTAATTT AAGGAATTCT TGTCAATTATA 60
 AGCCCTCCAT TTCATGATTT GATTGCCCAC TCGGTAACCA TTGGGGTTAC AGCTTCACTA 120
 GGGGAnATAC GAACCTC 137

15 (2) INFORMATION FOR SEQ ID NO: 1286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286:

25 GCTATTGATT ATGGTTAGCm TGTGTTCWC TTTACTCATT GTTCCTTGGt TAAGCTCrAA 60
 AAAAGCACGT ACTTTAAAGA AACATGCAGC TAATGAACAG GCCCGATTTT TAAATCATT 120
 30 TTATGATTAT AAAGCTGGTA TGGATGAACT ACGTCGATTT AATCAAATTA ATCATTATCG 180
 AGATAATTTG ATGGCTAAAT TAAATCATTT TGATAAATTA CAACTTAAAG AGCAACGCTT 240
 TTTAACGATT TATGATTTTA TATTAAATAT TATTGCTATG CTTTCGATTT TTGGTAGTTT 300
 35 AGTTCTAGGA TTAATTCAA TTAATGCAGG CCAACTAAAT ATTATTTATA TGACGAGTAT 360
 AGTTTTAATG GTCTTAACTT TATTTGAACA AGCTGTACCA ATGACAAATG TCGCGTATTA 420
 TAAAGCGGAT ACTGACCAAG CATTGCACGA TATTAATGAA GTGATATCTG TACCTTCTAC 480
 40 TAATGGAAAA AAACGTCTTA ATGATAAGTA TGATGCAACC AACATTTATG AAGTTAAGGA 540
 TGCTAGTTTT AAGTATTGGA ATCAGCAAAC GTATGTrTTG TCGGATATTr ATTT 594

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(2) INFORMATION FOR SEQ ID NO: 1287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287:

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TGAAGTAGTA ATAAACCCGG AACCCCTAAAA CTGGATGGAG GATGAAACCA AAAAGGAACC 120
 AGCCAAGCCA AATTGGGGGAA ACCAGGACGG CCCAATGGAG GTCCAACCA TCCAAACCCC 180
 ATTCCGCTAA TgNCTATGGG TCCCAATTAG GAATCCAATG GATGGATGGA TTh 233

(2) INFORMATION FOR SEQ ID NO: 1288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288:

AATCCCTGTA CGTTCGTAAA GCTAGCTGGn TAATAAAAAA GAGTCTGGAA AGTAGGCAAC 60
 AATCAATGAC AATGAGCAGA TCCAATCGCA GTATGCTTAC TCGTGTAAGA AACGCAAACA 120
 TGGTGCGTCA CG 132

(2) INFORMATION FOR SEQ ID NO: 1289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289:

TATCTGATAA TTCTGTACCC AGGCGTTTTA ATATGTTTAT CTGGTGTCAT GATACATAAA 60
 CATTGTACCT TTAGGTCATA CGATGTCGCA AATAACTGCT CTTGCCGTTA CAACACCATT 120
 ACGGTTATAC ACTTnTAGCC AATCATTATC TGGG 154

(2) INFORMATION FOR SEQ ID NO: 1290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290:

AAAAGTGGCA CATGCGGCTG TAAAGTCCTC TGTtTCTGAT AAATCATAAC CTATATACAT 60
 GTCTACCTTC CAACTCATCT AAGAAATAAG TCATATTTTT TTGAATGTTG GATAATCAAT 120

(2) INFORMATION FOR SEQ ID NO: 1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291:

CTTAATGCTA TATATTCTTT GTTTTTGATA CCATTCATC GTCTTCTCTT GATTTCTAAA 60
 CAATTTAGAA AATAAAAGAA TATACGCTTC AGACTTATTA AAACCCGCTA TATCATCTTG 120
 ATATTGTATT AACAATTGAG TAAAGCTGTG TATTAAGTCA TCTTTCTTCG ATGCAATGGT 180
 AGTTAATGAT TTTACACGAT AAGCATATTT ATCTGTAAAT AACTTAGCAA CTACCCACCC 240
 TAAATCATGT CCTAGAATAT GTGCCTCATG AATATTTAAC TTCTCCATTA GAATTTTAA 300
 ATCCTCAACG TGATCGTTTA AATCGTATGA TTCACTTTTA GAAGACTTGC CATGACCTCT 360

(2) INFORMATION FOR SEQ ID NO: 1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292:

TGTGTTAGTT GTTTATGTTG TTGATATATA CTGCTCGTGC ACATGGTACC CAGACGATTC 60
 AACGnTGAGT ACACAAAATA CAAAATCTAC GGCACATGGT ACCGTTTATA AAAGATGTGG 120
 AACCTTACTA GCATTTGTTG AGAACGCTAC ACGTTTAAAT CAAG 164

(2) INFORMATION FOR SEQ ID NO: 1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293:

TTAATTTTCT ATATATTTCT TAGGTTATAT TGGTATCTAT GCCAGTAAGT GACATGACGT 60
 TAGATCATTG AATCCAAGAT CGAnACATTG GGACATATTT ATTAACGACA TGGCTTCAAC 120

(2) INFORMATION FOR SEQ ID NO: 1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294:

GTCATGCnTA ACAGGTGAAT ACCTAGTAAT TCAGATATTA TCATTTATAT ACCCTCTTAT 60
 ATTTTAGTGC ATTATCTCGA AATCGAGATA CTTAATGTAA ATTTTGTAGTG CAGCCTACAC 120
 TTCGTGATTG GGCANTAGTT CTTAAACGCT GTGTAAGAT GTTAATTCAT CCTTGGTTAA 180
 CACACAAACG CTTGGTTAAT GCTCAGCAGC TAG 213

(2) INFORMATION FOR SEQ ID NO: 1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295:

AAGAAGTTTG AAGTCTATGA AAACAATCAA AAATTGCCAG TGAGACTTGT ATCATATAGT 60
 CCTGTACCAG AAGACCATGC CTATATTCGA TTCCAGTTT CAGATGGCAC ACAGATGAAA 120
 TGTTTCTCGn CCAATGAGAG GGAGAACATA GTATCAATAG ATG 163

(2) INFORMATION FOR SEQ ID NO: 1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296:

TAGCTTTAAT ACATTCTGAT TTTTAAACGC TTCGAAATGT TTTAGTAAC TAATTTTGCC 60
 ATAATCCCAA AAATCCTTG ATTATTAACT GCnTTTTGAT TGGCTACATT AAGGCTTTAT 120
 ACACATCAGC TCACCATGCC CATATCTACT AATGGTTATA TCCCTAGAGT CCCAGCGATA 180
 TAACATCAAC GCTTACnGGA GTTTCAG 207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297:

ATGGCATCGG TTGGTTATGA AAAGnCAAGC CATGGGGAGG CCATATTTGG GGTGGAATCA 60
 TACCTGGAAC CTTTGGTGCC TACCACCAAT TGGTAACGGT TTTACCATCG GATTTTTAGT 120
 GATACAGCGA TATGTTTTGT ACAGG 145

(2) INFORMATION FOR SEQ ID NO: 1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298:

TCCAAAAGTT AAAGGTCAAT TGAAACAGAn AAAGCTTATT ATGTCTGGAA AAGTATTAAA 60
 AGTAATGGTA TCAAATGACA TTGAACGTAA TCATTTTGAT AAGGCATGTA ATGAAGTCTT 120
 TCAAGCGTTG AATTGTGGT 139

(2) INFORMATION FOR SEQ ID NO: 1299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299:

GATATTGGCA ACCTTCAGCC GATGACCTCA TGGCAAATGA TTGGGAAGTT ATAAACCCAA 60
 CTAGAGACCA GGAATTATTG AAGCAATTAT AGAAATGCTA TCAATGATAC TTTTAAATT 120
 GTTTTAAAC TCATTTTCAA AGTAAACAAC AGTCTTGTCT GAAATTGTTA CATGATAAAT 180
 AGTGTTACTA GCATACACGC CGTTTAGGAA CCCAGAGTTT TTAAGTTTAT TTAAATCGTA 240
 TTTTACATCT TCGAAATGTA GTTTTGTAAA ATACTTTGTA TGTATATCTT TAGCACTTCC 300
 AAAATTTATT GGCAGGTAA TTTAATCGAA CCTAACTTTA CACATTCTAA ATAATCTTTG 360

(2) INFORMATION FOR SEQ ID NO: 1300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300:

CTACAGTGCA ATTTAACCAT GAAGTTGTTG ATTTTGAACA ATTATCAAAT GGTCAATGGG 60
 AAGTTACTGT TAAAAATCGC CTAAGTGGTG AGAAATTCAA ACAAGTAACT GACTACGTAT 120
 TCATCGGTGC TGGCGGTGGA GCAATTCCAT TATTACAAAA AACAGGTATC CCTGAAAGTA 180
 AACATTTGGG TGGATTCCCT ATCAGTGGTC AATTCTTAGC TTGTACAAAC CCAAGTTA 240
 TTGAACAACA CGATGCCAAA GTTTATGGTA AAGAGCCACC TGGTACACCA CCAATGACTG 300
 TACCTCATTT AGATACGCGT TACATTGATG GTCAAAGAAC ATTATTATTT GGACCATTG 360
 CTAATGTTGG ACCTAAATTC TTGAAAAATG GTTCTAACTT AGATTTATTC AAGTCTGTTA 420
 AAACATACAA CATTACAACT TTATTAGCAG CAGCAGTnAA AACTTACCT TTAATTAAAT 480
 ACTCATTTGA CCAAGTAATT ATGACAAAAG AAGGTTGTAT GAACCACTTA CGTACTTTCT 540
 ATCCAGAAGC ACGTAATGAA GATTGGCAAT TATACACTGC TGGTAAACGT GTACAAGTTA 600
 TCAAAGATAC ACCTGAACAC GGTAAAGGAT TCATCCAATT CGGTACAGAA GTGGTTAACT 660
 CACAAGACCA CACTGnAATT GCATTATTAG GTG 693

(2) INFORMATION FOR SEQ ID NO: 1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301:

CATACTTGGG TAATGCTGCC CATGGnACGC TGGnACAAGG TAAAGTTGCA CGTTTAATTT 60
 GTGnATGTAT ATAAAACAGA TGGGAACACC ATTTGAAGGG GATCCTCGTG CAAACTTAAA 120
 ACGTGTATTA AAAGAAATGG AAGATTTAGG cTTCACAGAC TTTAACCTAG GACCTGAACC 180
 AGAATTCTTC TTGTTTAAGT TGGATGAAAA AGGGGAACCA ACTTTAGAAC TTAATGATGA 240
 TGGTGGATAT TTCGATTTAG CACCTACAGA TTTAGGTGAA AACTGTCGTC GTGATATTGT 300

TCAACATGAA AtTGACTTaA ATATGCAGAT GCTGTTACAG CATGTGATAA TATCCAAACA 420

TTTAAATTGG TTGTTAAAAC AATCGCACGT AAACATAATT TACACGCAAC A 471

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(2) INFORMATION FOR SEQ ID NO: 1302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302:

CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTTT TGTTTGGATT 60

TTAATGATTA TTTATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA 120

20

ATTTGCATCT AGTTAATAAT TGCAATTATC AAATTTGTCT TATTGATCCA ATCTAATTTG 180

TACTCACAAA CTAGTTTTAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC 240

ATAAACCAAT GAAGCAATCA GAAACACTC TAATTTTCTa TTAGAAATTT GnTTTAATAT 300

25

AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT 360

GCTTGGTGAT CThTTATTCT GCGTAATAAT GCTAAACCTG 400

30

(2) INFORMATION FOR SEQ ID NO: 1303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303:

40

AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC 60

AAAAGACTGG GGTAAACTnC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT 120

ACAACATC 128

45

(2) INFORMATION FOR SEQ ID NO: 1304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

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TCCTTCGGAT TCTAAATGGC ATTGGACAGT GTTTACAAGC TCGCATTCTT CCACTTTTTTG 60
 CAATTTCTTT TACAATTTCT AAAGCTTCAT CAAAGTTTCC TTCAATAGnA AACGATTTCT 120
 GCACCATACA TTACTGACTT G 141

(2) INFORMATION FOR SEQ ID NO: 1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305:

GACTGGTAAA CACTAAGTGA ATTAGCTGGA CAATGAAAAA TATCCACAAT CATTAAATTAA 60
 CGTACGCGTA ACAGATAATA TCGGTTGAAG AAATGTTGAC GTTAAGAGTT ATGACTAANT 120
 AGAGTAGAAT GATGGTGAGG TCGATTTTAG TAGACTCTGG AC 162

(2) INFORMATION FOR SEQ ID NO: 1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306:

TTCTTAGTTG CTCGAATAA TAATTTGCTT AATAATGATs TAGCTGTTAT TGTGTCATAT 60
 TCTAAAGGTG CCATAAATTT AAAAATAATA GTAGTTGTTT TAAATTTAGT TGTGGTGAA 120
 ACTTTGATAT GTATATTTGG TTGAGATTGT CTAATCAAAT ATATAGCCTC CTCTATATCT 180
 TCTTACATCT ATATTTTCT AGTGATTTTA AATTGAACTA AGCTATTTT CATATAATTT 240
 AATGAATACA AAATAGGTTT ATCTGATTCA TTATAGTGCG TA 282

(2) INFORMATION FOR SEQ ID NO: 1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307:

AAGGAAAAAA CCCTTGGCCT TTGGAAAAAA CCCAAAAGGA AAGGGGTTTA AAAAAA
 120
 AAGTTTAACC CGTTTGGCCC CAATTCCCGC CCGGGGAACC CAAAAGGANT TTTAAAAAAG 180
 5 GAAACCCAAT TCCCGGCCGG AAAAGGGTTT TTAAGCCCAA CCGGATTTTA AGGAAAACCA 240
 TTTTAAGATT ACCTGGGAAA AAAAACCGTT TAGGAA 276

(2) INFORMATION FOR SEQ ID NO: 1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308:

20 TGTATTTAAT GCTCGTACAC ACAATTACAA AACTGCAAGA GAAAAGCAT TGAGTAATAA 60
 TCATATTCCA GAAAATGTAT ATGACAATCT AGTAAAACT GTACATAAAT ATTTACCATT 120
 GCTACATAGA TATACTGAAT TCGCAAAGA ATTGCTAGGT TTAGATGACT TGAAAATGTA 180
 25 TGATTATAT ACACCATTAA TTAAAGATAT TAAGTTTGAA ATGCCTTATG AAGAAGCTAA 240
 AGAGTGGATG TTAAAAGCAT TAGAACCAAT GGGTGAAGAA TATTTAAATG TAGTTAAAGA 300
 AGGCTTAAAC AATCGTTGGG TCGATGTCTA TGAGAAATAA GGTAAACGTT CAGGTGGCTA 360
 30 TTCATCAGGT GCACATTAA CTAATCCATT TATTCTACTT AACTGGTCTA ATACTATTTT 420
 AGACTTATAC ACATTAGTTC ATGAATTTGG GCATTCAAGCA CATAGTTACT TCAGTAGAAa 480
 35 ATTCCAACCG TCAATTCTA GTGACTACaC TATTTTTGTC GcTGAAGTTG CaTCAACTTG 540
 TAACGAAGCA CTTTTAAGTG ATTATATGGA TAAACATCTT GATGATGAAA AACGCTTATT 600
 ATTATTAAAC CAAGAATTAG AnCGTTTCAG AGCTACATTA TTCCGACAAA CAATGTTCCG 660
 40 AGAATTTGAG CATAAnATTc ATGCAATTGA AG 692

(2) INFORMATION FOR SEQ ID NO: 1309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309:

GGACTATTCC ATGATAGCTT TTTTGACTGG ATTTACTAAA ATGAAAGCAA GTACTATATA 60

atCGAGTAAT ATCTATATAT GACATTTTAA A

151

(2) INFORMATION FOR SEQ ID NO: 1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310:

TGTGCATTTG ATAATATTCA CTATGATTCTG TGGTCATTCA CATCGTCTAC GTCACCGGT 60
CTAAACGTAC CTAACCCAAC ATGTAATGAA CAAATGCGAT ATTAnCACCT TTATT 115

(2) INFORMATION FOR SEQ ID NO: 1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311:

CACCCAACTG ACCTCAATGG TATAATGCAT TTGTGAATAC CGAATATCAT TGGAAATATCT 60
CCTATCATAG GAATATAATA TGTATATATC TTCGTAATCn TGTTCAATTTT TAAGAAAATC 120
AATAGAAGTG TATCGATTAA AACTACATTT GAACCATTAC TTTG 164

(2) INFORMATION FOR SEQ ID NO: 1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312:

GAGGAAAATC GAAGTGAAAT TATTAAAATA TGGCGATGGT GGAATACGAA TAGATGGTGG 60
TTTAATAGGC GGCTTTATTC GGGTGTATT GTATGTAAAG TGAAAAATTT AAnCCCATTT 120
CAAATTGGTG ATATCGTTGC G 141

(2) INFORMATION FOR SEQ ID NO: 1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313:

AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA nTCCAGAGGA TTACAATTAT 60
TAGTTTCAAT AATCACGATT AGTTGAGATG GTTAGCCACA ACTTTCTAGT GTATCACCAT 120
TATATGTATC GGT 133

(2) INFORMATION FOR SEQ ID NO: 1314:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314:

TTGCAATTAG AATGCTGTTT CACCCCTTTA AACCATACTA TATATTTAAA TTTAGAGTCC 60
CATTTACACC AGGTTTAATA CCGAAAAGAC GCGAAGAAAT TGCAACTAAA ATTGGCCAAG 120
TGATTGAAGA GCATTGCTT ACAGAACTT TAATTAATGA AAAATTGAAA AGCGAGCAAT 180
CACAGCAAGC AATAGAATCT ATGATTCAAC AGCAGTTACA AAAGTTGACG AAAGATCAAT 240
TGTCAATAAA ACAAACTACT TCTCAAATCG tATTGATTTA GAACAAGTAT TACaAACTAA 300
TGGAAATCAA TATATTGAAT CACAATTgAA TAATTATTAT aCAAAGCaTC AAAACCAAAC 360
AATAGCATCT TTATTGCCAA ATCAACTTGT AACATTTTTA AATCAGCATG TAGATAACGC 420
AACAGACTTA TTATGTGATC GTGCAAGGAA TTATTTATCA TCTGCAAAAG GCACACAAGA 480
TATTAATGAT ATGTTGGATA CTTTTTTCAA TGAGAAAGGT AAGTTAATTG GTATGTTGCA 540
AATGTTTATG ACAAAAGAGA GTATTGCAGA TCGCATTCAA CAAGAACTTA TACGTTTAAC 600
ATCTCATCCT AAAGCAAGAA CAATTGTGA 629

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(2) INFORMATION FOR SEQ ID NO: 1315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315:

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	ATACAGGTAC GTTCGTTATC AATGGTGCAG AACGTGTAAT CGTATCTCAA TTAGTTCGTT	120
	CACCATCCGT TTATTTCAAT GAAAAAATCG AAAAAAATGG TCGTGAAAAC TATGATGCAA	180
5	CAATTATTCC AAACCGTGGT GCATGGTTAG AATATGAAAC AGATGCTAAA GATGTTGTAT	240
	ACGTACGTAT TGATAGAACA CGTAAACTAC CATTAAACAGT ATTGTTACGT GCATTAGGGT	300
	TCTCAAGCGA CCCAAGAAAT TgntGACCTT TAAGGGGACC AATGGAATAT nTACCGTAAT	360
10	ACCTTTAGGA GGAAAGACCG GCACCTGAAA CCACTGGAA	399

(2) INFORMATION FOR SEQ ID NO: 1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316:

	ATAAACATTT TAaATGTAA TnAGAAATT TTTTtagTAC AAAATCTTTC TTAATAATGA	60
25	TTAAGGAGGT CAGTAATGAT TGAAATTAAA ACATTAAACGA ATAATGATTT TAATGAGTAT	120
	AAGAGACTTG TTTCGACAGT CAATGAAGAA TTCACTCAAG ATTACATTA TAGTCAAACA	180
	ATGactGACA CCTTAATACA TGACATTTTA AATCAAGGTT CACCGAAATG TATTGTATTT	240
30	GGCTGTTATG AAAACGAAAC ACTTATCGCA ACAGCTGCCT TAGAACAAAT TCGATACGTT	300
	GGAAAAGAAC ATAAATCATT AATTAAATAC AACTTTGTTA CTAATAACGA TAAATCGATT	360
35	AATAGCGAGC TCATTAAATTT CATTATTAAT TATGCACGGC AGAACAATTA CGAATCTTTA	420
	CTTACATCAA TTGTGTCAAA CAACATAGnn GCTAAAGTTT TCTATAGTGC ACTAGGATTC	480
	GACATTCTTG GTTTTGAGAA AAATGCAATT AAAATCGGAA ATACCTATTT CGATGAACAT	540
40	TGGCTTTTTT ATGATTTGAT TAATAAGTAA TACAGTTTTA TATATTCTAC rTTTCTCATA	600
	AATTCAAATC ATATAGGTTT TATTTTTTCAT ACAACTACTC TACTATTGAG TAGTTGTTTT	660
	TTATTTGATA TGATAACAAT AAGTTTTTTT CAGAATATTC TATGTTTTAG GGGTGTCAAA	720
45	ACTTAATGGG TAACCGCAAT TATTCATGGA nTTATCnTAA GCGATTGGGT CCTAAnTT	778

(2) INFORMATION FOR SEQ ID NO: 1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317:

5 TGCACAAGGT GGTGCAGCAA TTGCAGCGTT CTTTATTATT AAACAAAATA AGAAGTTAAA 60
 AGGTGTGGCA TCTGCCGCAG TATTTTCAGC ATTACTTGGT ATTACAGAAC CGGCTATGTT 120
 TGGTGTACT TAAACTAAG ATATCCATTT ATTGGCGCTA TCGTTGGATC AGGTATTGGT 180
 10 TCAGCATATA TTGCTTTCTT CAAGGTTAAA GCAATCGCAT TAGGAACTGC TGGATTGCCA 240
 GgATTtATTT CAATCAATCC AGTACATGCA GgATGgTTAC ACTaCTTTGT TGGTATGACA 300
 ATATCATTcA TCATTGcTAT AACAGTTACT TTAAtTTTAT CtAAaAGAAa AGCAAATAAA 360
 15 GAAGTTGTAG AATAAAAAA GAGGTATGAC AGTAATCAAA GTATCASTCA TTGCAATGC 420
 AATAGGATGA AACTTTAAGC TGTACATCCT TThAATTGAG TTATA 465

(2) INFORMATION FOR SEQ ID NO: 1318:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318:

30 GACTTAATAT AACTGATCTT TTGCTATTAT TGAAACATAT TTATAAGAA AATAGCATTG 60
 CATAATACCC AAGCAATAAA TACTATAATA TTTTGGAAGT AACTAATCAA ACATCTAAGA 120
 CATGATTGAT AnCACCACAG AAAAATAAGA 150

(2) INFORMATION FOR SEQ ID NO: 1319:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319:

45 CCACCTTTTA ACGTACGTAT CCATGAATCA TATGATTAAT TTAATATCAT TATTACTTAT 60
 TTCTTATCTT TATTnTCTTT TTTTCTTCTG AAAAGTAGTA ATGAACCTAT TGATGCTAAT 120
 AATCCCCAAA T 131

(2) INFORMATION FOR SEQ ID NO: 1320:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320:

10

TAGTGTCCAA ATGAAAGTGT GGCTACCTAT AGCTGGTCCA TGAAGCTTTA TTTTAACTG 60
GTTTGTACAA TATTTAAATA TCAAAATCTT CTCGCGnTTT GGACAGTTTT TTTGGTATTA 120
ACCATTAATA AACGGAAAGA 140

(2) INFORMATION FOR SEQ ID NO: 1321:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321:

25

CTTATTATAT AATTCTAATC CTAGTACATT ATACATTTTA TCAAATAGTC AACTGGATAA 60
CTTTGAAAGT GAATGATnCT TTTAAATAA AGAAGATAAT ATAAAGTGCT TGATAATGGA 120
TTTGTAGTTG ATGATTTAAA 140

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(2) INFORMATION FOR SEQ ID NO: 1322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322:

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TCGTTGCAAC ACAGGCACTA TTTTACCTTT ATATGTTGTA ATAGTTTGAT TGCTGCCATT 60
TAAACAACCA CCTTTCTTAC TCCACAAATT TACCATGAAT AGCGCGCGCG CCATAGCGGG 120
ATACTAAAGT GTTCTGCACC TTGCCTGTCT CCTTCAAnTT TCGATTACTG TAGAGCACAA 180
GTACG 185

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(2) INFORMATION FOR SEQ ID NO: 1323:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323:

ACCTGCAATT TTCGTTATTC AAAACAATAA CTATGCAATT TCAACACCAC GGAGCAAGCA 60
 AACTGCTGCT GAAACATTAG CTCAAAAAGC AATTGCTGTA GGTATTCCTG GGTATCCCAA 120
 GTTGGTGGTA TGGTGCGGTA nTTGGTTT 148

(2) INFORMATION FOR SEQ ID NO: 1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324:

GAAAGCATTG ATGGACAAAG ATGAACCACC AAATGAATGG CGATTAGATT CCAATTGATA 60
 TGGCTCACGG AAAATTTATG CTACAATTGC GTCCAGTAAA CAGTGGCACT AATAGTCCAC 120
 TTAnGCTCCC TAGTGGATGA A 141

(2) INFORMATION FOR SEQ ID NO: 1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325:

TTATACTATC GTGAAGGGTT TATTACTCAA TTAATGCCTA AAAAGGATAA AAGTTATTTA 60
 GTTATTGATA ATTTTAATCG TATAGATACA GACATTTTCC AAACGTATAT TAATGTGTTA 120
 GAAGGCTATG AAGTAACATT ACCACGTTAT AATAAGACG GTAATATGAT TAAATGGTCA 180
 CGACAAAAAG ATTCTTTCTA TTAT 204

(2) INFORMATION FOR SEQ ID NO: 1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326:

TTTGTTAAAA GTCTTCATTT CGGATGAAGC TTTATCTATT GAACGCTCCA AATTATTTAA 120

AGCAGCTTTT TCTTTATTAA CAGCTGT 147

(2) INFORMATION FOR SEQ ID NO: 1327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327:

CATTnAATGA AGAAACTGAA CCCnGAACTA TACGACGCAG AAGGCAATTT AATTAATAAT 60

AGTAAAACAT CCAGCTTAAT CCATTGATGT GTTATAAAAG TGAAAAGCTC CAATCAAAGT 120

TGACGCTCAA ATAGTTTAAC TTTGATCGGA GCTTTTTTAT AATGTATACC GAAAGGTTCA 180

AATATTATAT AATGGTAGAA TTGAAAGAGA ATATAAAAAA GTGAGGATAT AAAATGAAAG 240

TTAATCCTAA TAATATAGAA TTAATCATTG GTGCAGTAAA AGAAGAACAA TATCCAGAAA 300

CAGAATTGTC TGAAGTGCAC TGACCGGTCTG ATCTAATGTA GGTAAGTCTA CATTTATCCA 360

ATAGTATGAT TGGCAGAAAA AATATGGCAC GTACATCACA GCAACCCGGC AAAACGCAAA 420

CGTTAAATTT TTATAATATA GATGAACAAC TTATTTTTGT GGATGTTCCA GGGTATGGAT 480

ATGCTAAAGT AAGTAAACA CAACGTGAAA AATTGGGAA AATGATTGAG 530

(2) INFORMATION FOR SEQ ID NO: 1328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328:

AAGAAAGTTT GATCTAGGCC AACCTTTCTA ACAACGATAC GACAGTTTAA TAATGTCTCA 60

TATCTTGACT TCCCATGATG ATATGGTCGT TAATCACATC AATGACTTAA ATCTGGATnA 120

ATAGATGCGA ATGGATCTTG AAAAATCATT GTA 153

(2) INFORMATION FOR SEQ ID NO: 1329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329:

5 TGTAGTTCGT TTGTGCTCTA ATTAAACGGT CGAAACCATG GATTAGACCT GCGATTACAA 60
CTGCAATGAT ACCTGAAGCA TGAAGTTCTT CTGnTAAAAA GTATACGACA AAAGG 115

(2) INFORMATION FOR SEQ ID NO: 1330:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330:

20 AACAAAGTTAT CTACATCTGC TGATAGGCAT ACTATTACTA ATAAATAATG CATCTTTTTG 60
CCAGATGTTT TCTTAATCAA TTGCACCAAC GAATGGCACT CTCATCTGTA Gn 112

(2) INFORMATION FOR SEQ ID NO: 1331:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331:

35 TTCATTGCAG ACAnTTGGTG AACCATGTGG ACGAACTAGT CCTAGATTAA GATAAGAGAT 60
TAGTGAnCAT TGCCACCACT GCAATTAAAC ATTCTTGGAA AAATTAACCTT AAGTTAGAAT 120
CTTAATGCAT ACAGATACGG CGAAGATGAT GCCAAAGAAC GTCACGACTT TATGATGATG 180
ACTGAACCCA GTTTTTACGG AAG 203

40 (2) INFORMATION FOR SEQ ID NO: 1332:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332:

55 ATGATGTACT AATATCTAAT AAGCTTGCTA AGTCTTGAGA CCTCATTTTA ATCACCTTTT 60

GACTATCTAT TTCTGTTAGT ACGTTTGACA TATTAATCAC TCCaCyTTAA CGCAaTAWAw 180
 TTTAwTAGCG TTGGCTATTG TTGTTTAACG CGATGGnATT TACAACTTGT AACGTAAGAG 240
 5 AATGAAAAAT AAGCTGnATA TGTTGTTTG 269

(2) INFORMATION FOR SEQ ID NO: 1333:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333:

TAGCTTTTGC CCAATATGGT GAATCATGCG CCGTTCTGTA ATAATCTTCA CTTGGCATTC 60
 20 TTGGAATTTG AACACATCC TGTTCATTTT TATAGAnTGC TTAAATGGTA CAGCTGAAAA 120
 ATCAAAGTAA TGTCCTTTTC TG 142

(2) INFORMATION FOR SEQ ID NO: 1334:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334:

35 ACTGATGCCC AATATGCATC TTGnCAATTG CAGGTGTGCA TGAATAACA CATGACAAAT 60
 CTGCCTGACT TTTTGCTGAC CCATAAATAA TTGGnCTAAC TTTTTCATC TTGATCTTGC 120
 ATCCTTGCCT TCCTATTTAA AATGCTACAA ATAAATTTGC CGGCGAGTGA ATTTTAATGT 180
 40 TTTACAACGC TGTTCAATAC CTGGAATAA G 211

(2) INFORMATION FOR SEQ ID NO: 1335:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335:

50 CTTGAATCTC TTGTGCCTCT GTGATGTATC ATCAAATTAT TTGCACTGCT TCTTCTTTTA 60

55

TCCGCTCGC

129

(2) INFORMATION FOR SEQ ID NO: 1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336:

15	CATGATGGCn TCTTACCAAA GGCGATTTTA AGAGCAATGA TACCAAGATA TTTTAAATAC	60
	TGATCAAAGT TCAGGTGGTA GCACAATTAC ACAACAACTT GTTAAAAATC AAGTTCTTAC	120
	CAACGAAAAA ACATATAGTA GAAAAGCAAA TGAATnCGCC TAGCAATTAG ATTAGAACAC	180
20	CTACTCTCAA AAGATGAAAT TATATATACA TATTTAAATA TAGTTCctTC GGTAGAGATT	240
	ATAATGGCGC TAATATTTCC GGAATTGCAT CCGCTTCATA TAGTCTATTT GSTATTCCAC	300
	CAAAAGATTT ATCAATTGCA CAATCTGCAT ACCTTATCGG TTTGTTGCAA AGCCCATATG	360
25	GCTATACACC CTACGAAAAA GATGGAACGT TAAATCGGA TAAAGATTG AAATATAGTA	420
	TTCAAAGACA ACATTATGTA TTAAAGCGTA TGTTAATCGA AGATCAAATC ACTGaaaaAG	480
	AATACAACGA CGCATTAAAA TATGATATTA AATCACATTT GTTAAATCGA AAAAAGCGTT	540
30	AATTGATGCT CACTTTTTTA AGTAACCACA ACAATGAATC CAAATATTAA AAACAGCAGT	600
	AAGATTATTT TCAATTAGAA AATTCTCAC TGC	633

(2) INFORMATION FOR SEQ ID NO: 1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337:

45	ATCAATATTT AGCAGTTATC ATTATGCTTG AACGGTGGT AAAGGCGGAG AAGTCATCCA	60
	CTTTTTCCTA TACTACAAGG ACCTTTACTT TAAACAACG AATTACAAA ATAAAAGGCA	120
50	TAATTTCTTT TCTGTCACAT CGCTCATTCT AACTACTAGA CTTTTAAAT CGTTCCTGTA	180
	ATTTAACTC AATCAACTnt CAATTAATGA TGCATAATAT GATTATAAGT ATAGTAGTTA	240
	ACTTCAAATA TCTTAGAAAT GTCCTGTACT ATATCTCTTT TATTCTCAA AGTCATAGGT	300

(2) INFORMATION FOR SEQ ID NO: 1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338:

TACGGCATAT ACCTCGTTCA TCAATGTTTCG TAAACATTAT TTAAACATC TCTTACATCT 60
 TCGGTTGGAA GTTCTTCATA GTCGAATTTC ATTGTnTTAT CAAAGTTTTTC CATTGCGAC 120
 ACTCC 125

(2) INFORMATION FOR SEQ ID NO: 1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339:

GAGCTTCGTT CCATTGTTAT CAAACGATTG CCATTCTGAA ATGCTGTAAA TAGCATGCTT 60
 CAAATCATCT TGTGCCTGCA GCAGTTTCTT TGAATATGC TTCATATCAT T 111

(2) INFORMATION FOR SEQ ID NO: 1340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340:

TCACACGTTT AGTTTTCTAT GAATACCAAT ATTTTAACAC CATGTTTAGC CAATTTGTCT 60
 GCTAAATTAA TCGTGTTTGT CCTCCAAATT GACACGCACC TTTAGTTTTT CTAAATAATG 120
 ATATCATCAC ATCTCTCAGT TAAAGGTCAA AATATTTG 158

(2) INFORMATION FOR SEQ ID NO: 1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341:

5 GCTTCAGGTC AATTAAAACG TTCAAGAGCT TTCACATCTC ACTTATTCGC AAACAAGAGC 60
 ACTAAACAAA AACGTCAATT ACGTAAAGCT AGATTAGTGT CTAAGAGCGA TATGAAACGT 120
 GTAAAACAAT TATTAGCATA CAAAAAATAA GAACAAATAC AGAAATCGGT AGGAATTACC 180
 10 TAAGGAGGAA TTTTATATGC CACGAGTTAA AGGTGGAACA GTAACAAGAG CGCGTCGTAA 240
 AAAAACGATT AAATTAGCTA AAGGTTACTT CGGTTCAAAA CATACATTAT ACAAAGTAGC 300
 TAAGCAACAA GTAATGAAAT CAGGTCAATA TGCTTTCCGT GACCGTCGTC AACGTAAACG 360
 15 TGACTTCCGT AAATTATGGA TTACACGTAT CAACGCAGCA 400

(2) INFORMATION FOR SEQ ID NO: 1342:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342:

25 GTTGAACAAG GGCAACAAA ATTCGAGCG AAACAGATTT TTGAATGGTT ATATCAAAAA 60
 30 AGAGTAGATT CGATTGATGA AATGACGAAC TTATCGAAAG ACTTACGACA GCTTTTAAAA 120
 GATAACTTTA CTGTTACAAC TTTAACAAC GTAGTAAAC AAGAAAGTAA AGACGGTACA 180
 ATTAATTCT TATTTGAATT ACAAGATGGC TATACAATTG AACTGTTTT AATGAGACAT 240
 35 GATTATGGAA ATTCAGTATG TGTAACGACA CAAGTAGGTT GTCGCATCGG ATGTACGTTT 300
 TGTGCTTCTA CACTTGGCGG CTTAAAAAGA AACCTGAAG CTGGCGAAAT TGTTCACAA 360
 40 GTTTTAACAG TTCAAAAAGC CCTTGATGCT ACAGAAGAGC 400

(2) INFORMATION FOR SEQ ID NO: 1343:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343:

50 GAAAATTTCA TCAGGTGTTG GCgTGAACG TACATTCCCA TTACACACAC CAAAAATTGA 60

55

TTTACGTGGT AAAGCTGCTA GAATCCAAGA AATTCGTTAA TCAGCATTTA AACAAAGCTA 180
 TGATGAGTC AAATTCGACT CAAACAATAA AGCCATCTAG GTCACITTTA TGGAGTGATA 240
 5 TAGATGGCTT TTTTGTCTGT TTAGTTAATG TAAAGTTGAT AATGTAATTG TTTATTCCTT 300
 CTCTATTTCAT AACGTGTTTG CTCAAATGG TTATATAAAC AAAAATCTAC TAAGTGCCAT 360
 TGAAAAGGAC TTAGTAGATT TATTAAATAT ATGCGTANA 399

(2) INFORMATION FOR SEQ ID NO: 1344:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344:

AAC TTACAAC ACCAGGTAAT AACAGCAATA AAGGCACCAG TTAGTGCGGT AATGCCANTA 60
 TCTAGGCCTT TAGGTTGCCA TAGTACGAGA TGTAGAGGTA CTAGAGGAAT GAGTGTGCGT 120
 25 AAAGTTGTCG TCGT 134

(2) INFORMATION FOR SEQ ID NO: 1345:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345:

TCATAATAAA CAAGTTCACA TGAATCACAA CATCTGAAGA CAATGTTCAA AATGAGGCTG 60
 40 GCACAATAGA TGATCGCAAG TCGnATCATC ACACAGTACT GAAGCAAGA 109

(2) INFORMATION FOR SEQ ID NO: 1346:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346:

CCATATCTGG nACGACCGAC ACCTTTACCA CCAACGATTG GTGCCATTTG TTTGCATAAG 60

55

(2) INFORMATION FOR SEQ ID NO: 1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347:

CAATTGAAAG GTGAATTTTA TAGGTCCATG ACAAATAAG GCTTGTTAAA GCTTATTAAAC 60
 ACAGTTTCAT CAAATAGTTA AATTAGTTTT TGTTTTGCAA TAAATTGGGT ATAGATTACA 120
 AntG 124

(2) INFORMATION FOR SEQ ID NO: 1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348:

CATCAGTGGC CTGATCACCC CAACATTTGA CATCAATGCA TACCAGTTGA TTTGAACAAT 60
 GATTGCATTG AGCTATCATC AAGTTTGTCT TTAAGCTACT AAACCCACGA ACCATGTTAA 120
 CCCCCTGGTC ACCATCACCA ATTGCTCGAT CTAATTCAGT TAATTCAGAT TCATGTTTTT 180
 TAAACGTTTC TTCTAAATTT AATAAACGTG CTTTCATATC ATcAtTTTCAT TGTGCaCtaT 240
 AAaTgLaTAT TaTTCATATT CACTTCTnAT TTAAAGTATG ACTTGTGTGTT GGTGCTAAAA 300
 ATGChTCCAA ATATTCTGGT TTATnAGGCA CGATAGT 337

(2) INFORMATION FOR SEQ ID NO: 1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349:

CAGCACGTAA ATACAACAAA GCGATCCCCA GCTTGTGGCA CATCATTAAAT ACCTGTAATT 60
 TCAACAGGCG TTGATGGACC AGCCGTTTTG ATTCTTTGAC CTAAGTCATT ACATGCCGAA 120

(2) INFORMATION FOR SEQ ID NO: 1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350:

CAATTTTACT TTGAATTTCT TTTTATCTT TTCTAGTTTT ATCGTCCCAC TCTTCAATCC 60
 ATTTTATTAGC TTTATCTTCA TTATTAGTCA ACTTGCCTAT TTCTTTTAAT ATTCTTTATG 120
 ATTGTATTTA TTGTATGTAT ATGGGATTGT TGGCGCTATT TTTTGGTATT TTTTATATT 180
 TTTATCCATA GcATCTACAA CAATTAAATC TGTTTTGcT TTAGCAACTC TTTCAACATC 240
 ATTTTCTCCA ATATAATCAA CCCCTTTTAA ATAAGGTTTT AAAATTGAAG AATCTTTAGT 300
 TATATCTGAA ACAGCAATTG GTTTGATTCC TAACTTTATA AAATCACCAA CATAAAATCC 360
 AGTTAATACA GCAACTCTTT TAAGGTTCTC nGGGACTTT 399

(2) INFORMATION FOR SEQ ID NO: 1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351:

TAAAACTTAG GCGGTTTTGC ATGATTATAG CGCTCAACAC GTTGAAATT ATAGGTCATC 60
 TCTGGTATTC TTGTACGATT CTTTTTCCAA TCTAAATCAA AGTTTCAAT TTCTTCTTTT 120
 GAGTTTAGAC TTAATCGATC ACGTTCATGT TCTTTAAAAG ATGGAATAAC TTGTTTAAGT 180
 GACCCTTCCA TTCTTAATTG ACCATGTGAA AACCAAGCTA TGTAGTTACT CACTTGTGaa 240
 ATTTTATCAA TATCATCACC AATTGACACA ATCGTTAAAT TATTTTCAAT ATAATCATTT 300
 GTTAATTCAA TCGCACGTTT CATAAATTGT GGTGTTAAAT AGTCAATAAC ATGATTTAAA 360
 ATAATAATAT TTGATTTTGA TGAGCGTGCA ATACTTAATA 400

(2) INFORMATION FOR SEQ ID NO: 1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352:

5 AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGcGgCcGCT CTAGAACTAG TGGATCCCCC 60
GGGCTGCAGG AATTCGGCAC GAGCATATCT AGTATTTTAG GACGGAGGnA GTACATT 117

(2) INFORMATION FOR SEQ ID NO: 1353:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353:

20 AGTTCAGGAG AGTTATAAAT ATTAGGGTGG TACATGCCCC AAATCATTGG AATTGTTAAA 60
GTAGATTTTA CAGTTTAGAG ATAACAGACA TGTCTATATG AAGGGCTGTC TACCCTCGTA 120
AGGTTATATC CTACAGnTGA ACGTATCAAG CTT 153

(2) INFORMATION FOR SEQ ID NO: 1354:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354:

35 TGTTGTAACA GCTCTCTATG TTTACGTTGG AAGTATGGTT TATTTTTCAT CTTACATTT 60
AGTTCCTTAT TTAAAAGTGA TAGAGCAATT GCACTCGTAG GTCAAGAAGC GGGATGCCAA 120
CACAAAGTTC ACAAGAnAAT ACACTTTTGA AAATATTGG 159

(2) INFORMATION FOR SEQ ID NO: 1355:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355:

50 CGnCTTCCTT CAACCATTGT AGAAGTTGTC TCATATACTT ACTACGGCTT GCTAATACTC 60

55

(2) INFORMATION FOR SEQ ID NO: 1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356:

GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA nCTTTACACA ACCAATTGGT 60
 CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA 110

(2) INFORMATION FOR SEQ ID NO: 1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357:

TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGn GCCTCACTAT CATTATCAA 60
 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATTAGTC 120
 GTTGAAGATA TCG 133

(2) INFORMATION FOR SEQ ID NO: 1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358:

GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAAATG 60
 ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTCGAAC 120
 GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCATATAG 180
 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTAAGTT 240
 TAGGAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGATAGG 300
 GAATATTGCG CAATTTAGAT ACGACCATTA TTTACAATA TTTAATGAAA TTTCCAAATA 360

(2) INFORMATION FOR SEQ ID NO: 1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359:

CTGTTTTAGT CTTATTGATT GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA 60
 ATTGAGCAAT GATTGGAATG TCGTATTTCT TTCTCGTTTCG TGAAATGACA TTTGTTAACT 120
 CTTCTAGGTC GTAATACGTT TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT 180
 CTATTTGAAT TCAGTATGAT AAAGAATAGT TTGTAAGCTG ATATCCCCCT GTTTGGATAC 240
 CTCTAAACCC CACCAACTGG GGCCCAATAT ATACGTAAnc TnTAATTGGC nGGCTTTTTT 300
 GCGATGCGAC GGGGGGCTGG AGGATGCTTA ACCTTAACCT CCAGACCGAA CCGTTTAACC 360
 TTTCCAAAAT TGCACCATAG GAATGGGTGG AT 392

(2) INFORMATION FOR SEQ ID NO: 1360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360:

CCATGGTTAT TTCTTCACA TTTCATGTAT ATATATTTGT TTATTATCTG TCTCTACTAG 60
 ACTGTAACT CCAACATATC TGTTTTATAA ACCAGAGAGC AGTCATTCAA TAAATAAACA 120
 GATCTGAGGG CCAACTGGCA TGTGTCAAC TTATGATATT 160

(2) INFORMATION FOR SEQ ID NO: 1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361:

GTATCCTAAA GATTCAGTTA ATCGGAGCGT TGTATTGCAT GAAGGTACAT TGCGGAATGC 60

ATATTTATTTC ACGATnTTAT TTAGCGAC

148

(2) INFORMATION FOR SEQ ID NO: 1362:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362:

15 AAAATTACTA TGAAGATTGC ATTAGGATGC GACCATATTG TTACAGATAC AAAAATGCGT 60
 GTATCTGAAT TTTTAAATC AAAAGGACAT GAAGTCATTG ACTGACACTT CACTCATnAG 120
 TGGCGACAGT GTACGTATCA GACTTAG 147

20 (2) INFORMATION FOR SEQ ID NO: 1363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363:

30 CTGGCAAAGA AGACAACAAC AAGCTGGTAA AGAAGCAACA ACAAGCCTGG TAAAGAGACA 60
 ACAACAAnCT GGCAAAGAAG ACGGCAACAA GCTGGTAAAG AAGCAACA 108

35 (2) INFORMATION FOR SEQ ID NO: 1364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364:

45 GACAATGTTG CTGTAATGGG GAAGGnAATG GGTGGGTACC GCGAATTGAA TAATTTAAAA 60
 CCGTAATATA TAATCGTAAT TGTTAAGCCC TCATTTTAT AAATTTTGA CCTCTTGAAA 120
 AAGTTACGTT TTCAAGAGGT TTTATTTATC CTA 153

50

(2) INFORMATION FOR SEQ ID NO: 1365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365:

TAAGAGAATT ATATGCATT CAAACGAAAC AACAGAAAA ACGGACCAAA CTAAGTGTCA 60
CAAGTACAAT CGCTGTACTA CTGCAAAACA CGCAAAACGA AACTTTACGT ACACACAAAA 120
AGACCACCAT TCACGTCGGG ATTATTAAAA AGGTAGTCTC GTACATTTAT TAACTACTT 180
ACGT 184

15

(2) INFORMATION FOR SEQ ID NO: 1366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366:

25

ACATTAGATG GGTCAATCAT GTTATACACG GTGATTTAGG GGAGTCAATC AAATATAAAA 60
GGCCGGTAAT TGATGTTATT GAGGAAAGAA TTCAAATAC AATATTACTC GGTGCTATGT 120
CATTAATTAT TACTTATATT ATCTCATTG CTTTAGGAAT AACGTCAGGT AGATATTCTT 180
ACAGTTTGAC GGATTATACT GTGCAAATAT TTAATTATTT GATGTTAGCC ATTCCATCTT 240
TTATTGCGGG AGTATTTGCA ATTATTATTT TTTCTTTTGA ATTACAATGG TTCCCGTTTC 300
AAGGTTCTGT TGATATTAAC CTAAAGAAG GTACTTTTGA ATATCATATG AGTAAAATAT 360
ATCACACATT TTTACCTGCA TTCACCTTAG GTTATTATC TACTGCTGGT TATAWTCAT 420
ATTIACGTAA TGATATTATT GAAAATTCTA AA 452

40

(2) INFORMATION FOR SEQ ID NO: 1367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367:

50

TTGTGAGTAA TTGGACAATA TAAGTGTGG TCTTGGATGG CATATCCTTG GTACGACCTG 60
GGCAACTTGC TTCATAGCGC AGTTAGGAAC TGATCAATCA TTGGCGTTTT GATACCTAGC 120

55

(2) INFORMATION FOR SEQ ID NO: 1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368:

TGGTGCAAAT TAAAACGGTT GCATATGCAC GTACGACGTA TTGCTAAATA CAATCAATTA 60
 TTACGTATCG AAGATGAATT ATTGAAACG CTAAATATGA CGGTATCAAA TCATTCTATh 120
 ACTTAG 126

(2) INFORMATION FOR SEQ ID NO: 1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369:

TGhAAAGTTC ATCAGGGAGC CATTTTTACA ACACAGGGCA CATACGGGTT GTGTTTAGGT 60
 GCAATTGCCC CAAGCGGACA AAGCATTATT TAAAGTTTCA AGTTCTTCAA CGATTTATTA 120
 GTGCACAGGA TCCTGTTAAG AGGTATTTTG AAGACTTCCG 160

(2) INFORMATION FOR SEQ ID NO: 1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370:

AGTAATTCTG CAAATGCCGC AGATAGCnGT ACTTTGAATT ATGAGGTTTA CAAATACAAT 60
 ACCAATGACA CGTCAATTGC TAATGACTAT TTTAATAAAC CGGCAAAGTA CATTAGAAA 120
 AATGGTAAAT TGTATGTTCA AATAACTGTC AACCCAGTC ATTGGATTAC TGGAATGAGT 180
 ATCGAAGGAC ATAAAGAAAA TATTATTAGT AAAAACACTG CCAAAGATGA ACGCACTTCT 240
 GAATTTGAAG TAAGTAAGTT GAACGGTAAA ATAGATGGAA AAATTGACGT TTATATCGAT 300

AATGGACCA CTGATGTAGC AGGTGCTAAT GCACCAGGTA

400

(2) INFORMATION FOR SEQ ID NO: 1371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371:

CATCAAGAAC ATGTGAGACC ACAATTTGAA TCACTTGAAA AAATAAATAA AGACATTGTT 60
 GGATGGATAA AATTATCAGG AACATCATT AATTATCCAG TACTACAAGG TAAGACAAAT 120
 CACGATTATT TAAATTTAGA TTTTGAGCGA GAACATCGAC GTAAAGGTAG TATTTTtATG 180
 GATTTTAGAA ATGAATTGAA GAATTTtAAT CATAATACTA TTTTATACGG GCACCATGTC 240
 GGTGATAATA CGATGTTTGA TGTGTTAGAA GATTATTTAA AGCAATCGTT TTATGAAAAA 300
 CACAAGATAA TTGAntTTTG CAATAAATAT GGTAATCTCC ATTGC 345

(2) INFORMATION FOR SEQ ID NO: 1372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372:

TTGAAAAGCA GTTTGGATTT ATGCTCAAAC CATGGACGAC GGTTAGGTTT ATGAATGTTA 60
 TTCCAAATAG GTTCATCTAT AAAAAGTAGT GGAAAGTGA AAAAATnAGT GGACCTTCGA 120
 TAATACGATG TATTTATCGT TAGAAGCAGT AATA 154

(2) INFORMATION FOR SEQ ID NO: 1373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373:

GAGCCTAATT ATTCAAGCCA AATCGCATAT GAAATTGATA AAGAAGTTCA ACGAATCGTT 60

CTATACnAGA ACTATC

136

(2) INFORMATION FOR SEQ ID NO: 1374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374:

15	ATCTTTAACA ATTAAAACCA TACTATCTTG AATCATCATC AAATTTAACG CATGTGCGTC	60
	AAGTTGTTTC ACTTTAAAGA CTTCAATTATT AAGACCGACC TTAGACTGCT TTTTAAAAAT	120
	AGGTACATTC GTAATCATAC CTATACTTTG ATTGTCTAAG TGTAATTTGT TTTGGTGATA	180
20	TCGATTATAA TCTTGTGCAG TAAAAGCTGT AATCATTACT GATTGTCTTG AAAATATCGC	240
	GCCTTCATTA CCAATGAAGT CTATTGGAAT aTCATCACTA GCCTGTTTTA ACTTGTAATA	300
	AGCACGATTC TnTTCTAAAG AAGCTCTAAA TAATGTCGTT TCATATACTT TGAAGTCT	358

(2) INFORMATION FOR SEQ ID NO: 1375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375:

35	ATATTGTGTG CTAAATTGTC TTAAGTATGT TTTTGTGTTG nAAGTAAGCA TATGTTATTG	60
	TCTTTTAAAT TGTTGTAAAA GTGCTGTTTT CATAGAATTA ATATCAGACA TCTTTATTAG	120
40	TA	122

(2) INFORMATION FOR SEQ ID NO: 1376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376:

50	CATTTTCTTC GGTTTCTGTC TTTTATGCG TAGATTATT TTCTGTTCT TGGTTATTAC	60
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CGATAATTAC GATGGTAATA AGAAGTTTTT TCAAATATAA CGCCTCCATG TTAATGAAAA 180
 GTAGTTGATA CGTGAAGCTA AATAATTnAT TTCAATATTG CCATAATCAT TTTAAAAAAT 240
 5 AAATATTAGA AAAGTAGGCG ATATTAAATAT TTTCAATTGTt TTTTGTGTAC TTCAATTAGT 300
 ATAACAAAAC TGTTATGTAT TTATAAATAT AATCATTAGT ATTTTATATGG CTGAAAAAGT 360
 TATAATAAAA GTGTAAGGAA TAAAATATTT GTATGGAAAA GAGAGATAAT TATGAATAAA 420
 10 ACCAGTAAAG TTTGTGTAGC AGCAACATTA GCATTGGGCA CACTGAT 467

(2) INFORMATION FOR SEQ ID NO: 1377:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377:

AGGTGTTAGA ATTTATTTTA AGTGTATAC GTGTCTTCCA GAAATTGTAA TGGCATTATA 60
 25 TTTATnAAAG TGTGGCAGG TTATTTTCAG GTGTATTAGT TTAGGTATCA TTCGTAGTAT 120
 GCTTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 1378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378:

GGACGCTAGA GGATCCCGGT CTGGAAAATA TCGTCCAGAA CTTAGAAATA TGAAATATT 60
 CCCAAGACCA ATCGATAATA TATTGCCAAT ATGGCGTGCT GTTGGTGGTC CACCTGCAAG 120
 TGCTATTAAA GCGGGAAAAC AAGGTGTGCC AATGATGATT ACAACCCCTG GTGGCCCAGC 180
 45 AATGAACTTT AAAGTTCTA TAKATGCTTA TCGTCAAKCG GCAACTGAaG CAGGTTTCGA 240
 TGCTTCGCCT AAGTCTTTAC CAGTAAGTAC AGCGAGTCTG TTTTATACAG CTGAAACAAC 300
 TCAGGATGCT ATGAGAGAAT TTTATCCACA TTTGAATACA GGGATGTCAT TTATTCGTGG 360
 50 TnGTTGGTTA TCCGAAACAG CAATnGCTAA TTCGTCAGTT 400

(2) INFORMATION FOR SEQ ID NO: 1379:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379:

10 AACTACAACA ATTAAACGAC CAACCTTAAA AaAATACGCT CTTATGCATT GGATTAGTCC 60
 TGATTATACA ATTAACTGA ACAAATACCC ATCATTTAAA AGACTTAG 108

(2) INFORMATION FOR SEQ ID NO: 1380:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380:

25 AAGTGGGGGG AATCAGTATG TTACATTTAC ATATATTAAG TATTAGCGAT TATTTTATTT 60
 ATCGCTACAT ACTTAACCAT TTCAAAAATT CAAGGCGGnT CACCATTTTC CAACCCGT 118

(2) INFORMATION FOR SEQ ID NO: 1381:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381:

TCATGAAAAC ATTTATTTTA AAATTTGATA TTTGTTCAAT AATATTCGAA ATTAACThT 60
 40 GTGTATAGAT TTTCTTTATA TCCTGAGAGA CATGTACTAT AATGTTTGTG AATA 114

(2) INFORMATION FOR SEQ ID NO: 1382:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382:

CGGTATTGAT CATATAAATA GTGTTTAGAT GCTATAGTCG GntGACTTAA GTAATTTAAA 60

55

GTTCCTTCT GCCTTGCTTA AAGATATATG ACAGGGTGCT GGCAT

165

(2) INFORMATION FOR SEQ ID NO: 1383:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383:

TTTGGTGTGA TGGAGTATAT TTAGGTGTGG AAATCAAGAG GGAATTCCAT TTTCAAACAT 60
 CCAATTAGAG TCGnAATAAG AACTCGCTAT CGGTCCAATT AACTGATTCA G 111

(2) INFORMATION FOR SEQ ID NO: 1384:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384:

CATTTAAATA ACGTTGTGAC CATGTGCTTT ATGCTATGTG CTAGAAAATC CATGTTTTTA 60
 TCTAATTTCT TAATAAATTG ACATTAGTT GGATTCTTGT CnCTTCACG TTTCGACATT 120
 GGATGACTGA ACGCATGAAA TCAG 144

(2) INFORMATION FOR SEQ ID NO: 1385:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385:

TCGTTGTGCA GCAACTGCAT TACGCTGTCT CATTAAATGTA AGCGCAATGG CCATTGGTT 60
 TTTCnATAGT GGAATACTTG TCAAAATTGA ACATTGTATC TTC 103

(2) INFORMATION FOR SEQ ID NO: 1386:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386:

5 CCAGnACAAA TACAACGTTA TATTCAACAA TTAGAAGACT TAGnATAGAT ATAAATTGAG 60
 GGAGGACATC GATATGGCAT TTGAAGGGTT ATCAGAAACC TTGCAAGCGA CGATGCAAAA 120
 AATGCGTGGT AAGGGTAAAC TTAAGTGAAGC TGATATAAAG ATAATGATGC GTGAAGTAAG 180
 10 ATTAGCGTTA CTTGAGGCTG nACGTAACT TTAAAGTGGT AAAAGAATTT ATTAAAACAG 240
 TATCAGAACG CGCATTAGGT TCCGATGTAA TGCAATCATT AACACCAGGG CAACAAGTTA 300
 TTAAATAGT TCAAGATGAA TTAACGCACT TGATGGGTGG AGAAAATACG TCGATTAAAn 360
 15 TGTCAAATAA ACCACCTACT GTTGTATGA TGGTTGGTTT ACAAGGTGCT GGTAAAACAA 420
 CAACTGCAGG TAAATTAGCA TTATTGATGC GTAAAAATA CAACAAnAAA CCTATGTnAG 480
 TTGCAGCAGA TATTTATCGT CCAGCAGCGA TAAATCAATT ACAACAGTA GGG 533

(2) INFORMATION FOR SEQ ID NO: 1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387:

30 TTATTTACAA GCCATTAATA TATTTTAGGT TTGTTCTGCA TCGATTCATT GGTGCTATTT 60
 TATTTACATT CAATAATGAG ACTTTTACAn CAAACCAATT GGTCAAATAT AG 112

(2) INFORMATION FOR SEQ ID NO: 1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388:

45 ACACCTACAG TTAATAGTAT CAGTGCACAC TAAAGTCCTA ATACTTTCAA CCATGACTAA 60
 TGATGTATCh TCTTGCCCAA CGAACGCGTT GTGCCAAATT GAATTAGACT GGACGGAC 118

(2) INFORMATION FOR SEQ ID NO: 1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389:

CGACGACACA ACTTTATAAT AAAATCTTAG ACAATAACGA AGGGTATTAA CAGAACTTGG 60
10 TGCTGTTAAT GCAAGTACTG GAAAATATAC TGGTCGTCGC TAAAGCAAAT TTTTGCTCTG 120
ACCTnCAATG GTACTTGTTG GGAATA 147

(2) INFORMATION FOR SEQ ID NO: 1390:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390:

TTTTTGATCA TGATTTTTGG GCATGGATCA ATCACTTGCT TGGCCAATGG TCTTTCAACA 60
25 ATTTGGATAT CTGACCTTAT TCGCTTTATC TAGCACTTTT GnCAATTGT TGGCATTGGA 120
AAACATGTGT TTAGATTTTT GTATGCCTCT CGCAGGCTTT T 161

30

(2) INFORMATION FOR SEQ ID NO: 1391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391:

40

GCCGCACGCG CGCGATTCTC GGCCTAATAA GAAAACAAAT AATTCCAATT CATATATGnA 60
CATTTTTGCC TCCTTATTTT TGAAAATGT GGAATTGGAA TT 102

45

(2) INFORMATION FOR SEQ ID NO: 1392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392:

55

AAAATGCTAT TAACAACGTA TTAAATAATC AAGATTACCA TGGTATTAAA GATAAACCAT 120
 TCGCATTATT CGTAACTGGA TTTTTCGACA ATGTAACAGA TAATACTGTT GGTATTAACT 180
 5 TTAAGACAAA AGACGGTTCA ATAGCAGTAT TTATGCGTCC AGATATTGGA GAAACATTTA 240
 GCGAGTTTAG AACATTCTTA GCCGTCTTGT TAATGTTGTT ATTATTTATC TCGATTTCAT 300
 TAGTTATCGC ATCAnCCTAT TCAATCATTG GTCCAGTAAA AAAGTTAAAG CTAGCGACCG 360
 10 AACGCTTAAT TGATGGTGAT TTTGAAACAC CTATCAAACA AAcnCGCAAA GA 412

(2) INFORMATION FOR SEQ ID NO: 1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393:

AGCAAntGGA TTGCAATGAG TTTCTTATAT TTACAAGGTG GTAGATTGAT TGATGTTTTA 60
 25 ACTGCGATAT TAGCAGTAGT CTAGATACCT AGTCACTGAG ATTTTAGATC GAGTTACACG 120
 CACATTATCC GATCTGTCTA TATGGATATC CGTATGACTA CCTATCCCAC GGACTGCACA 180
 TACTGG 186

(2) INFORMATION FOR SEQ ID NO: 1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394:

TCTTTAAAAG AATCAGGAGC TTGGAAGAAG TATATCAGGA TCATTAAAGTC AACAAATTAC 60
 45 GCGATATGAA AATTGGAATA ACAATTTGnA AAAGCATGCT TCCGATAATC AGCAAGCC 118

(2) INFORMATION FOR SEQ ID NO: 1395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGTTACCTCG GATGGATGAT TACTATTTTG GGCTGGGCGC CGGCTTTnGT TATTAGTGGT 60
 GGCAATAGTG GCAAAGTGTC ACAAAAAAAT CCAATAGCTG GAAACCCGGG TATATTGGG 120
 5 TATTAACGCC GGTGGCCGGG ATTTGGCCAA TCGCATTAAT TTAATGGCCA TTGGG 175

(2) INFORMATION FOR SEQ ID NO: 1396:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396:

AGAAACTTAG ACGATTAGTA TCATATATTA GAACACnGCA CCGAACTTGA AATCATGGCT 60
 20 GATATCGCAC CTTGAAGAAG CAAAAATGCC GCACGACTTG GCTTTGATAT ATTGGCACGA 120
 CTTACATGGC AT 132

(2) INFORMATION FOR SEQ ID NO: 1397:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397:

AGAGGTCCGG CTATCTATCA AATAAAGTGG TCATTTAAAG CGTACACTTC GGGTGCGTTG 60
 35 ATTTCTTACT TTAGGTGTAG GACAATTGTA TCGCATCTAT CTTTACnCTA CCTGCATTGT 120
 T 121

(2) INFORMATION FOR SEQ ID NO: 1398:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398:

CGTTCGTATA ATCTCACTTG CATCnTGAAT TGAACAACAT CCTGTCATTT TAAGACTGCT 60
 50 AAANGTACAG CTGAAAACCA AGTAAGTCCG TTTCGTCTGG CTGTGAAATG GATCAAGGAG 120

AAACACCTCA TCCAAAGTTC AG

202

(2) INFORMATION FOR SEQ ID NO: 1399:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399:

15

CGTTGGATCA CTGATGCATT CATAAATGGG TGAACnTAAT GTAATGTTAA ATCTATCACA 60
 GCGCGATAAC AGCAAGAATA TAGTGAACAC CATAAATTGA GCATATCAAT GCCATATTCA 120
 TGGATACACA TAGTTCACCT GGTGGTCGGT GAAAGCCTGT AGATG 165

20

(2) INFORMATION FOR SEQ ID NO: 1400:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400:

30

ACACCTTTGT TTTTGCAAAG CTGTACCACA AAGTACTGGG TAGAATTCTA CGTTATATGA 60
 GnCTTGCGT ATAGCTTCTT TTAATTCATA AACTGTAAAT TTCTTCG 107

35

(2) INFORMATION FOR SEQ ID NO: 1401:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401:

45

TTTTGTCTAG nAACATCTGC TTCTAATAAT GATCGATCAG CAGCCATTGT GCTTAATCTT 60
 TCATCCCACA TCACAATCTC AATAGAAGGA TAAGCTTCTA ATAATT 106

(2) INFORMATION FOR SEQ ID NO: 1402:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402:

CAATGTTAAA CCTACACCGT TAACAGCACA CATGATACTA AATTGTTGGG GTGTCATATT 60
 5 ATACAATGTT GAGTAA TAAA TGGCGATGCA GATGAATAAC TA 102

(2) INFORMATION FOR SEQ ID NO: 1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403:

TTTATTATTT GTGCTACAAC TACTTAAAAA AATCAGTAGA TATAGCATTAA AACATATTTT 60
 20 CATCCCCyTG AATTTTAAAA ACTTTTTC AAAGCAACACC TCTAAAAATA AATaCAATAT 120
 ATTATAGCAA ATAGAAATTA TTATTTTGTT AAATTATGTT GTnCATGTT 169

(2) INFORMATION FOR SEQ ID NO: 1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404:

TTAGTTGATA AGTAAATCCG AGTGACATTG GGATTACCCC CAACCGACTC TATTCCAGTC 60
 35 TGAAATACGT GAACCCATAA nATCCTATGT CCAGATTAT ATTTCT 106

(2) INFORMATION FOR SEQ ID NO: 1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405:

TATTTTTGCA GCAGAGATGT TCGCGACAAG GTTTACGCCA AATTGTCACT GCTACTGCGA 60
 50 TGTGTATTGC ATGCAAGTGC AGGnAATATA TTGAACATTT AAACGATCAG TTTAATTGCA 120

CTTTAATAAG CAATTTGTAC TGACTGTCGA CATTGCGTCA TGGTCTGTTT TTGTTTAACT 240
 ATACTATnGG TGCGAAGTAG GCCTATGTTT AGAGGTCTAA CATGCCGTAG GTCTAATGGA 300
 5 TCAGGAACC 309

(2) INFORMATION FOR SEQ ID NO: 1406:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406:

GTGGACCTGC AGTTAATTCA ACGATTTCAA GATGGGCGCC AAGAACGAAA CGTGGCCGAT 60
 20 ACTTAGGATT CTGGAATCAT CACATAATCG TGTGCATGAG GTGTTTCACT TTGGGGTCTA 120
 ATGATTCTTC ATGGAAnGTA TAGG 144

(2) INFORMATION FOR SEQ ID NO: 1407:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407:

ACCTTTGCGT CCAGAATTAG CTACATGGTA AAGCTTCGTG TTACTATTTT AGGGATATCT 60
 35 TCAACnCGTT TCACTTGTAT AATTTGTTTT TGTAATTGGT GAAGTCATAG TATAG 115

(2) INFORMATION FOR SEQ ID NO: 1408:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408:

ATTGGTATTG GCGCTGTAGT ATAGCTTCAT TATCTGATGC CATTAGTATA CGCACACTnT 60
 50 TTATTTATGG GCGTGGTATT CATCCTTATC GGGATCAATT ATTGGGTAC ATTTT 115

(2) INFORMATION FOR SEQ ID NO: 1409:

55

(A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409:

10 AACCAGATGa AAAGCAAATA TACATATATA ACTCTACATG GGGTCGTGGT TTGGATATTG 60
 TTCATGATGC ATTCCGTATG CCAATGACAA AGCAATATAA AGATAAATTn CAAGAAGATA 120
 AAA 123

15

(2) INFORMATION FOR SEQ ID NO: 1410:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410:

CTnTTTATAT TGAGGATTTT GTATCATATA TGGATAATCA TTAAAGGTGT ATGCTCTTGT 60
 TATCAGATCG CTACGGGTAA AATCGCTTCT ATAGGGCATT TACATGCGGG CTTCTGCCGG 120

30

(2) INFORMATION FOR SEQ ID NO: 1411:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 455 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411:

40

TCTCGTATTG CGTTTAGAGA ACATGCGCAC AAAGGACAAA TTCCAGGTGT TAAAAAATCA 60
 AGTTGGTAAA ATCAAATTC GTACTTTAGC CCATTTACAA TATCAATAAA ACAATGTACA 120
 GTATATACGA ATGCTATAAA CTGAATGTTT TCTCATATTA ATAAGGAAAC ATTCGGTTTT 180
 45 TAATTTGTCAT TAAAAATAA TTAGTTTTTA AAGGGGCTAT TTAAAGTGAA AATATTTGAT 240
 TACGAAGATA TTCAATTAAT ACCTAATAAA TGCATAGTTG AAAGTAGGTC TGAATGTGAT 300
 50 ACAACTATCC AATTTGGTCC GAAAAAATTC AAGCTACCTG TAGTTCCTGC GnATATGCAA 360
 ACAGTTATGA ATGAGAAATT AGCGAAATGG TTTGCTGAAA ATGATTACTT TTATAATCAT 420
 GCATCGTTTT GATGAAGAAG CAAGAATACC TnTTA 455

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412:

ACAAATGTCAA ATCACAATAG CTGTTGTAGG CATTGTGATTA CAATGAACTA AAGGCAAAAT 60
 TGGAGCAGTT ATCCATGAAT GATTAATAAC AACAAAAAGT ATGGGGTCAA GTTTAGGG 118

(2) INFORMATION FOR SEQ ID NO: 1413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413:

TGTTGACGAT ATAGGAATTA GCAAGAAATA GGCTAAGATA GTTTCGCACA ACTTGGGGCC 60
 CAACTTCTTG CTTGTTTGTGA GAATTAGGGG TCCATTTCTC GTGTTGGGGC CCGAACTAAT 120
 AGTATGAATA TATATATCTA ATATTAATAAC GGCAATATTT ATATGGTATA CATTTTTATA 180
 TTTAGTATTT GTATAGACAT GCTAATTAGC ACTTTCTAAA AAGGGTTGAA ATGATATACT 240
 GATGA 245

(2) INFORMATION FOR SEQ ID NO: 1414:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414:

TTTTTGTAT TCAAAATTTA GAGTGTGTTA TATGATAACG GTTTTTTCAT AGCGACTTGA 60
 TCATTTTTTCG AAATGATGAA AGATATGCAA GTTCAATCAA TCGGAACAAA AATACTATAT 120
 TATGGTAAGA AATTCCCGAA GACTAGCGCA CTCACACACA AGTGCATCCT CGCGAACAAT 180
 GCGCACTTTT CACAAGCACA CAAACACAAG GCACAAGTGC ACGCATTATT AGACAATGGT 240
 CTACCTACCA GA 252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415:

ATCTGCTGGA AGAGAAAAA GACGCTCTTA AACTGGCTT TAGAAGGTCA AGATATAGAA 60
GnTATTAAAT CTAAAAAGA AGGAACTGA AAAAGTGATT CCAGGAATTT TC 112

(2) INFORMATION FOR SEQ ID NO: 1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416:

CTCAATTACA TTCAAGAAAA TGGGTGGAAT TACACAACGT TGGACTGAGA AGTATAGTTA 60
ATAGCGCAAA TGChATAAGC CTTATATAAA AATGGGCACA ATTATTTTCAT GTACCAACAA 120
GAAC 124

(2) INFORMATION FOR SEQ ID NO: 1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417:

TTCAAGAGCA CATACTGTAA CTCGTACGAG AATTTTTTCA AAATGACGCG TCAATCTCAA 60
TATCATCATA TGGTATTCCG AGTAATACCC CTCGnCACCT TTTTtaggTA GCGTCAATAT 120
T 121

(2) INFORMATION FOR SEQ ID NO: 1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418:

CTACGCCATC AAGAGGGTGT TAGTGCTATT AACTATTGCG GCGAGAGCAA TTAGTCGAAT 60
 5 GCAAATTAGG ACAAGTTGAT GAGTAACTAC nGCCAATATC GGTAAGTTTC ATGGCGGTTTC 120
 AGC 123

(2) INFORMATION FOR SEQ ID NO: 1419:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419:

20 CTTATAATCC TTACnGCAAT TTCACCTTGT ACGGAATTAA ACAACGGAGG CATTACTTA 60
 CCCCCTTTAC TTAATACGTA CCAAACTTG GTCGTATTCA ACCATTGGG 109

(2) INFORMATION FOR SEQ ID NO: 1420:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420:

35 GCTGTnGTGC TGCCAAGATG CTGATTGAAA AGTATATATG ATTGCATCAG TAGAAGAGCG 60
 AGCAGAAAGA AGATATAAAG ATAATCAGTT AAGAGGTGTC GAATCAAATT TTGAAGATT 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 1421:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421:

50 TGTTTTTTACA GTCACATACA CTAGGCATCC TAGCATTATC TAAATTTAAT ACCATCGCAA 60
 CTTGCGCTTT AATCTTCAAG GCCAATTAAA CCTCCTTCAT CTTTCTAACT GCTTAnATAT 120

55

(2) INFORMATION FOR SEQ ID NO: 1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422:

GCCAATCATT GTCAATGTTT AGGCATCANA TTTATCGAAT GATTTTCATT TGCCATGATC 60
 AGTCAAGGCG GGGATTTATT CAAAAATTAT GACGCCTAGT AAAAAATTTT 110

(2) INFORMATION FOR SEQ ID NO: 1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423:

ATTACCTTGC ATGAATTTCC ATCTGTCAAA TGTGCGCCTT CACGAATTTG TTCGATAAAG 60
 ATACGTTGGT CACCGTGAAT AATTTACCA GCTGCATTTn TCCATGGACC A 111

(2) INFORMATION FOR SEQ ID NO: 1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424:

TGTTGTGTGA TTGCGTATTC TCAGGTGAAT TCTTACATAT ATAGTACTTT TTGTTTCCGC 60
 TTGATTTGAC CTTGCATATC TTTACATTC TTCGAAAATT GATCAAAGCh CTATTGAAAA 120
 ACCGTATCAT ATACAnACCT CTAATTTTTT TGACTAACAA AAAGAATTCT TTGACGTATC 180
 AACTATATCA TCATGACTTC 200

(2) INFORMATION FOR SEQ ID NO: 1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425:

5 TTTCTATAAT TTTAGACTAT TTCTACCATG TTGCTGAACA ATTTACTTAG ATAAAAATTA 60
 TAAAAATTTG GTCAATTAAC AAAGTTAGTT TGTAAAAACG TATACTTTAA TTATTCCGG 119

(2) INFORMATION FOR SEQ ID NO: 1426:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426:

20 AAAATGGCGT TGCAATTTTAC TCTAATAACG CTCAAGGCGA CGGCAAAGAT AACTAAAGG 60
 CACCTATTAT CGAACATAGT ACTCCTAaCG GACCTGGAAT TTAAATCAGA GCGGCC 116

(2) INFORMATION FOR SEQ ID NO: 1427:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427:

30 TTTTATTTTAC GTATAAGTGG GCGTTAGGTG TCACAGCGGT TGTCGATCAA AATATCATCA 60
 35 TCAATCTTGT ATATGGGTTT GCGGATTCTT ATTTTATGAT TTTACAGAAC TATCCTAGGC 120
 TTATTCTTTA TTAAGAGATG CAACnAGTTA TATAAAAAGA CGAATCTATC AACGCGAGCT 180
 40 GCTCACAAGG CATCTCnTAT AGCGTCCACA TC 212

(2) INFORMATION FOR SEQ ID NO: 1428:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428:

50 GAAAAATTGG TTCTGAATAT AATGGTGCCG TATACTTTAC GCCTCAAATC AAAGATTTTA 60

ATTTTAATGA AAAACATCGG TCGAATATAA CATAAAAAAA CGTCTATATC AAAAGCATCA 180
 TGAATAAACA GAGGAGCACA AAAATGAnTA AAAATATAAT CATCAAAAGT ATTGCGGCAT 240
 5 TGACGnTTTT AACATCAATA ACTGG 265

(2) INFORMATION FOR SEQ ID NO: 1429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429:

CGTACGAAGG ATTTGCAAAC TTCTTCATTC AACAAAGCTAA AGAAGAACGT TTCCATGGAC 60
 20 AAAAGATTTA TAACTATATT AACGACAGAG GTGCACATGC AGAATTCAGA GCAGTTTCAG 120
 CACCAAAAAT TGACTTTTCA AGCAT 145

(2) INFORMATION FOR SEQ ID NO: 1430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430:

ACACCGCTAA GCGTATTAAG ACAGGATCTG AAAATGGACA CATCGCAATC GAATTATTGC 60
 35 AATGCCAAGT CATATCGGGG GTGAACCGCA ATTTCAGGnA TTAAGTGGAT AGGTA 115

(2) INFORMATION FOR SEQ ID NO: 1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431:

nATGTATTnG TGAAAAGGTC CTGAGTGGAC AAAAGACCTA AATATTTAAT GGTGATTAT 60
 50 CGCACGTCCA TAGTTGGTGA ACAGGAAC TT ACACGTACAT CTAATCGCAG ACTATGCGTA 120
 AACTTTGGAA ACTGCTAGTC ATTGAAGCGT GGTATGTGTA TGCACGTAAA TATGCATTAG 180

(2) INFORMATION FOR SEQ ID NO: 1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432:

GGAATGATTG ATAAATTGGA CTA CTAAAG ATTTCGGTAT CGTGCATTT GGCTCAGTCC 60
 ATGTTTAATC ACCTATGnTG ACATGGTATG ATATTAGTGA CTACCAGAGA TATGGATGAT 120
 TTGGAACGTG GAGGACTTGA TCGTT 145

(2) INFORMATION FOR SEQ ID NO: 1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433:

TTTATTGCAT TTACATAATA ATATCCTTTT GTTGT TTTGG TATTTCTATT CATATACAAG 60
 ACCATACCTT TAACTTTTCAG AGCTTCCCCC TTATTTTGAG TTGCCATTTT AGAACCAATA 120
 ATCCATGTAC CTTTATCATT TTTATCAAAT TCGTCATCAC GATAACCTn 169

(2) INFORMATION FOR SEQ ID NO: 1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434:

GATCTATAGT TCTGTAATCT GACGTGCTTT GCCATGTGCA CCACTCGTCn TAAAAATCAC 60
 TTACACTTAA CCCTTTTCCA CCTTTATCGT ATCCACCTTC AA 102

(2) INFORMATION FOR SEQ ID NO: 1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435:

5 TTCTTATTAT ACAAATAGAA GCCATGTGTG CTTATATCGC AGCATCATGA CTCCTTTTTC 60
 ATTTGAATAT ATAAATAATA CAGnCGCTTT CGAATAAATT TAGGCTAATT CTACCA 116

(2) INFORMATION FOR SEQ ID NO: 1436:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436:

15 GGGGGTTTAT GTACTGGTGG ATCTGCAAAC TACTTGGCGT AAAGAATATA CAGATATGGT 60
 20 AAnGAAAAGT TTAGATTCAC ACGCCATCAC AATGGATTAG AAAAACCGAA TTTCTTCAGC 120
 AATTCTACAA TTTCTAGTAT ACGC 144

(2) INFORMATION FOR SEQ ID NO: 1437:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437:

30 GTTGCTGGGn AACCTATGGT CGAACATGTA TTGGTAAAGT GTGAAAGGCT CTGGTGGCGA 60
 TCAAGTTGGT AACCATCGTA GTACATGGTG CTGTAAATGT A 101

(2) INFORMATION FOR SEQ ID NO: 1438:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438:

45 AAAGATGGTG ACATTTTATA TAATCCGAAT GTGCCAAGTT ATTCAGCAAA GTATCAATTA 60
 50 AGTAATGATG ACTACAATGT GAAGCAACTT AGAAAGAGGT ATGATATACC AACTAnGAAA 120

AATTTAGAGT TTACATTAT AGAAAATAAA GAAGAAAACA TCTATTTTAC GGATAGTATT 240
 AATTTCAAAC CTAAGAATA GGGTTAATAG AAGTTTGAAA TGAAAATTC nTAAAGTGTG 300
 CAAAATAATT TGTCGCTTTA G 321

(2) INFORMATION FOR SEQ ID NO: 1439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439:

CAGTTGTAAT GGGACCTGGG CCAATCGGAT TACTTGTAGC ACAAGTGTTA AAAAGTAAAG 60
 GCGCAACTGT TGTGGGTACT GGGTTGGGAC AATTGACCAA GTCAGATTAG ATTAAAGCCA 120
 GAAAGCCATT GCCAC 135

(2) INFORMATION FOR SEQ ID NO: 1440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440:

AAATTATTTT GAACACTTTA TGAAATTTT ATTTCAACT TCTATTAACC CTATTCAGTA 60
 GGTTCGAAAT TAATACTATC AGAAAAATAC ACATTnCTT CTTTATTCT 110

(2) INFORMATION FOR SEQ ID NO: 1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441:

TCTCTTTTGG ATTCATTAAG ATTGCnGCAT CGATACCAAC GTTmAACGGT GATTGTGTAA 60
 TGAATTTTGG CCACCAAGCT TTTTAAACAT TATTCTTTAA TTCAACACCT AAAGGACCAT 120
 AATCCCATGT GTTTGATAAA CCACCGTAAA TATCACTACC AGGGAACACA AAACCTCTGT 180

GAAAACGCCC CATGGAAAAT AACAGCATAG TAAATATGCT TTACTTCCAT GGGACGAGTT 300
 AATATTTTAA ATTGTATATA ATACAAAAnA AGTnACGTAT TTAACCCGCG GTTCCACCCA 360
 AATTAGTGTA GTCACTCGCT TTTATTTTAA AATGATTTCGT TCGGCCAATC TTATTGTTAA 420
 GCTTACACTA TCCTTA 436

(2) INFORMATION FOR SEQ ID NO: 1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442:

ATTTTGTAGAA GCATACTGCG AACGTCATCA CATCGATTTA CATATCAAAA AGTTAGATTT 60
 GTCGCATAGT CTCGACCGAA ATAACAGCAT TCAGAATGAA GCTCGAATTA AACGTTACGA 120
 ATGGTTTGAT GAAATGATGA ATGTATTAGA AGCGGATGTA TTGCTAACGG CGCATCATTT 180
 GGACGATCAA TTAGAAACTA TTATGTATCG TATTTTTTANT GGGAAATCAA CACGTAATAA 240
 ACTAGGATTT GATGAGTTAT CGAAGCGAAA AGGTTATCAG ATTTATCGAC CACTTTTAGC 300
 TGTCTCTAAA AAAGAAATAr AACAAATCCA AGAGAGATAT CATATTCCAT ATTTGAAGA 360
 TGAATChAAT AAAGATAACA AATATGTTAG AAATGATATT CGTAAnAGAA TTATTCCAGC 420
 TATTGATGAA AATAATCAAC TTAAAGTATC GCATTTATTA A 461

(2) INFORMATION FOR SEQ ID NO: 1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443:

AAAGGTGATA AAAAACAAG GCATTGTAAA TTAATTGAAA ACCAAGTGAG TTATTACAG 60
 ATTCTAATTG GGATAATGCG CGATATTTTA TTCCACACTT GTTACATTAT TGCTTTACGT 120
 GGGGGTTAGC GTGGAnTCAT CAC 143

(2) INFORMATION FOR SEQ ID NO: 1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs

1743

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444:

TGGTGTGGT TCATCAGTTG TAAACGCGAT TGTCACAAGA CTTAGAAGTA TATGTACACA 60
GAAATGAGAC TATATATCAT CAAGCATATA 90

10

(2) INFORMATION FOR SEQ ID NO: 1445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445:

ATTGAACAGT GACAACAAAT GACAACAATG AATGACCAAC TGAGTTGCAG AATTGACCGA 60
CCTGACTTGC TGTnAGATGT GCATTGCCTG TGACCAGTTA ACTGCTGTTT GTACATTATG 120
ATTGTGCACG TGAAGTCTTT GCAAATGACT TTAAACATTA TGCTGCTAGA GCCATCTTTT 180
AAAGATGTTT GGACTAACGT nCATGATGTG AATATCTG 218

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(2) INFORMATION FOR SEQ ID NO: 1446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446:

TTTGACTTGA CATTATAGAA CACAAATTCA TTGAAACTA TGTTTTCAAA TTTATTTATT 60
GTTACTGGGA ATTCACATT ATTAGATTTA TTTATTTTCT TTTGA 105

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(2) INFORMATION FOR SEQ ID NO: 1447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447:

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AGACTGAAAA CTGCATATGC AGAGGCGATG AACCAAAATG CCAT

104

(2) INFORMATION FOR SEQ ID NO: 1448:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448:

TTGAATTAAC TGAAGAAATA GCACTGCAAG CAGGATTGTT GATATGACAA CATTGAGTC 60
 AGAATGGCAA CAACAACGTG ATTCGTGCAC TCCAAGCAGG TGCA 104

(2) INFORMATION FOR SEQ ID NO: 1449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449:

TATTAATTTT TTTTAATATG GAATATTCAT TGCATCGCTT TCCTATTCTT CAAGCCCACT 60
 TTTTATCTTC ATATACATTA ATTAACCACC kTCAAACATT GTCGTTAGAT TCGCCAAATT 120
 GAATCTATTT TTAGCACAGC AAAAAACCGA ACTGCTGAAA TAATGCATCT CCAACAGTCC 180
 GGTCTATTAA ACTATTTACT TATCTTTATT AAACAATTGA CATGATTTAT TAGAATAACC 240
 CAATTGGCAT GACCATGCAT CAGTAACATC CATGTTTAAT GGCTGCTGGT TTTTtaggTA 300
 AACCAGGCCA GAGTCATGGn TGGCACCTGn GCAACGCnAC GATAAAGCC 349

(2) INFORMATION FOR SEQ ID NO: 1450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450:

GATTTTATAT AAATATAGCT TTTCACAAA ACAATGATT GAATTTCTAG GAATTGAGTC 60
 ATTAAAAAAA CACTTGAAAA ATTCAGGTGG GATTGCGCTA TTGCCGGAAT TTATTGTTGC 120

AGAAACAACA TTGaTAATTA ATCCTGAATC GAATAAGCAm GTACTTGAAT CTTTTGTAAA 240
 AGATGTTTTT TTATAATTAT TGGTGAAAAC GTGTAGTTAT GGTGAAACTC AAAGATAATA 300
 5 ATTTAAATGA GATGTTAATG AAAAAGTAAT TCAATATAnA ACAGGTGATT TanATCTTAA 360
 TAAGGnTAAT TCCAGGTTGA ATTCCAATTG CGGGCATCAT 400

(2) INFORMATION FOR SEQ ID NO: 1451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451:

20 TCGGTTATAG TTGCTATTCT CAATTATGTT CGCGATAATT TTAAGTAAAA GTAAGCACAG 60
 ATATTGAATT TGATAGGAGT TAATTGATAT ATACATACGA ACTTTCATGG ATCACTTAAA 120
 TTTg 124

(2) INFORMATION FOR SEQ ID NO: 1452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452:

35 TGTATTAAAA ACCTTCCACC TTTAAAAGCA ACAATGCGGT GTCCTTTAAA TTCAAACATA 60
 ACCATATACG AATTACTCGA TAATTCTGTG TGTTTAATTG ACAGATGTCG TGTGAATTGA 120
 40 TnATTT 126

(2) INFORMATION FOR SEQ ID NO: 1453:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453:

50 ACTTTGGCAA CATCTGGAAT ATCATATAAA TCAAGTAACT TACCTAACCG ATGATTAATA 60

CTAACAGTTG TTTCCATGCC TACACCTCAC GATATTATCA CTATTCATAT TAACATTATA 180
 TGTAAGAAAT TAAAATCTTT TGAAGCATT AAGATTACTTA TCATTTnTAA ATTTCAATTT 240
 5 AACTAACAG TAATTTATGT AGCTTTTGnA ATTCTCATAA 280

(2) INFORMATION FOR SEQ ID NO: 1454:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454:

ATATTCTTTA AATTAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTG 60
 20 ATGATGATTG CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT 120
 CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT 180
 TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GgCCCTTTT CCTCTAATTG 240
 25 TT 242

(2) INFORMATION FOR SEQ ID NO: 1455:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455:

ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 60
 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT AntGGTATTT TATTCAGATG 110

(2) INFORMATION FOR SEQ ID NO: 1456:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456:

50 ACCAGTGGTT GCCTTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA 60

AAAGCGCTTG CAATATATTT TCGATTGTt ATTCAACmAA ACGTTTTATT tTATTCGCTG 180
 TAGTCAAATG TATACCCTTA TACTGACTCG aTAATCATTT GCTTATnATT TGAGAcTAGG 240
 5 ACATAAAATca ATGCTCTAGA ATCCAAAAAG TCACATTAGT AGTAGTTAAC CGAACGAAAA 300
 TGCACCTTGTA ACAAGCTTTT TTCAATTAAA GTCAGGGGCC CCAACATAGA GAATTTGAA 360
 ATGAAATTCT ACAGGCAATG CGAGTTGGGG TGGGACGACG AAATAAATTT TGCARAAATA 420
 10 TCATTTCTGT CCCACCTCAC TCAAAATAAA TTTCACTATC CGTAAATAA ACAACTAACT 480
 ATTTAAGTAT CATCTCTCCC CTAATTAACA ATTATAAAAA TAAGAACCAA TATTCGAGAC 540
 15 AACCTAATTA A 551

(2) INFORMATION FOR SEQ ID NO: 1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457:

ATCnGGGGCT GCATAAGCGA TATCAAGTGT GAGCATTGAA CGATTCAGGA CTGACCAGCA 60
 30 CGCCGTTTGC CTGCTTTGAA AGATCCACCG ACAAATCCGC CAACATCGT 109

(2) INFORMATION FOR SEQ ID NO: 1458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458:

ACCAGAGCCT CTTTGACTTC CTAAGTCGAA TAGCATCGTT GATATAGTTA AAGATGACGC 60
 45 TAGATTTAGn AATCCAAACT CATAACACCT CCACCATTC ATCACATCTG GA 112

(2) INFORMATION FOR SEQ ID NO: 1459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CCCCAACCAA TTTTTTAAAA AAGGGGGCCT TTGGGGGGGC CAACCAAGGG GGAACCCCTT 60
 AACCCCAATT TTGGCCAATT TTAAAGGGAA GGCCTTGGAA CCTTTTGGG AATGGGCCGG 120
 5 TTTTAAACCC TTGGTTTCCG GAAGGGGAAA ATTTTAAAA AAACCGGAAT TGTTGGCCC 180
 CCTTTAAATT AAAAAGTTCC CThAAAAANA AATTCCCCCA AGGG 224

(2) INFORMATION FOR SEQ ID NO: 1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460:

20 TTTGACAAT CAATTCGACG TCACTGCCAC TCCATCTATA GTAAAGCGTT GATACTTTCA 60
 ATAATACTG GATCACTGTC TAATTATAAA TGGATTCTTA CATCCCACCA TAATAATTn 120
 CATATGTTCA TCACC 135

(2) INFORMATION FOR SEQ ID NO: 1461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461:

35 TTATAGAACC TCGTACTCCT nTCGACACTT GAATTTAAAT CAGAGCCGCC AGTGGAGAAG 60
 CATGAATTGA CTGGTACCAC TCGCAGAAAG TAATGATTCT AAGCCACTTG ATTA 114

(2) INFORMATION FOR SEQ ID NO: 1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462:

50 GTTGAATTGT TGGTGATGTG GTTACACGAA TTTGAATAA TTGTTCTTTA CGTCAAAACG 60
 TATCGTTCCA AAGTAATCCC CnGGTAATAG TTACCAACAA GTTCA 105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463:

TTGTATGACT CTTCCGACTT TGGTAAAATT GTGAACGCTG GntGAATGAT TTTTGTTTGA 60
CAATTGGCCT TATCATCATT AATCGTATTT TTAAGCTGCT CGGATATAAG TTCTCAGCGA 120
GTTCTTTTGT ATGTATCATT AGTGTAGAAA ATAGCTGTTT GT 162

(2) INFORMATION FOR SEQ ID NO: 1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464:

TAAATTGGAA AGTCACATTC AAnATGCGAA AATGTTTTAA AATGTCCTGT AGGTGCTTAA 60
TAGTTTTGCA TTTGCAAATT TTA CTGAACC GGTTTAAACG AAT 103

(2) INFORMATION FOR SEQ ID NO: 1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465:

AAATTGTATA ACTACCAAGC TTATATGAAA TGGTAAACAA AATATTATCA CTTGTTTGAT 60
AAGTAGCGTG GAAAATATTG TATCTTTCTA AATGTACACG TTAGAANTCA TGCTTATGTA 120
TTACACGCGG GGCAC TGGTA CCTAAGGGCC TAT 153

(2) INFORMATION FOR SEQ ID NO: 1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466:

TTTCAGTAAC ATATGAAAAC TTAATTAACG ATGTTTCAGTA GGTTTCATACA TTTTACTTTA 60
 5 TGATGCTTAA TTGAATTACA nTTAAGATAT GACCAGCTAA AAAGAGTTAA TGTGATATTT 120
 AACC 124

(2) INFORMATION FOR SEQ ID NO: 1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467:

AAGGAATTAA GTTTGCGACA CCAGCAAATA GTACTAATAA AGGAATATAT GGTAAGTCAA 60
 TAATTGAATA ACCGATATAT AAGAATATAC CTAAAATAAC ACTGACAGTT ACTTGACCTT 120
 GAATGTAAGA TTTTAATGTA AAGTTTAAAT CAGTTAATAA ATCTACGAAA AATACTTTAC 180
 25 GTTCACCTTT GAnAAATTTA GCAACAGCTG GGATAAATTT TTCATGGTCT TTTAACATAT 240
 AAATTAAGAA GAATGGAACC ATAATCAATA AGAAGATGGT TGAAATTAAT GATGTAATGT 300
 30 ACTGTAATGA ATTAGATAAn ATATTAGnAA CGCCATCACC CATTGATTTA ACCA 354

(2) INFORMATION FOR SEQ ID NO: 1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468:

TGCAAACTAG GAACAATAAT GTTAATATAA CTATGATGnA AGTTAAAAAA TAAAAAGGAA 60
 45 CACTCTATAA TATGAATTAG GGGTTACAGT TTTTGTAGTA TTTTACAGTA TCAAAGTTTA 120

(2) INFORMATION FOR SEQ ID NO: 1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCTAAATGCT GACTAAAACT AGCAACACGA GACTCATTAT TATTAGACAC GATTGTAATA 60
 GTGATTCCTT TTTCATTAGC TTCCTTAAAC CATGCTTTAA CACGTTCTGT AGGTTCTTTA 120
 5 ACATCCCAAC CTACTAGCGT ATTATCTAAA TCTGTAATAA TACCTTTAAC GCCTTTGTCC 180
 ACTAACTTGT CTAAATCAAT TTGAAATATT GATTGAACAT ATGAATTCGG CATAAAAAAC 240
 10 TTGCGAACTA AACCCATTTA ACTCACCTTT ACCTTTTAT AATTGAGACA CTAATGCTTC 300
 AACAGTTTGA CTGATGATA CAGCTGCTTT TTCTAAAAAT GCTTCGAAGC TCATTTCCGC 360
 TTCTCCATTT GCTAAGTCTG AACTGCACG AACTACAACA AATGGTACAT TAAATTGATA 420
 15 ACATGTTTGT GCAATTGCAG TTGCTTCCAT TTCAACCGCC ATCGCATTG GAAATG 476

(2) INFORMATION FOR SEQ ID NO: 1470:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470:

CACCATACAT GGGTAAGGAT ACTACTCAA TCACTTGAA ACCAATAATn CATGACCATA 60
 TGTGTGCCAA TGAATTCAAT TGGAAAGACA ATGATGAGAT ACTATTAAAA CGATTATATT 120
 30 TATTGTCACT TGTCAAACG CACTCCTTTT CCAAAT 156

(2) INFORMATION FOR SEQ ID NO: 1471:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471:

AACAAAAGTT TGAAAAGCC GGGTGCCAGC GAAACTTAA AAAGCACTTT ATCAGAAAAA 60
 45 GCTAAGAAAA AAGATTAATA TTCATTCAAT AAATATAAAT CCAATTTAAT TTGTTGTTTA 120
 AGGTCTACAA GTGTATGTTT AATATACAAT TCATCGTTTG ACGGTAAATC AGATACTTTG 180
 AAATCTTGTC GCTCAACCTC TAGTAAATCG AAATCGCTAC CAGCTGAATT ATAGGTTTTA 240
 50 AGTTCACCCT CTTCAATGAT TCTGTTTTCA AAGTCTTTAA TAACTATAAA TACTGGTTTA 300
 CCGTTGTTAT TAAACAACCT GTCTCTTTTG TCTAATAAGC TTATACAATC CAAATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 1472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472:

CTAGGATTnC ATCTATTTGG GATGAAAATA AGCGTTTCCT GAATCCACAA GAATATCCAG 60

TCGATTTAAG CCAGGCATGT TGGGGTAATA ACATAACGTT TTTTGA 106

(2) INFORMATION FOR SEQ ID NO: 1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473:

TATCTTACCT ACATTGTTAT CTGATGGCTG TAATCATTAA ATCTATAACA CCGAGTTCTT 60

CCATTAAATTT TCAGCTTCAT TCGACTGCCT TTTTATnTTT CGTACTATTA CGAATTT 117

(2) INFORMATION FOR SEQ ID NO: 1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474:

ATGCATGGCA CTGGAAnCAG CTGGGAGATA TAGGTAGTAT CCTAAAGAAG TTCAGTTAAT 60

CGGAGCGATT GTATTGCATG AAGGTAACAT TCGGAGTGC CAACAGGCCA AGTAAACTT 120

AACGGCAACC ATGCCCTTATA TTAAATGCCC TTCCGGGAAA GGAC 164

(2) INFORMATION FOR SEQ ID NO: 1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475:

5 ACAGCAAGAC GTGACAAATC AGATACTATT AGTCATCAGC GTTAACATGT GGATAnGTGT 60
 GAGGTACGAA TanCCGAAAG GAAATACGAC CTTTAACATT CGCGCACAAA ATGAGCTCAG 120
 GCGCCTGCCT TGCCCATTTT TTAAATTATT TCCCTGGAAA TGATTGCTG TGTGCTGTTC 180
 10 TGTCCACAAC AACACGATTA ATGCCATGAC 210

(2) INFORMATION FOR SEQ ID NO: 1476:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476:

20 AGGGTGATTT CACGGTTCGT CTGCCCATTT AATTGCGCAT TTTGCACACC ATCTACCGTT 60
 TGCAATTTTG GTATTAATTG TTGCATGCAG TACTGTCCGT TGACTTTGnt GCAAGTGCAT 120
 25 GCTCTTTC 128

(2) INFORMATION FOR SEQ ID NO: 1477:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477:

AAAATCTGGT AAAGTAACTA GAGTTTAATA AATATATTGC ACATAAAAAA TGTGACCTTA 60
 40 TGTGGAGGAC ACATTTACTT AAGAACTAAG AGCTCAACCT CTTAGTTCTT TTTTGTAC 120
 CAAACAATAC ATAATGGTTC ATAGTGAAAT TCGAACTATC AATATAATTT GGTAAATACG 180
 TTTAATAATG GTTCTCTGTC AAATTGGACT TATGGGTTC AATATCGATTT TGGCACATAA 240
 45 ATCAATGTAC TAGGACCTAC AATTTTCCTT TCAATAATAA ATCAGCCAT AATCTTCATT 300
 AATTACAGCG TGATTCATCT ATTATTATGT TATAAATkCT ATCTATAAAC GTCACCTTAT 360
 TAAATAACTC ATGCACTTTA TTAAAAATCC TCACAAATTT GAATATACTT AATTTAAATC 420
 50 TGTACTTCTA ATTTGCAAAA TCAACCCATC ATGTACAGTT ACTTTGCTT GCAAAGACTC 480
 AATTCATTT GAAATAGTTA AAGTAGAACC TATATnAGC ATTTGTCTAG CTAAATTATA 540

GATAACTCTT ATCTTTTTCa ACTGTAGGTG ACCTTTAGGG C

641

(2) INFORMATION FOR SEQ ID NO: 1478:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478:

15

TTAACCGTGA TGCAGAGTAG TAAGTGGATn CATGCTCTGT TATGGATGAC AAGACAAAGC 60
 AGCGAATATT GCGTACTGCG ATTGATGAGC AGATGCATAT GATTGGATTG GTGCAGCTGT 120
 C 121

20

(2) INFORMATION FOR SEQ ID NO: 1479:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479:

ACCATTGCTT AGATAAATAC CTCGCACTGA ACCGCATTAG TATAGCACTT CTAGCTGATC 60
 GCATCAGTAA AGTATGCTAT TAATGTCTCA GTTTTATCTG TAATGCATGT TTAAGTTAGT 120
 CATAGCATTa Ttn 133

35

(2) INFORMATION FOR SEQ ID NO: 1480:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480:

TTTTGGGGnT TTAAATTTT AAATTCCCGn TGGGGGAAAT TCCCTTAAAA ATTCCCAACC 60
 CTTTTAAGGG GTGGGGGTTT TTTTAGGGAA AAAGGGGCCC GGGGTTAATG GTTCCCAAAA 120
 AATTGGGGAA AATGGCCCC CAAATTTTAA ATTCCCGGTT TTAAATTGG GGTGGGTAA 180
 ATTGGAAAAA CCCCCAATT T 201

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481:

CAGTATCAAG CATAGTAAAA AATGAGGGTA GGA CTGAAAA TACGGCGTTA TTGGTGGTGC 60
 ATTCACGGTA AATATGTTGC ATGACCAGCA AGTTTTGGnC TTCTGATGCA CC 112

(2) INFORMATION FOR SEQ ID NO: 1482:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482:

CAAAAAACAA GTTCTGATAT GCAGTAGCTG AATAATTTTG CTAGTTACAC CAnAGTGATC 60
 TTCTGGTGT TTACTTTTTA TAAATGTTTT CATATATTTT ATATGTATAA AAATGGGATT 120
 TAGCGTA 127

(2) INFORMATION FOR SEQ ID NO: 1483:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483:

AGTGGTGTAT TGGGTGAGTA ATGCTTAACT TCATACCTGG TGCATTGGCT GTTCAGTATC 60
 ATTATATCTG CATGGGCGAT ACT 83

(2) INFORMATION FOR SEQ ID NO: 1484:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TATTATTGAT GTTCTTTGGT TCATTCTTTG GTAATAATTT TGCACCTTGAA AATTTACAAC 60
 CGTTAGCTGG AACCTAGnCA AAGGGATGGG TTTAGTGGTC TATTGTGGGT TTATTGGTAT 120
 5 TCCGTGGGCC ACCCCATGGG GCCATTATGG TTTGGGAATT TTGGGAATAA ATTAATTTnC 180
 CCAACCAAAA ACCAGGCCAA G 201

(2) INFORMATION FOR SEQ ID NO: 1485:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485:

20 CTCACAGCAA CATCAAAGAG GCAGATATTA GTCAAGTTCA ACGTAATAAC ATCTACCTTC 60
 ACAAGTCGAT AAAGGAGCAC CATCATTAAT AAGTAGATCA ACAAGTCAAC GAGAATTTTA 120
 ATGTGCAGAA TAGAGAAGTA CACCACACAn ATAATCAAGC GATGTAATTA CTACTACATT 180
 25 TThCATGACA GAGTGAACCT CAACAGCGGT 210

(2) INFORMATION FOR SEQ ID NO: 1486:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486:

35 CAGGTTATGT TTGCATTAGA AGTTCTTGGA AAATCTTTAT GGAACGTGGT TTACACCCTG 60
 40 ACTTTGAATT GCATCGATCT GATGAAGATA AATGAAATTG AATGGGATGG CChACATGGA 120
 ATGCAACCTA TGACTTGGAT GGAATTAGAT GAAGCGGG 158

(2) INFORMATION FOR SEQ ID NO: 1487:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487:

TTGCAGCATA TAGAGGTAGA GGCATCGCGA CAAAGTTATT AACGTCATTA CTTG

114

(2) INFORMATION FOR SEQ ID NO: 1488:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488:

15 TGCTAAGTGA TAAAAAGAAT GATAAGCCAG GTGTACCAAT GGGTCCTGGA TTAGACCATT 60

TGGGAGATAT CGTTGTACCA CATGTTGATC AACTAACGTT nCCACATG 108

(2) INFORMATION FOR SEQ ID NO: 1489:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489:

CAAnACGTAA TTTcatgatG AAAGTGGTCG ATAATTTCTT GAAACATCGC TTTcAGTAAT 60

30 AACGCCTGCT TTAAGGTCAC GTTCCGCATA GGTGTACTGA GGATGTTGAT GT 112

(2) INFORMATION FOR SEQ ID NO: 1490:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490:

CAGAACGTTT AAAACAAAGT TGGAAAAGTT TTCTAATCGT ATTAGCTGCA TGTTTAATAC 60

45 TTATTATTGC AAGTGAAACG CTTATTTTCC TTTAGTCATT TGACCGATGT TAAAGAGGTG 120

AGATGGTTAT TTAGAATCAT TGTATTGATT GTTTTTGCCG TAGTGATGTT CACAATTTAT 180

ATCTCTTATC ATCATTATAT GAATGACTTT TTAGTTACTA AGTTATTTAA TATTTCCGCA 240

50 GCGACGCCAt AGTTATTATG TCTAT 265

(2) INFORMATION FOR SEQ ID NO: 1491:

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- (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491:

10 CAAAAATTGGC CAGGGGCTCA TCCAATATTA AAATAGGCGT ACGAGGGATT AATAGACCAC 60
 CTAATGAAAC GCGTTGGTTG TTGGACCTCC AGATAAATCC TGGGGGTCGG TGG 113

(2) INFORMATION FOR SEQ ID NO: 1492:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492:

25 ACTAAGAAAA TCCGAAATCT TTTCCGCTTC TTTTAAATAC GTAATACTTC CTTTTTTTCG 60
 CTCTAAATGT TTGGCATTCA ACTCATAACT ATTCATTAGT TTCGTTAAGC CTTCTGCATG 120
 ACTCTCATTT TGAGAAAAAA TTTCCAAATG GTACGAAGAT GTTTCAGGGT TATTCACTGA 180
 30 GCCACCTGCC AGAAAAGCTC CTCTCAAGTA ACTGCGTCTC ATTTGTCAT CTTGAATCAT 240
 TGAAATGATC AATTTTCATGG CGnnAAAATG CCGTCT 276

(2) INFORMATION FOR SEQ ID NO: 1493:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493:

45 GATGACGAGC GCCAATTATG TCACTTTTAT GGCAAAAGCT GGAAGTAAAC AACCAAGCCT 60
 GCCAGTAAAA TTGGCAATTG GGACGTTCTT AGCAGGTGCG TCATACATAC 110

(2) INFORMATION FOR SEQ ID NO: 1494:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494:

5 AAAAAAAGG TTTTACCC GGAATCCAA AnTTTAAATC CCTTAAAAA AATTCGGCC 60
 AACCCCAAA CCCAAGGTTT TTTCTTAAC CTTGGAAnTA ACCAAGGTTT TTTTCCAAA 120
 AAATTTTCCA AAAAAGGAAT TACCCAAACC CTAAAGGTT TAAAAATTGG GGGGGGAAAA 180
 10 AGGCCCTTTT AGGGGGGAA 200

(2) INFORMATION FOR SEQ ID NO: 1495:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495:

20 AAAAAATTTG GTGCATTTAT CATATGGAGT ATTAATCTGT AGAAGTAAAG GCGATATAAA 60
 TGTTACTTTG GTAATAAAGA TTACAGCGAA CGTTATTATT GCTCAGGTCA GATCAAGAAA 120
 25 TTGGTGTCCG GGTGACAAGA CTTGGTGGCG CGGTGTAGTT TGTCAGTTGT GTGGTCATCT 180
 TAAATAACGC TATCGTACGG TGTGTATCAC ATGAAGGGAC TCTTACTAAT TCTGCAAGTA 240
 30 CACGTCACGC nnt 253

(2) INFORMATION FOR SEQ ID NO: 1496:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496:

40 ACGCTAGCTT CTGAAAAAAT AAGTGAAC TAAGATGCAAT GAnCCTATTCT CTGAATGATA 60
 45 TTAGACGTAG CGCACCTGGT GCAGAAGCC AATAAAAAGA CAAG 104

(2) INFORMATION FOR SEQ ID NO: 1497:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AGGGAGGCGC CCAAATGGCT CTATATTAAA AAAGGACTCT CAGAGCATTAT ATGAAAAGTT 60
 GAAGCTCAAA AGGAAnCGAA AGAAACAAGT ATCAAAACAT 100

(2) INFORMATION FOR SEQ ID NO: 1498:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498:

TGGAACCTTG GGAAGTCAA ACGGTTGTAA TCGTTGAACA TAAAGTTAAA CACATTCTGG 60
 ATCATGTCCA nCGCGTCCAT TTGATGGATA TAACGGGAAT A 101

(2) INFORMATION FOR SEQ ID NO: 1499:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499:

AGTTCTGGTG CATCGTTTTT CATTGTATTT GTGACGATTA TCATTCCAGC ATTAGAATAT 60
 TATGCATTAT ATTTAGGTGT GATAGGTGCA TTTATAGGTG GTTTAACTGT TTATACACTT 120
 TCAGGTG 127

(2) INFORMATION FOR SEQ ID NO: 1500:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500:

TCCCCGCTTT AATACCTTCC ACGATTTCTT TAATTGCTTG CGGTTGGTCA CCTTGAGGCT 60
 CAAAATCAGA ATGTATTTTA AAAGGATAAT GTTCAACCAT TGTCACATAT GCCTCCTCTT 120
 TCAACGTATT ATTTATATTT CCGCTCAACT CTTTGCTTTC TCATnACATA TnTTAGCAAA 180
 GTAGTCACAC AAAAaGCAAA CGTTkGTTTCG TAAAAATGTC GAACAAaGAA AnACAAACAT 240

AAATACACAT TATATTAATC ATCATTTTGT TTCAACAAAT TTGTTTGAAA CATTATTTTA 360
 AAGTTAATCT TAGCGATCTT CATCTTGATG TTTATGAAAT TCGAGTTGAT CTATAATTAA 420
 5 ATAACCAGCT AATAATGACA CTACATCAAT AAAAATAATC CACTCGTTAT GGAAATACTC 480
 TTTATAGATT GAGGCACCAA TTAAATTAA TGTCAGAATA GTACCGACCC ATTTACTTCT 540
 10 TGTTATTACA CTAAATAATA 560

(2) INFORMATION FOR SEQ ID NO: 1501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501:

ATTAAATCAT ACTnACAATT ACCGATGACA TTATTCCAAT TCAATCTAAT TCCGTGATGA 60
 AAGAGCCACG TTTTGGTTAC TTCGTGGGCG TGAATTATTA TG 102

(2) INFORMATION FOR SEQ ID NO: 1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502:

TATGGTAGCT CCAAATGGTT GTATCGTCAC ACCATCATCT TCAAGTGCAA TGCGATGTAA 60
 TCGATTGGCT GTTGTCTCTG TTACCCATAG TACTTTTTCA TCTGTACTTA AAGCAATACC 120
 40 ATTTGCTACG CTAATATTTT GAATGATAGG CGTCACTGTT CTAAAGTCCG GCGAAACATA 180
 ATAAACGCCT CCTAGTGGAT TGGTAGAGTA TCCTCTAAAA TCTGTAAAAT AAAATCCACC 240
 TTTAGAATCA AATACCATGT CATCAATACA ATATGCTGTT GAAAGATCTT CAATAATATC 300
 45 TTGTAAGTTG TCACCATTTT CTGTAGCTGC AAAAATGCCT CCGGAGATT TAAAATCTCC 360
 nAAAATAACC AACGnATAAA TCGGGCAnCT TATGGAATTG 400

(2) INFORMATION FOR SEQ ID NO: 1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503:

5 TACAGGTAGT TAACAGTTGA TGTTAAATGG CGTACTGGAT TCTTTACGCA CGATTTTTTG 60
 TTAATAAGTA TGGGATAGCA CATTACTATA TCCTACTTAC GACTTATTGG ATATGTCnTA 120
 GCTATTCTTA AGCTCGAAAA GTTTCACAGG ATACATAAGG GACCAACT 168

10 (2) INFORMATION FOR SEQ ID NO: 1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504:

CTACTGATTG TGTAATGTCG TTGGTAGGCT TGGGCTGTAC GCAGTATTAG GTGTAGGCAA 60
 CTTGGCTTTT GGCATCTACC TTGTATGTGT CGTGTATCTA nGGCTGGGGC TTGCTCCTTC 120
 25 AGTTGTTAGA CAGTAGGGGG TAATCTCAGG GGTGCAATGT ACTCCCTCCG TCCTAAAATA 180
 CTnTATATGC TCGTGCCGAA TTCCTGCAGC CCGGGGGATC CACTAGTTCT AGAGCGG 237

(2) INFORMATION FOR SEQ ID NO: 1505:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505:

CGCATTTACC ACCATATGAT GGATCCAnCG ACGTTTTAAT AAAGATAAAA GTGACAGTAG 60
 40 CGGGAAAACA GGNCCATAAT TCACATCTCT TTTGAAAAAT ATGTTCAAGC TAGGATCATT 120
 AGGAGAGTCA TATTAATAAT AAAAATGTTG CAATCAATCG ACGTGC GTTG AATCTTAAAT 180
 45 ACATAATAAA TGTTGTAGAA GATATGGGT 209

(2) INFORMATION FOR SEQ ID NO: 1506:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506:

AAAATGTGGC TATTGATTTT GACTTGAAC TTTTGAACA TTTCTCTCAA GGATTTAAAT 60
 5 GTAGGTAACA GGCAGGTAC TACGGTACTT nCCTATTTT TTATGCAAAT TTAAAAAAC 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 1507:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507:

20 AATGACAAGG TCAGCATTAA AACCATTAA AAATAACGC GTTATGGTTA CTGGACGTAT 60
 ACAACGTGTT TTGTTTAAAA ATTATTTAGA TAGACATAGC ACATTTAAGC CGAATGTAAG 120
 GATATTATTA AAAGAnGTAT TTGT 144

(2) INFORMATION FOR SEQ ID NO: 1508:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508:

35 CCGATTGAAT CTGTGTACAC TTCACCAAAG ATATCTTTCT TCGTTTCTTC AGATAAACTT 60
 TCCATTGCTT TCTTATCAAC ACTTGTTTCT ACTAATAAGT GTGTTAATTT GTGCTTnTTA 120
 40 ACAAACTCAA TAGCTTGTC 139

(2) INFORMATION FOR SEQ ID NO: 1509:

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509:

50 TCTGCCTGCC TCGGCCTCCC AAAGTGCTGG CATTACAGGC ATGAGCCACC ATGCCTGGCT 60
 55

CAAGTTAAAA TACAGATGTA AGACTTGACT TGATC

155

(2) INFORMATION FOR SEQ ID NO: 1510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510:

ATCCCAATGC TAATGAATTT GCATATACGA TAAATAATGC TTTTATCAT CAATAAAGCT 60
 ATGAATCTTT CAAGATCTTC ATTGAAC 87

(2) INFORMATION FOR SEQ ID NO: 1511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511:

ATAGGCGTTT ACCAGTTATT TTCGAATCCA TATAATTATG TTTGTCCGTT TGGTTTAATC 60
 CAATTAATTG ATTAAGTTTT TCCAATTCCT TTTTTTTTAA TTAAAATTCC AATCCTTAAA 120
 AAAAAATTGA AAAAAACCTT AAAAAAATT GGTTAATTTT CCCAAGGGAA TTAAAAATTT 180
 TGGGGTTTTT TnAGGnCCCT TTTGGGAAAA ACCCAAC 217

(2) INFORMATION FOR SEQ ID NO: 1512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512:

TGACATTGCA TCGGATTATG TTACATCAnG GACAACGGGC CTCAAAAAGC GGTGCACAAA 60
 CGTTCCGTAA TCATATGCCA GTGCAATCGG ATGTAAAGAG A 101

(2) INFORMATION FOR SEQ ID NO: 1513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513:

GATTTTATTG AAATGATTTT ACCTGTGATC AATTATTGTA ACAAATCTAC AATAAAATTG 60

10 TCTTACTGCA TGACCTAATA AATAGCAAC AGATATCATA CACACTTGTA ATTT 114

(2) INFORMATION FOR SEQ ID NO: 1514:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514:

ACATATACAG GTACGTGTTT AGTCCGTCGT ATACTGCAAA ATTATGTCCG ATGAAATTAG 60

25 GGGAAAATTG TAGAACG 77

(2) INFORMATION FOR SEQ ID NO: 1515:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515:

CCTTATAAAG TTAATGCAAG CAACATGGAC AAATTATTAT TTGAATAAAC TGCAAGAAAG 60

40 ACAACAATCA TTCTTCGGAA TGCTAGGAGA ATATATTTTA GA 102

(2) INFORMATION FOR SEQ ID NO: 1516:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1516:

CAATTTTAAA TAGGATTTT AAGACCTTGG TTGGGTTTTG GTACAATTAA TGGGGACATG 60

55 ACTAGGTCTT GCCACGTTTA TATGCATCT 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1517:

GTAAGAGTGC ATAGTTTTTA AATGTTGCTT GTCTGGTnTC ATTTTGGCAC CATAcAGTTC 60
 GTACCTGGAT TAGGGAAATG CCAAATGTCC GCGTAGTGAT AT 102

(2) INFORMATION FOR SEQ ID NO: 1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1518:

GAGAACTCCT TACCACAATC AAAAGTAATT GATTTAAATA TATGAGAAGA TAAAATGAAA 60
 AGGTGCAAGC AGTATTAAGA ATTTAGGTAG CAAGAAAACA AGAAGTGGTA CATAcGATGC 120
 TAACCTAAAA AGAATTGGAG ATTAAATGA TTATTAACTT TGAAACACAA CAAATACATT 180
 TTGATTTAGA ACATGAAATT CCTATTTTC AAGCACCTGA GAAAATAGG ATACGCTTAG 240
 ATATTGATGT TCTCAATAAA AAGCnAATTT CTAATATTAT TAATGTTATA TTTAATAACC 300
 AATCAAAGAC GAAATGTACA TTTTGTCTG AATACTTATA TCCTGTTAAA TTTAGAGAAA 360
 AAACAAGAAT TGGTCGTTTT TTTAATATTA CTAAGTGGTA CGAAGAAATC CATTCTACCG 420
 ATGAGAAGTA TGTnATTGCA ACTATTAA 448

(2) INFORMATION FOR SEQ ID NO: 1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519:

ATGGACGAAA GAAGATGTCA TTGCTTTTGA AAACCTAACA AATATTAAAG TAAATTTAAA 60
 AGGTAGCGGT TTTGTGTCCC ACCAATCAAT TAGTAAGGGA CAAAACTTA CTGAAAAAGA 120

ATTCAAATTC AGATGGTnAA GAAGAAATCT GACAGTTAAA ACTGACAGGG ATAAGTCGGG 240
 ACTnAACAGG AATGGGCTAC nTTTAAATTT AGGGATGGTA TTGGGCCACT ATTTGGTTTT 300
 5 TGAC 304

(2) INFORMATION FOR SEQ ID NO: 1520:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520:

ATGACGTCGC ATGCACGCGT AcGTAAGCTT GGaTCCTCTA GAGCGGCCGC CCTTTTTTTTT 60
 20 TTTTTTTTTT TTTCTGTTGG CCTTTGATAA TTTTATTGGA TCAGTAACAA CTMTTGTGT 120
 TTCAACTAAG ATAGCTAAAA TTCTAACT TATATGTAAA AATTACACTC CATTTTAGCA 180
 CAAATGTTAA CAGAAATTAA CAGCACAGTG CCATGAAGAA ATGAnAAATA CACAGCTTTG 240
 25 GTAGGGnAAT GGTCTGGAA ATAATGTAAT GCCAAGTnTC TGATCATTTA ACATATCACT 300
 CACCTCCTTC TTCATCTGAT GT 322

(2) INFORMATION FOR SEQ ID NO: 1521:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521:

40 TAAATACAAA CCCTTTAAAC ATATTTACTA AGTCGTTCAA TTGTTGATTT GATAAnTGAT 60
 GTGATGTGGT ATTTTGCATC GGTCTGCTT GATTCCAGAC ATGTC 105

(2) INFORMATION FOR SEQ ID NO: 1522:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522:

55

GATCGTATTT CCCAGATGTA AATTCnGTGG ACAATTGGCG TCAAATAGCT TCTAGTGG 118

(2) INFORMATION FOR SEQ ID NO: 1523:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523:

CnGCATATAA TCCCGCGACA TGTCTTTTAC GGGTGCACTT GTAATATTAT TACCCCCCGT 60
 ATAACCCATG TATATCTATA CTTTACCACA TAAATAATT CCGGGACTAT TTGGCACATG 120
 TTTTGGGTGA ATTTCTTTAG TGGCACACCA CCCCTGG 157

(2) INFORMATION FOR SEQ ID NO: 1524:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524:

ACTGAGGTAG GTTATGTAGG ACGAGATGTT GAAAGTATGG TTAGACATCT TGTGATCCT 60
 TGAGTAAGAT TAGTCAAGGC CG 82

(2) INFORMATION FOR SEQ ID NO: 1525:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525:

GATACAAAAA AGAAGTTCAA TTTGAACTAT GAAGAAATTT ATATTTTAAA TCATATTTTA 60
 AGAAGTGAST CTAACGNAAT CTCATCTAAA GAGATTGCTA AGTGCTCAGA GTTCAAACCT 120
 TACTATTTAA CTAAAGCTTT ACAAAGCTA AAAGATTTAA AATTGTTATC AAAGAAAAGA 180
 AGTTTACAAG ACGAAAGAAC AGTTATTGTT TATGTTACAG ATACACAAAA AGCAAATATT 240
 CAAAAACTGA TTTCAGAATT AGAAGAATAC ATTAAAAATT AAATCAAGGT TAATTGCGTT 300

AAAATTAAC TAAAATTTAA ATATTGAAGA GCTTAATTAA

400

(2) INFORMATION FOR SEQ ID NO: 1526:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526:

ACTGTCTAAT ATCACTCCC TTAAAGTGTT TTTCATATTT TTCTATTAAT GTTCATATTG 60
 TAGGGTGTTG AATGCATCTA AGCATTCNAA GTTATTCTCC AAGTTCATCA ATTTCAAAT 120
 GGAAC 125

(2) INFORMATION FOR SEQ ID NO: 1527:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527:

CATGTTTATT TATGTTTCGG CTTTAATGTT GAAGAGTTTT ACAAAGTTTA CCGATTGCAT 60
 TTTATAATTT TAATGCATTA TTGGAGCATT GGCTATCATC TATTACTGCG NA 112

(2) INFORMATION FOR SEQ ID NO: 1528:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528:

GCGAAGATGA GGATGAGATG ACTAAAGGAA AATATTGAAA AACAACCAA AACTGATGA 60
 ACATTATTAA AAATTTACAA AATCAAATCG ACAACTTGAG CGCAAGAACH AACAG 115

(2) INFORMATION FOR SEQ ID NO: 1529:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529:

5 ATGGATCTTC CGCTTCTCTT AATTGATCAA TTAAATCAGA CATTTCATGT TTTTGTAAT 60
 AATGATTCGC TTTAATGGAT TTTTACATG ACATCATGAT TGCTACATCT TCACGTAATT 120
 10 TTTTGATATC TACTTTTTTC TCTTCCAAA TTAGCTCAAT CATATCTTTA ATAATTTCTT 180
 CTACTTCATC TTTAGGGAAC CAAACTGGAT AGCTACTTAC AATATAATCA TGACCACCAA 240
 AATGTTCTAA CATGATACCT ACTTGTTGAA GCTCATTTT ATATTGATCA ATGACTAATT 300
 15 GTTCATCTTT TGAAAAATGA AATGTTAACG GGATTAATAA ATCTTGTAAT TCATTGGTAA 360
 CCTCACCTAT TTTATCTCGA AAATATTCAT ATTTATnCT 400

(2) INFORMATION FOR SEQ ID NO: 1530:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530:

TAACAGTCAA CCCACCCATT AATATATATT CAACGGCTGA CTGATACGAC GAACGTCAAA 60
 30 GAATATGAGA GGAATAGGA CAAGATCATC ACACATA 97

(2) INFORMATION FOR SEQ ID NO: 1531:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531:

TCATAACGGT GCAACTTAGA GCTGACGTAT AGTTCATTCC AACTATATAC GATGTATCAA 60
 45 CACCATGTTT CAGTTTTAGG TTAACGATAC TGTATACCGT ATTATGTCAG nGGCACCTTA 120
 TCTTCACGTA CTTTACGGCG AGATGATGAC 150

(2) INFORMATION FOR SEQ ID NO: 1532:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532:

5 ATTCAATTCTG CTAACCAAGTA AGGCAACCCC GCCAGCCTAG CCGGGTCCTC AACGACAGGA 60
 GCACGATCAT GCGCACCCGT GGCCAGGACC CAACGCTGCC CGCCTATCC TGAAGCCAAA 120
 GGAAATGAGA TCGGAATT 138

(2) INFORMATION FOR SEQ ID NO: 1533:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 460 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533:

20 GGGGnCCnGG CAATGGAGGC GTGCTTGGAT GGTGCTTGA ATCATCCCTT TGGCCTCGAT 60
 CATAAGCTTA AACTTTTGGT GCTGGnGCCA CTGGAGGGAA ATCTTCAATT CTGGCAAATG 120
 25 GTAATTnCCT ATACCAACAT TTAAGGCATG TGGTAATGCT GGCTACTCCC GCTTCGTTAT 180
 CAGCTACATG ACAAATACAG ATGCCATCAC CTTTGCCTCC ATTTTAATCG TTGATGCTTG 240
 GAAATGTTTT TTGTAAATAT CAATGTTATC CTTGCTGTA TGTATCGCAT TTATATCTGG 300
 30 TAGCAAAAAT GTTCCAACAG AAAGCCCTAT ACCTAGTTCG GCAGCTATTT TGGCAGATGT 360
 TGCGCTACTA CTTAATAACC ACATTTCTGG AAAATGATCA TGTGTGGTGC ACTACGATCG 420
 ACTTGCTTAT CTTTATTGTT AGATAATACG GAATACGnAA 460

(2) INFORMATION FOR SEQ ID NO: 1534:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534:

45 TAGCTAATA AATAGTTCAC TTTTCCATTT TGTGTAGTCA GTCATTGTA TTCTTCAATT 60
 TGCTCTTCAT TTAATGCCGC ATAAGCTTGA TCAATAATAT TTGGATTAAG TTGTCCAATA 120
 50 TACTCTAACT GGTCATGATA AACAn 145

(2) INFORMATION FOR SEQ ID NO: 1535:

55

(A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535:

10 ACGCGATTTA ATCGTTCGTT CCAACGATGT CCACTCCCCT ACTAATAATT AAAATCATT 60
 CAAATTATTT CAAACTTTAC AATTnAACT AACAGTTTTTC TCAATAAAAT GCAAGCTTTT 120
 CTCATTTGTT ATTTAGAATG ATTATGATTT A 151

15

(2) INFORMATION FOR SEQ ID NO: 1536:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536:

25

ATAATAGAAT CATTACAAAT TATTTTCAGAC TTTACAATTA AGACTAACAG TTTTCTCAAT 60
 AAAATGCAAG CTTTTCTCAT TGTTAA 86

30

(2) INFORMATION FOR SEQ ID NO: 1537:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537:

40

ACCAAAGTGT AAAGCCATAT ACTGAACATA TTGATAGCAT ACTCAATGAG ATCAAATTAC 60
 ATCGTGAATT TATTATAGAA GTACCTTATA TGAATTCAAG GAAATTTGAG CTAAGTATTG 120
 CTAACATTGA ACAACTTTCT GTCGAATGTC ATTTTAAGCG AACAGTCGA AAGTTATTTA 180
 TAGAAAAGCT TAAAAGTGTT CAATATGATT TACAAAATAT ATTAGATGGC GTAACACnAG 240
 AGGGTACTGA TGGTTAAAC AGTTTATGTA ACAGGTACA AATCATTCGA ATTAAACATT 300
 50 TTTaAAGATG ACGCACCTGA AGTACATTAT TTAACAAT TTATAAAACA TAAAATTGAA 360
 CAACTGTnGG ATGAAGGATT AGAATGGGnG TTAATACAAG 400

(2) INFORMATION FOR SEQ ID NO: 1538:

55

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538:

10 ATATCGTTAC TGCTGTATGT TTCAATATCT ATATTCATAA ATTTCAAATh CTGACACCTC 60
 AATTTCTTTA AAATAAGGGG CAGAACCCAC TATGACTATA GGATCTCTCA CAGGTCAATT 120
 CGCAAATCAC TCGTGC 136

15

(2) INFORMATION FOR SEQ ID NO: 1539:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539:

25 TAAATATCTC GGCACAATGA TGCGGGATAT TTTTTTACAA TAGGCATAAA GGCTGGAAAA 60
 AACATATCTA GTGCTATGAT ACTTA 85

30

(2) INFORMATION FOR SEQ ID NO: 1540:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540:

40 ACAATTTGTT TATTTCAACA AATTATCTTT ATTCCACGAT GTGCACAAGT GGTGAAATC 60
 AGCTGAAGAC ACG 73

45

(2) INFORMATION FOR SEQ ID NO: 1541:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541:

55

TGCAGGAATT CGATATCAAG CTTATCGATA CCGTCGACCT CGAGGn

106

(2) INFORMATION FOR SEQ ID NO: 1542:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542:

ACATCAACTC ACCCATAATA TATATTCACG GCTGACTGAT ACGACGAACG TCAAAGAATA 60
 15 TGAGAGGAAT AGGGACAAGA TCATCAC 87

(2) INFORMATION FOR SEQ ID NO: 1543:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543:

GCTTATTCTG AAAAATATTT AAATTGAAGA AAAGAATATT CTAACCTACGG AAGTGGTATT 60
 30 AACTAATAAC TAGTATCCTT TATAAATAAA CATAAAAATA TTCAAACGAA GGTCTACTAA 120
 ATAACCTATCC ATAAAGTGAG TATAAGTTTG TTTGTAAAC TGAAGTAAAA AGCATAAGGA 180
 ATTACACTTT AAATACATAT AGTACTTACG AATAGAAAAT AATCCCTTCA ACAGTAATTT 240
 35 TTAAACAAAA ATAAGTGTTG TTTTATGTTG ACTCTACTAG AATAACTTGA TATTATATAA 300
 AAGTCGTCAA ACGGCACTAA TATTTAnnAA ACAAATGTTT TAAGTTGTTG GATTThAAAA 360
 TATTGAATTA AAGTGTAAT TTGGACTATT GGAAATTGCG 400

40

(2) INFORMATION FOR SEQ ID NO: 1544:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544:

ATAACGCTAA TCAGCCACAT TCAGTATTGT TAAATGGACA CACAAGCAGT TGATGAAAAT 60

55

(2) INFORMATION FOR SEQ ID NO: 1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545:

GGCTGTTATT GTTGTGGAGT TAAAAATGAA GGAAAATTAT AAACATGGTA AGCGTGTTC 60
 TCGTATTACT TTACTIONAAC NAACGGTATA ACCATACCTA ACTTAGTA 108

(2) INFORMATION FOR SEQ ID NO: 1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546:

AAATATGTTT CATATATTAT GAATCTAGCC TTAATCATAT TGCATTCAAA ATAATTTTAA 60
 AAAATGAAAA GAAAGGATTT AGCATGCAAA AATTCAAAGA CTTTTTTTAC GATGATTTAT 120
 CGGTTACACG AGGAAATTAT TTTTAACTT TAATGGCAGC ATTTTTTATT ACTATCATTT 180
 TATTTATCGG CATAGTTGTC AGTGAAGTAC ATTTACTTTA TAGCATGCTA ATTGTATTAG 240
 TAGGTTTAAT TCTATTGAGG CTATTCAAAA TCAATTTATT CTCTTTTAAA AAATTAACAT 300
 TGTCTCAAGT TATTTATATT ATAGGCGGTG CACTATTAAT TTATGGGTTA GATAATCTTT 360
 ATTTATATTT TCATGACGTA CCGGCAATGA ACAACAATTA GAGCAAGCAA TACGGAAATA 420
 CACCATTCTA TATTTCTATT TtCACTGTaC CATCATCCCC GCTATTGTGG aAGAAaTTGT 480
 TTTtCGCGGT ATGATAATAA GGGkTATCTT CAGAAAACAC TTGTTTTTtag GGTTAATTGT 540
 GTCTAGTTTA GTTT 554

(2) INFORMATION FOR SEQ ID NO: 1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAAAGCAACA CTTTAAATCC CTTTGAACCT TAGTTTATCC GCTAAATCAT AAGCTTCTTT 60
 TTTGCTACTT ACAAAAATCA ATCCTTGTA AATTTACCT GAATATCCAT AGTAATCTGT 120
 5 CTTTGAATA ATATAATTAA CTCTTTCATC AGAAGTTAAA TATCTCAGTT TAGTTACATC 180
 ATCTTCTTTA ATACCTTGAT GTACATAATC AGTCACACCA AAATAATGAA ATGGGACATA 240
 10 AAATATCACT TTCTAATGCT GCTTGTAACC TTATTTTATA TGCAATATTA TAATCAAACA 300
 GTTCAAATAT ACTTAATTCA TCTGGATCTT TCTGGTGGTA GGCAGGTCAT TCCCAGCAG 360
 AACTTAGGGT TTGGAGGTAG GTTAAATAC TCGGTTGGAT 400

15 (2) INFORMATION FOR SEQ ID NO: 1548:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548:

CGCTCTAGAA CTAGTGGATC CCCCAGGGCTG CAGGAATTCG GCACAGCATA TCTAGTATTT 60
 TAGGACGGAG GGA 73

30 (2) INFORMATION FOR SEQ ID NO: 1549:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549:

GTATCCAAGC AGCTTTTAAA CAATATGGCA TAAACATTAT TAACGGCTAT GGTTTAACTG 60
 ATGGCACCTC TTG 73

45 (2) INFORMATION FOR SEQ ID NO: 1550:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550:

GTAACATGTA TAGTGAAGTG ACTACTAAGA AGnCGTATTG TGATATTGAT AGCAGCTGAT 120

(2) INFORMATION FOR SEQ ID NO: 1551:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551:

GGTATGTATT AATTAAAATG TGGTCATGAT TGAAACAGCA ATGTAAAAAT AGCACAACAT 60
 AATTnATAAA GGAGAGAAAC GGCATGCATG AACAGATTT TAGAATTTTA GAGGGTCAAG 120
 ATATTACTTT GCCAGAATTA GGTAGAGAAT TAGAnAATAT TACAGGACAT ACGATTGCTG 180
 ATTCTACTGG CG 192

(2) INFORMATION FOR SEQ ID NO: 1552:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552:

CTAAGTTAGA TGCTAGTATA CAAGATTTAC AACAAAAGGT ACTGGAATCG AATTGTGAAC 60
 TAGACAAACT AAATC 76

(2) INFORMATION FOR SEQ ID NO: 1553:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553:

TGTGTTGGGG CCCCGTATAT TGAAATTTG TTATAGGTGT ATTTCTTTGG TTAATATTG 60
 TTATATAACT TGTAATTTTA GGATGTTGAT TTTGCTTACC TTGTCTGCTA TGTAATGTCA 120
 CATCAACATG ATThA 135

(2) INFORMATION FOR SEQ ID NO: 1554:

- (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554:

10 TTTGAnATCA AATTCACCTC GCAAACGTGT CCAAGCGTGA GCAAAGGGCT AGATGATTAA 60
 TAGTTGCCCC ACTAACGGGA TCGCCCCAGT TATCCAACCTT ATCT 104

(2) INFORMATION FOR SEQ ID NO: 1555:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555:

25 AATAAGAAAC AnGACACTAG CTCACCACGA CGCGCACGGC CTGCGTGTA AATGTTGGT 60
 GGCGCGGGTT GGAGATCGTG TTCAACCAGA GCAGAAAATA 100

(2) INFORMATION FOR SEQ ID NO: 1556:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556:

40 CAATGAAATT ATTTATTATT TTAAGTGCAT TAAACCCCGA TGATGGCTGT CCGGTACCAG 60
 GTGCATTTTG GTGCCCATGG TTTACC 86

(2) INFORMATION FOR SEQ ID NO: 1557:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557:

55 GTCATGTTCC CATCAAACT AATTTGTACT TACTAAAGGC TCAGCAGCGC AACAAATTAGG 60

(2) INFORMATION FOR SEQ ID NO: 1558:

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558:

AACTGGTTAC AGAAATACCA CGTTCTTGTT TCAACTTTCA TCCAGTCACT TGATCGCAAA 60
15 TTTACCAAGTC TTCTTCCCTT TA 82

(2) INFORMATION FOR SEQ ID NO: 1559:

- (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559:

CCACAGCGGC ACTATAGCCA GCCCCTAATA TATACAGTAT TTGCATCTGA CTCATTGGTT 60
30 CATAAGTATA TGCACTGA 78

(2) INFORMATION FOR SEQ ID NO: 1560:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560:

ACCATTTGCT AACTTTTTAG CAGCGCAATG TTCTTATTAA CTGCTTACGC CATCTATAAA 60
45 AATAAACGTT CAACAA 76

(2) INFORMATION FOR SEQ ID NO: 1561:

- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

TTGGAACCCA AATTTTTTTTA ATTTTCCCAA AAATTGGGGG GGGACCCCCA ATTCCCTTAA 60
 GGGTTTTCTT TGGGGGCCCG GGGTTAATTC CACCCGGGGT TAAAATTTTC CCAAAAATTA 120
 ATTTTnGAAA AGTTTTAATT TAAGGAAACC CATtnGTCCG GAATTTTTTAC CCCATCCTTA 180
 TGGGGGGTCC CAAAGATTCC 200

(2) INFORMATION FOR SEQ ID NO: 1562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562:

AACACAGAGA ATAACCAAGA GAAGACGTTT TCATCTGAAG AAAGTAACAG TAMGCCATT 60
 ATGGAAGAAA ATCAAAACGA TGAGATAGTT ATAAAAGAAG ATTCATATAA TCCATTCGTA 120
 ACGAAAACAT CTGAAAGTTT AATAGCTGAT GATGAATCTT CTGGTTATAA TAATACACGT 180
 GAAAAAGATG AAGACTACTT CAAAAACAA CAAGAAATT TACAAGAAAT GGATCAAACA 240
 TTTGATTCAA ATGATGGTAC AACTGTGCAA AATTATGAGA ATAAAGCGTC TGATGATTAT 300
 TATGATGTAA ACGATATTAA AGGAACAAAA AGTAAAGACC CTAAACGAGG AATTCCATAT 360
 ATGGAATTGT TGGnCAGTCA TGGAACGTTA TTATTGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 1563:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 454 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563:

TCTTCATCAT CTTCTAATTT ACCAGCTGGA ATTTCTAGCA ATGGTTTTTC TACTGGTTTA 60
 CGATACTGTT TCACTAATAC GACTTCTTTT TTAGGTGTCA CTGCACAAAC ArCAACTGCA 120
 CCATTATGAT AAATAATTC TCTTGTGAC GTTTCACCGT TTGGTAATGT CACTGTATGA 180
 ATTTCTACAT CTACAATTTT GCCATTATAA ATAAGTGTTC GATCAATTGT TTTTTCATT 240
 AAATCCATTA TAATCACGTT CCTTTAAATT CATATTATAT ATTGATACAC TATGCTTGTT 300
 AGCTAAAGTG TATCGAAAGG AGAACAGACA TGCAAAAAA TATATTAAAA AGTGGTATTT 360

AAATTATAGG ATTGTGCTGT TGAAAATGGG TATC

454

(2) INFORMATION FOR SEQ ID NO: 1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564:

ACATCTCGCA TCGTCACGAC TTGCTTGAAC CACTAGCAGG TCAAACAAAG CTGTACAGGC 60

AACATCTGC 69

(2) INFORMATION FOR SEQ ID NO: 1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565:

TCCAGAACCA TTTTAAATCC CGGGAAATAT AATTACCTCC ACTAAGTAA TATATCCAAG 60

CCAAGACTAA TCCTCCTTAA GCCGGTTTAA GTAACCAGGT TGAGAAGGAT TTTTGG 117

(2) INFORMATION FOR SEQ ID NO: 1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566:

TATTGAGATT AACAGTCTGG GAAAAATGAA CAGCAATTGT nTAATGTGAC GATGCTGATT 60

ACITTTTAAAC AGTATCATTT AATAACTCAG AGATGCGCTT TAT 103

(2) INFORMATION FOR SEQ ID NO: 1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567:

5 AATGGATGGG ACAGCAATTA GTGCATAACG ACAATATATG CTCAATTTGT CGGCAACTGG 60
 TTAAGAATCG TATTGTCACA A 81

(2) INFORMATION FOR SEQ ID NO: 1568:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568:

20 AATGGATTCA GTAGGTATTG GTGAAGCGCC AGACGCAGCT GATTTGAAAG ATGAAGGTTC 60
 ACATACTTTT AGCATACCTT 80

(2) INFORMATION FOR SEQ ID NO: 1569:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569:

30 TTTTAAATA CGATTTTAAG GAGGCCATTA TAATGGCGAG TAAAAGTAGC GAATTAATGG 60
 35 TTTTGTTAG GAATTGGTCG TTTAGGCATT CAGGA 95

(2) INFORMATION FOR SEQ ID NO: 1570:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570:

45 CCCAATAAAA AAAGCCTGTT GTCACAATGG TCATAGACAC GTACATACTT TAAAGGTTTC 60
 50 TGTAATATAA ATATTTTATA TGCCACTTTA AAGTTGGnAC GTTCGTATGT TGTACTAA 118

(2) INFORMATION FOR SEQ ID NO: 1571:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 104 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571:

GACTTGATCA ATGAAGCATT GTGTGACAAT TGGTCTGTTT GCACACCGCA CGGATTGnGC 60

10

GTCATTTATT TGTACTAATT CAAAAACAT TGTTGTTTTTCTAG 104

(2) INFORMATION FOR SEQ ID NO: 1572:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572:

CCGAAGTGTGTA ATGGTCCTAA TGTTTTACTC ATACCATATT GCGTAACCAT TGAGCGGCGA 60

25

TTGTGTTGCA CGTCGAGCAT TGAGACCGTT GTACTCGTAA nGTATATCTC TGTACACG 118

(2) INFORMATION FOR SEQ ID NO: 1573:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573:

AGGGATCAAA GGTCCATCCC CCATGCATTG GATAGTGGGG GATGACTTTT GATCCTATGT 60

TCCAGTTGCT TATT 74

40

(2) INFORMATION FOR SEQ ID NO: 1574:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574:

AACCTTTTGA GTAAATTCAC CAATACTCAT CCCCTTATCA TTTAACAAAC TTTTATTAAT 60

GTTTTTGGTT ATATTATGAG TCTTTACTGC TTTTAGATTG TAAAAATTAT CGTCATAAAT 120

55

GTAATTAATG TAATAATAGA AAAGTGTATA TATCTCATAT CGCCACCTGC TATACAACTT 240
 ATTAAATAAT TAATTCCAAG ACATATTAAT TATCTAATTA TAACCTTAGT TnACGTTATT 300
 5 ACATAATATA AAAATATATA ATAACCTTATC CnCCGGCnCC T 341

(2) INFORMATION FOR SEQ ID NO: 1575:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575:

ACGTGTACCA ACTTTTGGGC ACCATTGATA ATANGTGTCA TAGGGTGA CT CAGCATAACG 60
 20 GGCAAGCCTA TTAATGATAG CCAGATTAAG ACATACAGTA CATATGTTT 109

(2) INFORMATION FOR SEQ ID NO: 1576:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576:

GCTAGATTGC GGAATTAAC AATCATCAGC GATTTAATAT TTGCACTGGA GACGTCATGG 60
 35 TAATAAAAAA TTGATGAGA 79

(2) INFORMATION FOR SEQ ID NO: 1577:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577:

ATGATGGCTA TCATGAGATT GAGATGATAA TGACAACAGT TGATTTGAAA TGATCGTGTA 60
 ACTTTTCAT 69

50 (2) INFORMATION FOR SEQ ID NO: 1578:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 104 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578:

AAATTGTCAC TnCAGGTCAT AACCAACCAG GTGGGACTGC ACGAGCGTTA CTAATGATCC 60

10 AACGGTCTTG CTTTGTGATG AGGCAACAAG TGCACTTGAT CCGC 104

(2) INFORMATION FOR SEQ ID NO: 1579:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579:

GCTCAATAGA TACAACTATT AGGACAACGG ACTATCGTTT ACAATTTATT CCAGATAAGG 60

25 ATCGCGCAGG TCGTATGCGT AACTATGCA 89

(2) INFORMATION FOR SEQ ID NO: 1580:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580:

TTGTCTCTAA TAATGGnTTT GGCTTTTCT AAAATTTCAG ATGTGGGTGC TGGTGAAGCA 60

40 CCGACTGGTT AATTTTCTTG TCGTCACGGC CACTTTTGT TT 102

(2) INFORMATION FOR SEQ ID NO: 1581:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581:

AAGGTGCTGT TATTAGGATA ATGnATTTAA ACCCCATGGT ATGAAGGATA TCTGGAAGTT 60

AGATTGGATA TCCCTTAACC ATGGGGGGTT TTATTTTGG GG 102

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582:

TTCAGGGGAG CTGAACATAT TGACGACTTT TGGGTCAATT CATTTTGCAT TTTACTTTTA 60
 AATGCGTTGT TGCATGTAAT TGTATTAACG ACATACATGG TGGGGCTCTA AATnAATGCT 120
 TGACTAATTT CTTGGATGGA GACCACGATT TACCAACTCA 160

(2) INFORMATION FOR SEQ ID NO: 1583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583:

TAAAAGCAAG TACATTAGAG GTTAGATCAC AAGCTACTCA AGACTTGAGT GAATATTATA 60
 ATAGACCGTT CTTTGAGTAT ACAAATCAGT CAGGATATAA AGAGGAAGGA AAAGTGACGT 120
 TTACTCCTAA TTATCAACTT ATAGATGTAA CTTTAACTGG GAATGAAAAG CAAAATTTTG 180
 GTGAAGATAT TTCTAATGTA GATATATTTG TTGTAAGAGA AAATTCTGAT AGATCTGGTA 240
 ATACAGCTTC AATTGGTGGT ATTACTAAAA CAAACGGTTC AAATTATATT GATAAAGTAA 300
 AAGATGTAAA TTTAATAATT ACTAAAAACA TCGATAGTGT TACATCAA 348

(2) INFORMATION FOR SEQ ID NO: 1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584:

AGCCAGCAGT AGATAGATAT ATTAATGAAT TCTTGGAGAA AGGTAGCTCA AATTGTCCAA 60
 TTGAGATATT GAA 73

(2) INFORMATION FOR SEQ ID NO: 1585:

- (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585:

10 GTAAGGAATG GTCACGTATT CCACACTTCT ATATGAATTA TTATGTATAT CAATACGCAA 60
 TTGGTTACAG TGCAGCTCAA AGCTTAAGTC ATCAAATTTT AHCAGAAGGT AAGCCAGCAG 120
 TAGATnGATA TATTAATGAA TTCTTGAAAA AAGGTAGCTC AAATTATCCA ATTGAGATAT 180
 15 TAAAAAATGC TGGTGTAGAT ATGACAACAC CTGAACCAAT TGAACAAGCT TGTGAAGTTT 240
 TTGAACAAAA ATTGA 255

(2) INFORMATION FOR SEQ ID NO: 1586:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586:

30 TTATTAGGTG AHTCCATTGG CAACATTGAT TGGTTTGTCA TTAGGACAAA TTTTATTATA 60
 CATTGGCGTT ATTTTACTA TCTTATCTGG TATTGAATAC TTTTATAAAG GTAGAGATGT 120
 TTTTAAACAA AAATAAATAT TTGTTTATAC TAGATTTTCAT TTTCATATGG AATCTAGTTT 180
 35 TTTTAATCCC AATTTTAGAA ATTAGCCACG CAATTGTTTA TAATGATATA TTGTAAACAA 240
 ATATTTGTTT ATTTTTTTAG GGAAATCTG TAGTAGCATC TGATACATTG AATCTAAAAT 300
 40 TGATGTGAAT TTTTAAATGA AATACATGAA AAAATGAATT AAACGATACA AGGGGGATAT 360
 AAATGTCAAT TGCCATTATT GCTGTAGGCT CAGAACTATT 400

(2) INFORMATION FOR SEQ ID NO: 1587:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 561 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587:

55 CAAAGCGTCT ATTATTGTTT GATTTTGATG AAACATATTT TAAACATAAT ACAAATGAAG 60

AAGTGATCAC TGCTGTATTG ACAGGAAGTA CATTTCAAAG TGTCATGGAT AaaATGGATC 180
 AAGTTAATAT GACGTTTAAA CCATTACATA TCTTTTCTGA TTTGAGTTCT AAAATGTTCA 240
 5 CTTGGAATAA TGGCGAATAT GTTGAATCAG AAACATATAA AAAGAAAGTC TTGAGCGAAC 300
 CATTTTTATT TGAAGATATT GAAGATATAT TACGTCATAT TTCTGCGCAA TATAATGTCTG 360
 10 AATTTATTCC ACAAAGAGCA TTTGAAGGTA ATGAAACACA TTATAATTTT TATTTTCATT 420
 CAACAGGTAA TCACAACAAT GATAGTCGTA TCCTAGAAGC ACTnnTCAGA TACGCAAATG 480
 ACCAAACTA TACAGCGAGA TTTAGTCGAA GCAATCCATT AGCTGGTGAT CCTGAAAATG 540
 15 CGTATGATAT TGACTTCACA C 561

(2) INFORMATION FOR SEQ ID NO: 1588:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588:

CCAACAGTTT TATCATTATG GCAAGTTCTG TTAAACCTGC TGAGAGTTAT TTTGCACTGA 60
 30 TTGCAAAACC AGAAATTGG 79

(2) INFORMATION FOR SEQ ID NO: 1589:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589:

GCAGATATGC AGCAATTTAT AGAGGACTAG TAAACGCATA TATGACTTAC AGCTTTCAGA 60
 45 CAAATAGCTT TGC 73

(2) INFORMATION FOR SEQ ID NO: 1590:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TCATTTTATG GTTGATCATA GGCCTCGTCT TTTTCCTTGG GGATTTTATC TTTAAATACA 60
CAGATTGGCG C 71

5 (2) INFORMATION FOR SEQ ID NO: 1591:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591:

ATACAATACA ATTCACACCA TATATGGATA AAATGCAAGA TGCAATTACT GCAGTTGCAC 60
AGTGCAAGTA GCAATACC 78

20 (2) INFORMATION FOR SEQ ID NO: 1592:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592:

30 CCAATTAATT AAAAACC GGA AAACCAATTT TTTAAACCA TTAAGTTAAA AATTTTTTAA 60
AATTGGGGCCC CAAACCTTGG AAAAAGGTTT AATTTTCCTT TCCCAATTTT CCCAAAATTT 120
35 TTAACCCAA AAATCCCGG TTTTGGGTTA AATTTCCCTn GGTTAAAT 168

(2) INFORMATION FOR SEQ ID NO: 1593:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593:

TGCTAGAAAG TATAGAACCT GGTTCAAACG CATGGTTTTA TGTCCTTTT TAAACnGATG 60
50 TTTATTAAAA AAATATGGAA ATTGGCCACG TCCGCCAATT TCCTTAGAAA AGAACGT 117

(2) INFORMATION FOR SEQ ID NO: 1594:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594:

AGACGAAGCC AAAAAGTTAT TCGCCAAATC TGAAATATTT TCAAAGACCT TAAAGGCGTA 60
AAATAC 66

10

(2) INFORMATION FOR SEQ ID NO: 1595:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595:

ATTTTATTTA GGCCAATAAC TGrCTACTTC TGAAATAAGT TGCTTTGCAT AGTCTGACGC 60
GGGATGTTTG GATAATATCT TCTGTGTTAT TGCATTGCAA 100

25

(2) INFORMATION FOR SEQ ID NO: 1596:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596:

GACCAGACGG CCGTAAACCT GGATGAAACC GTCCATTAGA TTCTGAAGTT GGTATTTTAC 60
CTAGAACGCA TGG 73

40

(2) INFORMATION FOR SEQ ID NO: 1597:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597:

CTTTATAAAA TTGTCTTTGA CTAACAGGAT TTTCAACGCT ATTCACAAAC CATGGTTTAA 60
CATATT 66

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598:

TATGGCACCC TCTTTGATnT TGTGACCGTT TTTGGTAATT CACCATTATT GTACGAACCA 60
 TGGAAATTCGC TGCCTTCCTT TAGGCAATAA CATAATTATA TTTATCCCCT TCTTGTCACCT 120
 AGAGGTGCTG ACAACACCA 139

15

(2) INFORMATION FOR SEQ ID NO: 1599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599:

CTCCTCTGCA TGCACATCTT GTTGTAGCAA GGTTCACATG TAATTTATTA AATCGAAACT 60
 CTATCCAACCT ATGTTATAAA GTTCATTCTA AACAAATnAG T 101

30

(2) INFORMATION FOR SEQ ID NO: 1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600:

TTGTACCAAG GTTCACATGT AATTATTAA AGCGAAACGC GTATCCAACCT ATGTTATAAA 60
 GTTCATTCGT AAACAAATAA GTATAAAAT TCAATATTTT TATTACTAGA ATATGGTTAA 120
 ATACATTTAT TTCTTATAAA AATTGTGATGT TTAAGATATT TTGCCAAATT GA 172

45

(2) INFORMATION FOR SEQ ID NO: 1601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601:

5 TTGGCACTGG CCGTCGTTTT ACAACGTCGT GCACTGGGAA AACCAAAACA CGACGTTGTA 60
 AAACGACGGC CAGTGCCAAG CTGTCATGCC TGCAGGTCGA CTCTAAGAAG GA 112

(2) INFORMATION FOR SEQ ID NO: 1602:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602:

20 TGCAATGGTT AATCATCTCA TATAACAACA CATAATTTGT ATCCTTAGGA GGAAAACAAC 60
 ATGACAAAAC ATTATTTAAA CAGTAAGTAT CAATCAGAAC AACGTTTCATC AGCTATGAAA 120
 AAGATTACAA TGGGTACAGC ATCTATCATT TTAGGTTCCC TTGnATACAT AGGCGCAGAC 180
 25 AGCCAACAAG TCAATGCGGC AACAGAAGCT ACGAACGCAA CTAATAATCA AAGCACACAA 240
 GTTTCTCAAG CAACATCACA ACCAATTAAT TTCCAAGTGC AAAAAGATGG gCTCTTCAGA 300
 GAAGTCACAC ATGGATGACT ATATGCAACA CCCTGGTAAA GTAAATTAAAC mAAATAATAA 360
 30 ATATTATTTT CAAACCGTGT TAAACAATGC ATCATTCTGG AAAGAATACA AATTTTACAA 420
 TGCAACAAT CAAGAATTAG CAACAACGTG TGTTAACGAT AATAAAAAAG CGGATACTAG 480
 AACAATCAAT GTTGCAATTG AACCTGGATA TAAGAGCTTA ACTACTAAAG TACATATTGT 540
 35 CGTGCCACAA ATTAATTACA ATCATAGATA TACTACGCAT TTGGAATTTG AAAAAGCAAT 600
 TCCTACATTA GCTGACGCAG CAAAACCAAA CAATGTTAAA CCGGTTCAAC CAAAACCAGC 660
 40 TCAACCTAAA ACACCTACT 679

(2) INFORMATION FOR SEQ ID NO: 1603:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603:

50 CATTTTAATT GATATAATTT AGACTTTAAC ATTTTCATGCT GTTCACGGTT TTAATTTGAG 60
 55 ACGTCATTTG GTATAACAAC TATAC 85

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604:

ACTGGTGTGA ATAGCTCCAG CAATTTCTTT AACCGCGATC ATAATCAACG TCACCTTTTA 60
 ATTTGCCA 68

(2) INFORMATION FOR SEQ ID NO: 1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605:

TGGGGGGTnT TTTTGGGTTG GGTAAAAA AGGGAATTGG CCCAAGGGGG GAATTCCTT 60
 AAAAAAACC CCAACCCCT TGGGAAATTA AAAATTGGGT TAACCGGGA 109

(2) INFORMATION FOR SEQ ID NO: 1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606:

GCTTATATAC ATGTTCCATT ATAAAGGAG TACGAACGAA AGTAACGCAT GACGTTAATT 60
 TAAAAATATT GTAATAATTA TGGATTAAAT TAAAAACCA GGGGTATTCC AT 112

(2) INFORMATION FOR SEQ ID NO: 1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607:

GTTCAAGTTG GTAACCTAAC AACACGnAAT TAGTTTAAAC GTTTGG

106

(2) INFORMATION FOR SEQ ID NO: 1608:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608:

CACACTGATA CCATAGGATT TATGATAGAT CAACAGCATG ACCAAATGTA TGACCTAAAT 60
 TTAAAAATTT ACGTACACCT TGT 83

(2) INFORMATION FOR SEQ ID NO: 1609:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609:

AAAAGAATAA AGTCACTGAA CAATGGTCTT TCACAATGAT GTTGCGTCAA TGCACAAGCG 60
 CATTATGTnt GTGACTTGGG CATTTTGGCT TATCAGCTGA ATATTATACG CATTACATC 120
 CCAATTAACG TA 132

(2) INFORMATION FOR SEQ ID NO: 1610:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610:

TTTAATGCAT ACGCTTCTCG CTTAGCAATT TCTTTGCACG TCTAACAAGC ATTAACGCTC 60
 TTAnTACTAT AATCACAACA AAACCAGCGA AATATAACAT GCGTATA 107

(2) INFORMATION FOR SEQ ID NO: 1611:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611:

5 TTGCGCACCTG GTATCGTTCA AACCACCAAT GATGGCCCGT CTCGCCGTGG CAACAGCCGA 60
 AGACCGCAGG TAAACCCTGA ACGC 84

(2) INFORMATION FOR SEQ ID NO: 1612:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612:

20 ACTCACATGT ACGATAACAC CCTTCGTAAA TCCATCTTTG GTTTGCCAAG TTCGTCGTTG 60
 TAAACTGTCT ATACTCGTTA AACCGCTACA TGTTTTCCTA AAnCCTGTGC CTAAATGCTT 120
 TACTGAA 127

(2) INFORMATION FOR SEQ ID NO: 1613:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613:

35 CGTTCAACTT TTTCAATTTT TAACGGCGTT TTACTATCTT TATCTGTAAC TAATTCAACT 60
 CCAAACATTA AGCCTCGTCC TCTTACATCA CCAACATTTT GATGACGCTT CAGCGCATGT 120
 40 AACTGTTTC 129

(2) INFORMATION FOR SEQ ID NO: 1614:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614:

50 nCAACTAGTG GATTTAAnAT AnACATAATT ATAAATGCAA ATGCTAATAG CTGAATACCC 60

55

GCACTAGGTG CATAATTTGT GTATTGAGCA AATAAAGCTA ATACAATGAT TGTAATTCCT 180
 TTAATGACAA ATAAAGGTAA ATTTAATCGT TTAAAGGTT GGTAAATTAA AAATACAATT 240
 GCAGCTATAT GCGAGCCACT AACTGCCAGC AAATGATATA TACCTATCTC TTTAACACGT 300
 TCCTTAAATT GCTCATTAAC TTCTTTTACG TCACCAGTAA TCAATGCC 348

(2) INFORMATION FOR SEQ ID NO: 1615:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615:

GAGCTCCACC GCGGTGTCGC CCGCTCTAGA ACTACTGGAT CCCCCGGGCT GCAGGAATTC 60
 GGCACAGCAT AT 72

(2) INFORMATION FOR SEQ ID NO: 1616:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616:

CATCACGTTA AATCATAACG CGTGACGTGC TTTTGCTATT TGTCTCTCGG TATCTCTATA 60
 TCT 63

(2) INFORMATION FOR SEQ ID NO: 1617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617:

ATTGAATTCA AGGGTGAAC TCATGAATTG GCTGGAAAAA GGTAGATTTA ACTGGATGGT 60
 TGNAGCCATA TATCGGTGCG TTTATTTATT TGGTATTTTA AAAATCAACC TCG 113

(2) INFORMATION FOR SEQ ID NO: 1618:

- (A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618:

10 GTACAATAAA GTGGTAAACA ACATGCCAAT GGAAAAAGGG ATTAAAGGTG TTTATGTCAT 60
TCTTAAAGAT AGTAACGGTA 80

(2) INFORMATION FOR SEQ ID NO: 1619:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619:

25 ATCTTATGTT TTTTTCCTAA AACTTCTGCT ACTTCATTTA TTTGATGTAT GGTAGATAAT 60
TCTGTTTGGA TACTCATATC AACTTTTTCT ATCATATCTG AAATCTCTTT TnTGGCA 117

(2) INFORMATION FOR SEQ ID NO: 1620:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620:

40 CGATAAACCC TTCGTAATCA ATCTTTGGTT TGCCAAGTTC GTCGTTGTAA CAGTCTATAT 60
CGTTAAAAGC TACATGnTTT CCTAAGCCTG TGCCTAATGC TTTACTG 107

(2) INFORMATION FOR SEQ ID NO: 1621:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621:

55 AATATCGTGT CTCTGTCCAG TGCTGTCCAA TCAATTTTGA TCCACCGATT GTCATACGTA 60

(2) INFORMATION FOR SEQ ID NO: 1622:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622:

ACCATCTGAC ATCATCAATT ATGAATTAAT GATGATATTA AAAATAAATT TGAACATTG 60
CCAATTGATA GTGCC 75

(2) INFORMATION FOR SEQ ID NO: 1623:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623:

TACCTGTGTA TCAGCTCTAT TAACAACCTA ACATATGTGA ATAATTTGCG ATCCTTGTTG 60
ATAATGCTGT AATTGAC 78

(2) INFORMATION FOR SEQ ID NO: 1624:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624:

GCAAGCTTTT GCGGCTTCTG ATGCACCATT AACTTCTGTA ATTAAACACA CAAAGTGAAA 60
CAGGTAGGTA ATGCAAAACT GCAACGGACA ATCGA 95

(2) INFORMATION FOR SEQ ID NO: 1625:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTGCGATTA CACAGTAGTG AATGAGATAT TTGACATGAA AGCTCCTGCA GCTTCTAAAG 60
 AAGAGTTAGC AGGTTT 76

5 (2) INFORMATION FOR SEQ ID NO: 1626:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626:

AAAAGCTAAA AAAGATTATC AGGTGTATCA CAAACTCAAA TTCTCATTAC CATTTATCTC 60
 AGTGTGAACG TCTTAATTGA GAACTAATCT NAATTGAGAT ATTAGTCATA TAAGGATGGA 120
 20 CAAGCA 126

(2) INFORMATION FOR SEQ ID NO: 1627:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627:

TGATACGATA GAACATAGTT CAGCACATTG TTTGTTGAAA TTGGATATTA CCGCCATTTT 60
 35 TTCACAATAT CAATAATACC TGAACGTGTT GGTThTTCCA CATTATGATT GTACAT 116

(2) INFORMATION FOR SEQ ID NO: 1628:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628:

ATTTTGTCTT ATCTTGAACA AATCCGATTT TTCTCAGACA CTGAATCCAA AGTATTCATG 60
 50 TACCATAAAC CATCTGCATG TTGATTTATG C 91

(2) INFORMATION FOR SEQ ID NO: 1629:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629:

ACAGAAAGTC AAACAGTAAA AGCGGCAGAA TCAACTCAAG GTCAACACAA TTATAAATCG 60
10 TTAAATACT ACTATAGCAA GCCAAGTATA GAGTTAAAAA ATCTTGATGG TTTGTATAGA 120
CAGAAAGTGA CAGATAAAGG AGTATATGTT TGGAAGGATC GAAAAGATTA TTTTGTGGC 180
TTGCTTGGTA AAGATATTGA AAAATACCCT CAAGGTGAGC ATGATAAGCA AGATGCATTT 240
15 TTAGTCATCG AGGAGGAAAC TGTTAATGGA AGACAATATT CAATTGGTGG TTAAAGTAAG 300
ACAAATAGTA AAGAATTTAG TAAAGAAGTC GATGTTAAAG TAACAAGAAA AATTGATGAA 360
TCATCGGAAA AGTCTAAAGA TAGTAAATTT AAAATTACTA 400

20

(2) INFORMATION FOR SEQ ID NO: 1630:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630:

GCTTTCCTTT TCGAAATCTA TAAATCTAAT CCATTGAAGT AAATAATTA TGATAATTAT 60
TAATTCTATA ATTGTnGTIA TCTTTAAATA ATTTGGAAAC CTTTCATAAT CTAAACCAA 120
35 AAAGAAAGTT AGACATGAAA AAAGTATCAT AAATAATGAT GCTAAACTTA AGGCTTGTGC 180
ACCTGGCTTT CGAAGAATGT CTATATTTTC CTTAGTAGTC ATATTTACCT ATCTCCTATA 240
CATTGATTTT GTAATAGCAT ATTAAGTATT TAAAGTTATA AGTACTTAGA TTCTTTTCGA 300
40 TTAAAAGTAT AAAAGCCTAA AATTATCTTT ATATTATTAT TTGATGACAA CTTTATGGTC 360
TCTATTGTTT TTTACTTAAA CGCTAAAAAG CTAnACAAAG 400

45

(2) INFORMATION FOR SEQ ID NO: 1631:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631:

55

TCTAGAGCGA

70

(2) INFORMATION FOR SEQ ID NO: 1632:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632:

15

CAACGAAGAT ATTCAAGTGT TCACTCATT TTTTGGACTG CTAATGAAAC TGATTCTTGT

60

GG

62

(2) INFORMATION FOR SEQ ID NO: 1633:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633:

30

CTAATGATTA GATTCAAAC AATAAAGACT ACAAAAACAA GTTGATAATG GTAAAGATAT

60

TATCCAACCTT GACATCTAAA G

81

(2) INFORMATION FOR SEQ ID NO: 1634:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634:

45

AATTCACCT TTGTCTAGTA ATTTATTTGT GTAGTGAAT CATTAATTGT TTAAATATCT

60

AGT

63

(2) INFORMATION FOR SEQ ID NO: 1635:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635:

	ACCAACTAGC TAAATGCCAG CGCGGnATCC ATCTCAnAAG TGCACAGCAA GACCGTCTTT	60
5	CCAACTTTTG AACCATGCGG TTCAAAATAT TATCCGGTAT TnAGCTACGG TTTCCCGAAG	120
	TTATCCCACT CTTATAGGTA GGTATATCCCC AGTGTTACTC ACCCGTCCGC CGCTAACATC	180
	cAGAGAAGCA AGCTTCTCGT CCGTTCGCTC GACTTGCATG TATTaGGCAc GCCGCCAGCG	240
10	TTCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA	300
	TACTAAATAA TGTTTGTAAC TAATAGTTAC GTTTTTGGAA TTAACGTTGA CATATTGTCA	360
15	TTCAGTTTTC AATGTTCAAT AATGTTCAAT CTCTTTTATT CTACTTCATT TATTTCTTGA	420
	AGTCAATAAC TTTTGAACG ATTACTTTAT TTATTCTATA TTGTTTTTAT AGTTATTTCA	480
	ATGGtAAGTn TTACACTTTT GaaATTCTTC TTTAAAAACA ACTGCGTCGt TTTGaCGcT	540
20	TTATCaTATT ATCmACTTTG GGaATTTAAA GTCAATAAC	579

(2) INFORMATION FOR SEQ ID NO: 1636:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 69 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636:

	TCGACATTAA GCAACGTTCT TCGCAAAGG TAGCGAGCGA CACGAGTTAA CTTTGCACGT	60
35	TTCATTATT	69

(2) INFORMATION FOR SEQ ID NO: 1637:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 116 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637:

	CTGTGACTTC GTCGCGATGA CCTTCGCCGT TGTTCTCATG GTAAGCTTTA AGTATCGTCG	60
50	ATGCAGTCnG TTCGCCATGT GCGCCAGCAG ACTGGTTGTA ATGTCGCCTC GTCCGT	116

(2) INFORMATION FOR SEQ ID NO: 1638:

(i) SEQUENCE CHARACTERISTICS:

55	(A) LENGTH: 71 base pairs
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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638:

10

ACAACATTTA GGTACTTTCA CGCATATCAC TACAGCTCAA CGTGATGATT TACCAAATCA 60
AATTTACAAA G 71

(2) INFORMATION FOR SEQ ID NO: 1639:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639:

25

GCGTGGCTTT GTGATTAACA TTGACAAGCA CGTGCAACAA CATATTCGAC GCGATAAAGC 60
GACATCTAAT ATT 73

(2) INFORMATION FOR SEQ ID NO: 1640:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640:

40

CGCGATCATT TTCATTTCTA ATTAATCTTC CAAGTCCTTG TCTAAAACGT GTAACGTCAT 60
CAGGTAATAC ATATTCCTTG AAAGTTGAAG TGAATTCAGA ATCCATAAGC CAATATTTTG 120
CATTATGCTT GTTCATAAAC GGTAACCTCG CTATCATCAC ACATTTAATA CCATTGCTT 180
GAAAATCAAA ACCTTCAAAA AATGTTGACG TACCAAGCAG TATGGCCTTA TCAAAATTAT 240
TAAACTGTTG TACTATTTTA TAATTTTGGT TCTGCTGTG TGTTAATACA ACATAATCTT 300
CAAATCTGG CAATTCATTT AAGCATATCT TGTACCATAT GCATCATTTT ATAACGCTA 360
AATAAGACTA AACATTTTGA TGACGTTATA GTCGTATATn 400

50

(2) INFORMATION FOR SEQ ID NO: 1641:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641:

ATTGTTGTAC CATGTATACT AACAATTGTA ATGTCTCATT TCAGTAAACA AAAAGCGAAA 60
 GACATT 66

(2) INFORMATION FOR SEQ ID NO: 1642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642:

ATTTGTCGG GAATAAATTT TGCCATTACA TAGAAATATC TAATAGATAA CGAAAAAGTA 60
 TCGTATGTAT TTTTAATATA GTGTAATAA TTATATGTAA AATAAAATGT AGGTTTTTAG 120
 TTAGAGGCAT TATAAGAAAA TTTTGAGTAT AGGTTAGCTT TTAATTATGA ATCTTATTGA 180
 AATTTGATTA ATAAAAATAT GATAGGGGAT TAAATGAAA CTATTTTATA TCGTATTTCT 240
 TATTATTATA TGGCTGAATA TATTTTATAGG AAATGAAATC ATCCATACAC TGACTGTTTT 300
 AATAACAACA TTGTATATTG TTAATTCACG AAGGGGATT AAAAATGACA GAGTTGAATA 360
 ATATTATAAA CGCGCTTGCA ATCTTTGTTT GAGTCCGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1643:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643:

AACTAGAGGA GGACATCCTA ATGGAAGCAA AACCCGTTGC TAGAACAATA AGAATCGCAC 60
 CTCGTA 66

(2) INFORMATION FOR SEQ ID NO: 1644:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644:

TATCAATTTC ATATGCGATT TGGCCTTGCA ATAATTAGGT CTCACCTTGC CATATCTTTA 60
 5 CCTAAGCAAT ACTTG 75

(2) INFORMATION FOR SEQ ID NO: 1645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645:

CATTCTCCTG CATCATAAAA ATCAACAATT GTATCATCAA AGTGTATCAA AATATTTTAA 60
 20 TATCCCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646:

AGTGACACTT TCGTTCCACC ACATCGTAAA GAAGTACTTC AAGCACGTGA AGATGACATC 60
 35 AAAGAAAAAG TTG 73

(2) INFORMATION FOR SEQ ID NO: 1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647:

CTGTGATTGG TGTGTGATT GTCTTGCTTC CTGGTTGTCC TTCTTGTTTC GCTCGCTCTT 60
 50 CGCCGGGTTG T 71

(2) INFORMATION FOR SEQ ID NO: 1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648:

10

AACTATAGAA AAATTCGGAA TTATACCAGA AATGGAATAT GAAATGGAAG AGGTTAAACA 60
 AAnCGAGCAA TATATTAGAG AGCAAGAAGA AGCTGGAACA ATAGAGGCGA TAACA 115

(2) INFORMATION FOR SEQ ID NO: 1649:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649:

25

TGTTGTCATG ATCTGAAAAG TCAAAGTCAA TAGAACATTG GCTTTGGCTT TTTATTTGG 59

(2) INFORMATION FOR SEQ ID NO: 1650:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650:

ACCGATAATA GTACACGGCA TAATGnAACA ACTTGGCATG CACCCTTTTT ACGTTCCTTT 60
 ATCTCTGCAT GATTGTCATG TTCATCATGG TTTGGCTTGC ATTAATAGAG AGGGTTGACG 120
 CAGAA 125

40

(2) INFORMATION FOR SEQ ID NO: 1651:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651:

55

TGATTACGC GAATGCCACT TTTACTACCA ATGTTCCCAA AGCTGCTTCT GACAAACGCC 60
 ATTGTACTCT G 71

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652:

10

TCACTACATG CACCATAAAT ACAGTATGAA CGTATTGAAA TGGGCATTAC ATGATACAGA 60

- (2) INFORMATION FOR SEQ ID NO: 1653:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653:

25

TTAATTGAAA CAATTGACAA ATGCAATTTG ACGCCAAACT TTGAACTTTG AATGGATTAT 60

CACATTATGA TTGTTTCATCC ATGGnCAATT AGCATGGACG TATTACATTC TGGATTATCA 120

AGC 123

30

- (2) INFORMATION FOR SEQ ID NO: 1654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654:

40

CTATGACGTC GCATGCACGC GTAACCTGGG CCCCTCGAGG GATCCTCTAG AGCGGCCGCC 60

CTTTTTTTTT TTTTTT 76

45

- (2) INFORMATION FOR SEQ ID NO: 1655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655:

55

TTTTAAATTT TCGTGAAATC GGAAATGTAC GATTAGTTAT TAAGCGTTAG AATGTGTGAT 120
ATGTGAACCT GGTATTGACG GCGCT 145

(2) INFORMATION FOR SEQ ID NO: 1656:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656:

TTTAGAATTC CAATACGCTA TTGCCAGCGA TTTAGCCACT TGTGGGTAAT GATATTGAAG 60
GTGTTAGTCA AGT 73

(2) INFORMATION FOR SEQ ID NO: 1657:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657:

CTTCTGAAAA GTAGTAATGT AACCTATTGG ATGCGAATGA ATCCCCAAAT TTAGTGGACG 60
TATGTGGCTT CATCTTCAGA ACCTGTATCT GGT 93

(2) INFORMATION FOR SEQ ID NO: 1658:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658:

AAGTTAACAT GCAAGTTGAC GATGTAATGA CTCAAAAAGA GTGGAAACAA AAACACGA 58

(2) INFORMATION FOR SEQ ID NO: 1659:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659:

TTAATCCAC AAACAAATGT ATGAAATTGA GTCAGTGATA TTAAATATGG GCTTGAAAGT 60
 5 GTCTA 65

(2) INFORMATION FOR SEQ ID NO: 1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660:

TGCATTTTTG TAAGAACGCA AAGCATTGTA AATTAGTTTT TATAAATTAG GATATTATCA 60
 20 TGTGTATTGA AAACAATGAA GTGTGCTATG A 91

(2) INFORMATION FOR SEQ ID NO: 1661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661:

ACATATCTGT CCACACAACA AGGACCATTT GTCTGAAGGG ACAGTGAGTG GGGAAATATGT 60

(2) INFORMATION FOR SEQ ID NO: 1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662:

TGGGGTTTTA ACCAGGGGAC CTAAAACCAG CCCCCATTTT CCAAGTTTGG ACCCCAAATT 60
 CCCNAAATTT AAAAAAATT TGTTTGGGGT CTAAGTTGGG CCGGTGCCTT CCTGCCTAAA 120
 TTTAGCCCAT GTCTAACATA GTACTTTGGG AACGTAAAAG TTAAATTTA 169

(2) INFORMATION FOR SEQ ID NO: 1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663:

	TGGCACAATT GCACCAATTA AATGAATAAC TTTATCATTT TTATATACAG GTACAACAAT	60
10	CGCTTCTTTT ACGAACTCAG ACTGGCGTAA TTGTGTTTCA ATTCTTTCTA ATTCCATTCT	120
	GTAGCCATTC AATTTGATTT GGAAATCAAT ACGACCTTGA ATGAACCATT GACCATTTTC	180
	AAACTTCGCT TTATCACCAG TGTGATATGT ACGAATACCG TCATCGAAAT TAAATACTTC	240
15	AGCTGTTTTT TGGTCATTTT TTAAGTATCC TAAACTTACA CTTTGACCTT CGATAACAAG	300
	TTCACCTTCA TCTGTAGTAG ATAATCTTGC GCCTGGTCTT TCAACGCCAA CAGGTAATGT	360
	CGGATATTGA TCTAAGATTT CTTGTGTAAT TTGAATACTT GTAAGTACTA CCGTAGCTTC	420
20	AGTTGGACCA TATGTGTTGT AAATCGTGGC ACTTGGGAAA CGGTTTACTA ACGCTTTTGC	480
	TGCTCTGTGA GGTAGAATTT CACCACAGAA GAAGAATTCG TTAAGACTAC CATATTGTTC	540
	TTCATTAAGC GTTGGTAATA ATAAACACAT TTCCATAAAT GATGGTGTTG ATACCCAAAT	600
25	GTTAATCGGT GTTGCTGTTA GCATTTTCATT TAATAATTTA GGTTTATTAA TCATGTTTTT	660
	ATCTACAAGA nTnAAnG	677

30 (2) INFORMATION FOR SEQ ID NO: 1664:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664:

40	GTTACAACAA TAGTGGTATA AAACGGGAGC AATTAGAGAT CAATATATGA TTATTAAGAG	60
	CA	62

45 (2) INFORMATION FOR SEQ ID NO: 1665:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665:

55

GTTTACGCAA ATGATAGCTC GGTAAAACAT GAGCAACATG TTGAAGCCAA TTTGGAAATG 120
 TGTATTATCGG AAACCACAAT CCACCTAATA CTGCTAAACC AATTGTTACG ATATTAGCTA 180
 5 AAGCACTTGT TTTTGAATA TCATTTAACA AAGAACCATA ATATGCCAAA AGTTATTAAT 240
 AGAGACGCAC CTAACCATAA AAATATTCCT GACTCTAACC ATTGAACTGC ACTCATTGCA 300
 ACACCTTTAT AAAAATGTCC AACCATAAAA ATAACATA TC 342

10 (2) INFORMATION FOR SEQ ID NO: 1666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - 15 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666:

GTCCAAGAAT TCAAAAACGT TTTCAACTTC GGCCAAAGCC CAATTTnTCT TTGTGGTTTA 60
 ACTTTTTAAT TTGAACGTT TTAGGGCATA AAAAAAAAAA GG 102

25 (2) INFORMATION FOR SEQ ID NO: 1667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - 30 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667:

35 TTGATAGTAG CCATAATCAT ACCACTTAAA TAATATGTTT GATCATCGGC ATAATTTTTA 60
 TTTATTGTCT GTTCGCAATA TTTGAGCAT TATCATAATT ACCACTAGTC ATATCATCTT 120
 40 TG 122

(2) INFORMATION FOR SEQ ID NO: 1668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
 - 45 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668:

AGAGATGAAA TTAAAATCGC AATTGAAAAT TTCAAATCAC GATGAGAGTG GGACAGA 57

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669:

AACTACTGCC AATATTAATA GCATTGGTAC ATCTTAGAGG CATTGAATTC CTTACTCAGA 60
 CTCATAATGC 70

(2) INFORMATION FOR SEQ ID NO: 1670:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670:

TTGTCTGATA TAATCCATT CGATTGGACT CCACACGTTA CACCGATACC TTCTTTACCA 60
 GCCCCGACCCG TAC 73

(2) INFORMATION FOR SEQ ID NO: 1671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671:

GAAGAATTGT ACTGTTAAAG TGACTCTAAA CTATCGCGGA AATAACAGTG AAATCACCAA 60
 TTAGACTAGC GAACTGAAG TCATTAAAAA CAGACATTTG TAGTGGTGCA CTTATCACCG 120
 CAAATACAAG AGAGTTTCTC 140

(2) INFORMATION FOR SEQ ID NO: 1672:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AACAACGTTT ACTATTGGCA CAGAACGGTT GGTACTTAGT CTAATACCAT TGTCAATCAA

59

(2) INFORMATION FOR SEQ ID NO: 1673:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673:

ATCTCTTTGA CTTGAAGGAT TGGATTAAAA TCTTGGTGAT TTGGGCCGTG AAATATTTCC 60
 AGAAAATTCC TCAGACGTAT TAGTATAATT GTAACGnTAC ATTCTAATAT ACCTTTCTTC 120
 GATG 124

(2) INFORMATION FOR SEQ ID NO: 1674:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674:

CACCACCACC ACACACACAC ACACAAACAC ACAACCCCCC CACACACAAA CCACACCACC 60
 AACACACCAA CACAnCACAA AAACCCACCA CACACACCAC ACACCAACC 109

(2) INFORMATION FOR SEQ ID NO: 1675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675:

TnGTCAACTG ATTTATGAAA TGGCAGAGCA TATGGCGTCA AAGGTTCTTA ATCGTTAAGC 60
 CAGACCACTG GAGGACCATT AGATGCAGCG TTGCTTTCAA G 101

(2) INFORMATION FOR SEQ ID NO: 1676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676:

TTTTTAAAT TTGnAAATTT TAGACCTTAT TTCACGTGCG ATTTAATCGA TGTGTTAATA 60
 5 AAACAATACT GGCATTCAAC ATGTAATCCG ATAATAAAAT AAGGTTGCAA TTATGTTATT 120
 GCATATTTTG TTTATTACTT AGAATAATAC GATGGTTAAG ATGAAATATA TGACAAAGAT 180
 AAATAATGAC ATTAAATTCA AGATGTTTAC GCCTTTTAGA TCTTTTTTAA GCATTTTAAA 240
 10 TCCTGTCACT TCKACATTAC CGACTAAGAG TAATAAGACG ATAAATACCC ACCAATTsTC 300
 TTTTGAAAA CTCATCGTCG TTAATGCTAA GACGAATAAT AACAACACAC CCATAATAAT 360
 15 TCTCAAAATG CGAGTAAATA CAACTTCCAT TTTAAAAATA 400

(2) INFORMATION FOR SEQ ID NO: 1677:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677:

TCTTACTCAT GCATATGAGT GCAAGGGCCT GAGCATTTCAT CAGCAAGATT AGAGCGATTT 60
 TTAC 64

30 (2) INFORMATION FOR SEQ ID NO: 1678:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678:

ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTACA 60
 TTTCA 65

45 (2) INFORMATION FOR SEQ ID NO: 1679:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679:

5 AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT TAGCGCGACA 60
 AAGTCCTGAA TTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTA~~n~~AA AAAGTTGGTT 120
 TGTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG AAAGTATTTG 180
 10 TAAACGTGAC CCACTTGGCA GGCAAAACAG TTACAGGCGG TATTATTACA ATCAATGATT 240
 CTGcATGGCA AATGAGTTTT ACAATCAATC GTGCAGCAAC AGTTTGAAAG ACCAACCTGG 300
 AAAATGGAAA TATCTACATG GGGTTTGATG CCTTATGATT CnGGnGTAAA CGGCGGTTGA 360
 15 TG 362

(2) INFORMATION FOR SEQ ID NO: 1680:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680:

AGATACTTCA GATTTAGCAT CATGAAGCAA CTTTAAAGC AATCGCTGAC GCTGGTATTC 60
 30 AGCCCGAGG 69

(2) INFORMATION FOR SEQ ID NO: 1681:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681:

40 TAACCATTTT TTTTGACGTT TTATGTTGTT TTAAGAAATA AATACCAGTT AATGTA 56

(2) INFORMATION FOR SEQ ID NO: 1682:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682:

55

(2) INFORMATION FOR SEQ ID NO: 1683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683:

CCCCAACACA ACAACAACA CACCCACCAC CCAACCCAC CACACCCACC CACCACCCCA 60
ACCCACCACA ACACCACnCA CCAACACACA CCACACAACA ACCCCACAC 109

(2) INFORMATION FOR SEQ ID NO: 1684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684:

ATTATGTTTCG CGATAATTTA AGTAAAAGAA GCACAGATAT TGAATTTGAT AGGAGTAATT 60
GT 62

(2) INFORMATION FOR SEQ ID NO: 1685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685:

CATAAGGTAC TTAAATTAAG GCATATCTGC TGTCTAGCAG TCGCATAAAT CATTAGA 57

(2) INFORMATION FOR SEQ ID NO: 1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686:

(2) INFORMATION FOR SEQ ID NO: 1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687:

CTTTATAGTA TATTGCTTTT TGTTTTTCTT TTTCGTCATA TTTCACCTTTT AAATAGATAC 60
 CTGCAACACT AATTAATATG ATTAACATAA TACTAGTTAA TATTAAnATT 110

(2) INFORMATION FOR SEQ ID NO: 1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688:

AATTACTAGT CTGCTTGTCC AAAGATTATT TATATTCTAG CTCAACATTA ATTTCTTTGA 60
 TTTTGGTACC ATCTATCGTG TCACCCATGC GATGCGGTTG TAGTTTTTTTT GTAAGTTCGA 120
 AAGTATAAAA CTTATCATCT TCCATTTTAA CTACAATTTT ACCTTTTCTA TTATTACAG 180
 CACCATATAA TTTTCTTCT TCCATCAATT TTTT 214

(2) INFORMATION FOR SEQ ID NO: 1689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689:

GCTAGTTGTA ACGTGCTTTT TCACCACCAG ATAAATCATA ATATCTTTTA ACATCTCTG 59

(2) INFORMATION FOR SEQ ID NO: 1690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690:

CCAAACTTTA TAATATGAAA TGCTTGGTAA TTACAAAGAT AAAATCATAC TCACG

55

(2) INFORMATION FOR SEQ ID NO: 1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691:

TAGACAGCAA TCCATTGCTA TAGGGGTGGA TATCTCATTT GCGTTTGGAG CTGTGCTTGT

60

TATG

64

(2) INFORMATION FOR SEQ ID NO: 1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692:

TGCATGGGAT TGCAGCTAAG AGAATCATAA AAATATATTA CTTTAATAAG TGTTAGTA

57

(2) INFORMATION FOR SEQ ID NO: 1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693:

CGATGTGTAC GTCTCACCTG ATTTGCGCAG GTAAGCTAGT GCATATTCAG CACCGCTACT

60

CGCCCAGCCT AGAC

74

(2) INFORMATION FOR SEQ ID NO: 1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

AACITTTTCAG ATGTTGATAG CTATAGATTT AGGCGCTATT CACCAAGTCT ACATGCAATA 60
 5 CGTACGTTAT AATGCACTGC AACGAATCGC GCGTTATGAG TTGGTAATTG TTGTTCAATA 120
 TTGGGTGTAT AGTTTTCAAC GTGGTTACAA GCAACTACCT AA 162

(2) INFORMATION FOR SEQ ID NO: 1695:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695:

20 AATTATCTCT ACACCTTTTC TTTCACATAA TTGACGCAAT ATAATCCCTA TATCT 55

(2) INFORMATION FOR SEQ ID NO: 1696:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696:

30 ATGCAACGTT GGCATTGGGA AATGGTCCTG CCTAAATTAA CACGCAATAA AATGTG 56

(2) INFORMATION FOR SEQ ID NO: 1697:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697:

45 ACTGTGTAGA AGATGCTATT ATTGTAAAAC ATAGTTTTAA TTTTATTTTC TGATATA 57

(2) INFORMATION FOR SEQ ID NO: 1698:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

AAAATTTTCC CCCGGGAACC CGGTTTTTTA AACCCCCCGT TTTAAAAAAA TTTTGGGGGG 60

CCCAAAATTT CCCAAAAAAA NAAAAAATTT TTTTTTTCCC GGGGAAAAA 109

(2) INFORMATION FOR SEQ ID NO: 1699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699:

GTGTTAACGT GGATTATATC AAGGAGCGG TCAGGTACAG TCCACACGCA CAGCGCACAG 60

AAGTATCACA TCCAGTAAAC AAGGCTAGTA CAGCATTGCA 100

(2) INFORMATION FOR SEQ ID NO: 1700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700:

AAGGTTAAAT GAATTAGGTT GATCAATGCT CTATACTCAT TGCTAAGTCA ACGCACCTTT 60

ACCACCTTTT CCCAACTCAG TAAGGCATTC GACGTATTTT TTAGCCAAGT TTACATATCT 120

ACTCTGCAC 129

(2) INFORMATION FOR SEQ ID NO: 1701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701:

CAAGAGGAAC AACTCGGTAC TGCGCATCAG CAGAGATGGC GAAATCACAC TTAGAAGACA 60

AGG 63

(2) INFORMATION FOR SEQ ID NO: 1702:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702:

10 TATTTAATAA ATCTTCAATA CCTTGTTTCAT CAGTTTGTG ATAAATAAGA CCTCTCCATT 60
 TTAAATCTTC AATTAATACA TTCGTCATTA TTATTTCCCTC CTATTTATAA TTATTTATTG 120
 AATACTTGTT AAAATACTTT AAAGKTTTTT GAACGTAAAA AAAACCCTTA CAACAAATAT 180
 15 GTAAGGGCGC GATTGCACGT TACCACCAAA CTAAACATA ATCATAAGAT AATGTTCACT 240
 CTATTAATGA TACGTTCAAT AATAAACGTA GGACATGTTA GTTATAAAGG TGTATTCATA 300
 TTATTAAAAA CACTAGTTCA CAGCGACCAC TAGCTCTCTG ATGATTTCAT ATAATATTAC 360
 20 TTGTCCTTTT ATCCTATTCT GTATGCATTT TCCCTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 1703:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703:

TCAATATTGA TATCGAAACG CTTTGCAGAT TGATATAAAT TATCAGAATC AAGTAATTCA 60
 35 TTTATTTTCT TTGGTGAAAG TACTTGGAAT ATACTATACT GATGAAACT TAAAAATGAA 120
 ATGAAGTATG GAAGTTGTTG CTTTGGGTAA GCAAAATTTT TAATACATAC TGATTAAACT 180
 40 GTTTGTTTAT TGnGAATTGC AACGCATC 208

(2) INFORMATION FOR SEQ ID NO: 1704:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704:

AAGCCGATGT AATTATTTAT GCAACACCTG TTCTAATGCA CAAAGAAATA TCTTAGCGAG 60
 55 CTTATAG 67

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705:

CCAAGTTGCA TGTTATTTTA AGCTGACTTT CCACCAACTT CTGAGTTTGT GGCC

54

(2) INFORMATION FOR SEQ ID NO: 1706:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706:

CAACTACACG AAAGGGTAGT GCTTCAAGAT AATAACGTCC AATTATTAGG AACTGTGGCG

60

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61

(2) INFORMATION FOR SEQ ID NO: 1707:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707:

ACCATTCCAA ATGAACCTAA ACCAATTGAT ACGTTGACGA CAACAGGTTG TTCA

54

(2) INFORMATION FOR SEQ ID NO: 1708:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708:

AAATTTGAAT AACTGTACAC ATTTTTTTGA TCATAGTCTA TATACTTTGT GAATTAATT

59

(2) INFORMATION FOR SEQ ID NO: 1709:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709:

10 GCACAATAGC CAATTAGATG GGGCCGGTGC GGTAACATTT TGCTTCATTC CTGCATTAT 59

(2) INFORMATION FOR SEQ ID NO: 1710:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710:

TTACAATTCA ATCAAGTTCT TCATTATCAG ACGAAGAAAT CCACCGTATG GTAAA 55

25 (2) INFORMATION FOR SEQ ID NO: 1711:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711:

35

TTTCTGCTTA TTGTCATTGC ATATCGAATT ATTAGAAAGT GCAGATTTTC CATCAG 56

(2) INFORMATION FOR SEQ ID NO: 1712:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712:

TAAACCTTTA GGATTGCTGG CAATAGTAGT GCAGTTGGCT GGACTTGTCA TGCCC 55

50

(2) INFORMATION FOR SEQ ID NO: 1713:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713:

5 CAAGAGGATT CGTGCAATGA ATTCATGGAG ATATTTAGAT CTTTCACTGG AGAGAAAATA 60
 AAAAGAAGAA AAGAGTAACC TTTAGATTGC TGGAThTGTG CAGTGGCTGC TTGCGTGCCT 120
 TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC CCGGGGTTTT ATTGTACACT 180
 10 GTGTAGGACG CAGACTTTAT GTGGTTG 207

(2) INFORMATION FOR SEQ ID NO: 1714:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714:

TGGTTATCGA CTGCTCGTAT ATTTTGACTG TTTTGACTGT TGTTCGTA GCAATACTAT 60
 25 CTCCTAAGCC TTTCATTGGC ATTG 84

(2) INFORMATION FOR SEQ ID NO: 1715:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715:

35 GTTTGAATTG ACTGACTTCG TTTTACCGCG TGTTTAATAT TGTTATACAT ATAT 54

(2) INFORMATION FOR SEQ ID NO: 1716:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716:

50 GAAGCCTGTC AGTGGATCAA ATTATTGAAG ATAAGTTGGG TGGCATTITT GGAAAGTCCA 60
 AATGCTGGGA ATGGTCA 77

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

GGGCCCTTTT TTTCCCAAAA AAAAAAACCC CCCCAACCCC AATTTTGGnC CCCCTTCCCC 60
 TTTAAAAATT TAAAAATTGG GCCAAAAGGC CCCCCCAAAA AAAACCCCCA ATTGGAATTG 120
 GAAAACCATT GGAACCAATT CCATTGAACC AGGA 154

(2) INFORMATION FOR SEQ ID NO: 1718:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718:

ATTGTCTACA CTGCCACTTT ATTTTCATTA ACCATTTTCAC AAATGTGTTC ATCATTCAAC 60
 ATGAACATCA ATTGTTCAAT TACATCGACA CCTGATGCCT AAnCACGCAC CTTTTCACA 120

(2) INFORMATION FOR SEQ ID NO: 1719:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719:

TTCAATTTGTT TGTAAGAGTG GCATTTCTAT GTCTTAAAG TGACGAACT TCAC 54

(2) INFORMATION FOR SEQ ID NO: 1720:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720:

(2) INFORMATION FOR SEQ ID NO: 1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721:

TTTGATTAT AAATTGACAT GTAAGTACGA GGCAGCTGTA CCCGATATAT AATTGCTAAG 60
 AGTTAGGGCT G 71

(2) INFORMATION FOR SEQ ID NO: 1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722:

TTTTATCTTT ATTACTAAAA CCAACTGCAC CAAAGTTTGC AGTCATTACC ACACGTTTAA 60
 CACCCGCATG TTCTGCAGCT CTTAAAATAC GTTGTATACC TTCAATTGCA GGCTTCGCCA 120
 TCACTTCTGC ATCGTCTGTT TTACCGAAAA ACACCGGAGA TGCTACACTC AAGACATACT 180
 TGCAATCTTT CATTGCTTCA TCCCAATGTh CATCTTGTGA TAAATCCGCT TCGACAAACA 240
 TTAAATCGCT CTGTGGAAAT GCCCATGTCT TGCATTGTTT NAATTACTTT ATCAGCTTTA 300
 CTTAAATCAA GnatCGTCGT TTGTA 325

(2) INFORMATION FOR SEQ ID NO: 1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723:

CAGTATTGCA GTCACGACAA TGTGATGACT AAATTATCCA AAGTATGAAT TCCATGCGGC 60
 ATTAATCCTA G 71

(2) INFORMATION FOR SEQ ID NO: 1724:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724:

10 TTGCAACGAT ATTAGGCTAT CTAGTCGGCA TATTTGTAAA ACAAGATCCA ATT 53

(2) INFORMATION FOR SEQ ID NO: 1725:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725:

ATCTATTCAT CTTCTACAC GGACAGGAAA TGAGTCCAGT AGATGCACAT TGGGAATTAA 60

25

TCGAAGCTAG C 71

(2) INFORMATION FOR SEQ ID NO: 1726:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726:

CATCTTGCAG GTCTACATTA TAAAATGTGA AGTTTTCTAC GATAACAATT GGGAAACTCA 60

40

GGGGCATCTC C 71

(2) INFORMATION FOR SEQ ID NO: 1727:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727:

TTCnTTTTTA AAAATTCCCC ATTCTTTTT AAATTTCTTT CCCGCTGGAT TAAATGGATT 60

55

TAAAAAATTC CACCCCAACT TAAATTAAA TGGCTTGTGG AAAATTAACG GGATTGGCAT 120

TCCAGCTTAA ATGGTTTTTT TGGAGGCTTC CACGTAAAAA ATGGCGGGTG GCTTT

235

(2) INFORMATION FOR SEQ ID NO: 1728:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728:

15

TAGAGTGGCT ATAAAGCTAA GTTCAATTGA CCAATTACA ACAGGTATT GAGGACAATA

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(2) INFORMATION FOR SEQ ID NO: 1729:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729:

30

ATCACCAAGA AGTTCTAATG CTTGGTATAA ACGTTGAATA CGACGTCGG TATT

54

(2) INFORMATION FOR SEQ ID NO: 1730:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730:

CGTCCCGAAG CGTTGGAGGC GGGAAACATCC AGAGTAATTG GCACAGATTA TGACCATAT

59

(2) INFORMATION FOR SEQ ID NO: 1731:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731:

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(2) INFORMATION FOR SEQ ID NO: 1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732:

TATGTGGTGT TCAATGCACT GGTCAATTATG GTGCATCTTA CCAGATTCGG CATTCTTATT 60
ATAACTATAC TTGTAATAAA TGGCGACATG CAGACACGnC AATAC 105

(2) INFORMATION FOR SEQ ID NO: 1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733:

TTTACGTTCC ATAGCAAAGT GATACAAACG TCAGCATCAA TGTAAGGCAT AGATCATAGT 60

(2) INFORMATION FOR SEQ ID NO: 1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734:

TTCCATCATA CATTGCGGTT TTACTTTTCT TCTGGTATGA TCAAATATTC ACATAA 56

(2) INFORMATION FOR SEQ ID NO: 1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735:

AAATGGGGAT GAAACAGTTA GTGTACAGGT GAAAGCTTAA CAGCAGCTAC AATTGCA 57

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736:

GATTTGCAAT TAAACTTAAA TGTAATTTTT CGGAATGTGT ATTGGTTTA CTTAAAGTAA 60
A 61

(2) INFORMATION FOR SEQ ID NO: 1737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737:

AAAGAAGCTA AAGAAAAAGT TGATAAAACA GCAAAAGTGA TTATTAGCTA CAGCATT 57

(2) INFORMATION FOR SEQ ID NO: 1738:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738:

CAATAATATC GCTAAAACCG CCATTTGTAC CAAATGAATT TGATAATGCT GCAG 54

(2) INFORMATION FOR SEQ ID NO: 1739:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739:

TAGAGCCCAA CCGGCAACCC ATCCATGGAA ATTCACCAA ATAATACATT GACCCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 1740:

(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740:

10 CCTTTTGGn AATTTAAGGG GGTTCCCAAC CAAATTCCCC CAAATTTTTT TGGGTAAAA 60
AAACCCGGCC CAAAATTTA AGGAATTTG GAAAAGGTT TGGTCCCTT TTTTCCCAA 120
GGCCCAAAT TTGGAA 136

15

(2) INFORMATION FOR SEQ ID NO: 1741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741:

25

CATTCAACCA ACGACTGACA ACAGAACATT TAAGACTCTA GGACATTGAT TGA 53

(2) INFORMATION FOR SEQ ID NO: 1742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742:

GCTCGTCTGA TTCAGTCACA AAATTGTCTT GTTATACTTG TCACCTATCA TC 52

40

(2) INFORMATION FOR SEQ ID NO: 1743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743:

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TGTTATTTAA AGAGGCTCAA GCTTTCATAG AAAACATGTA TAGAGAGTGT CAT 53

(2) INFORMATION FOR SEQ ID NO: 1744:

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- (A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744:

10 TCTGAGTTAA AGACGTCTCA CTTAAAGCTT TAGCAATTCC AACAATCAGA TATCTTCACA 60
CGTGTTATAT GTGTCCATTA ATATATCCTG TGGC 94

(2) INFORMATION FOR SEQ ID NO: 1745:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745:

25 GGAAAAAann TTTTAAAAA AAGGGAAAAG GGAATTGGGG TTCCCGGCCC CTTTTTAAAG 60
CCCCCAAATT AAGGAAATTT TAAATTTTGG GGAAGGGGAT TTTCCACCGG TTAATAAACC 120
GCCGATTTTG AGGGGGTTGA ATTAATTGGC CCAAATTTAA AAACCTGGAT GCTGGGTCCA 180
30 ATTTTTTACC GGGACCAATT GGTCTGTCAT GA 212

(2) INFORMATION FOR SEQ ID NO: 1746:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746:

TATCTTCCGA TGAAGAACAA GATGCACAAG AAGTACGCCA ATGATTTAAG AAAGTGGT 58

(2) INFORMATION FOR SEQ ID NO: 1747:

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(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747:

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AAAATTAAGn CCTTTTITAA CCTTTCCTT CCCCAATTGG GGCCT

105

(2) INFORMATION FOR SEQ ID NO: 1748:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748:

15

AGTGCCTATT ACTTTGATTG ATGTCCAAGT TTCCTATCAC ACAACTTAAT TT

52

(2) INFORMATION FOR SEQ ID NO: 1749:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 95 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749:

AAAGCATCAT CCGAACTCCA ATGATTATAC TCCCTAGATA TTATTATGTG ATGCTTTGAG

60

30

CATTAATTAG AGATGGGACG ATTCCATGAA AGATA

95

(2) INFORMATION FOR SEQ ID NO: 1750:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750:

TTGACACATC TACTCACATT AAAAGTAGAT GAAGCGTTGA GATTAACATT TCCACATTTA

60

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CAA

63

(2) INFORMATION FOR SEQ ID NO: 1751:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 116 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

TCGATATTTG AGACACGCTG CTGTAATAAA ACATCCTATA AAGTATATAC CAAGATCTAC 60
 CAATATAAAC AGCGGCTATA TGATATAAAT GCTCAGACAC ACCCnCTGCG ATCCAT 116

5 (2) INFORMATION FOR SEQ ID NO: 1752:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752:

TATGATTAAAG CTTAGTGCAG ATTTGATTTA TTnAACAAACG CTTCACTACA TTAAAAATAG 60
 GGCACTCGCA CATATAGTTG TATCAATAGC CTTTATCAAT TTTTGGGAA GGT 114

20 (2) INFORMATION FOR SEQ ID NO: 1753:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753:

30 AACTTCAAAT GTGCCAAGTG TTGAATCACA TCAAATCAT TTTTATTTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1754:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754:

ACTAATCCCT TGC GTGTTTC CAATCAATTG CATTATTAGT GGCCATTTGT TTGATATAAC 60
 45 TGACAAGCTT TAACC 75

(2) INFORMATION FOR SEQ ID NO: 1755:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755:

GTGAACAAGG GTAGATGTAA ATAGTTGATG CATGTGTACA CATCATAACA AAA

53

(2) INFORMATION FOR SEQ ID NO: 1756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756:

TTATTTGGGC AGGCAAATAC CCTTAATATA TTCAAATCAT GTTAATATCA TTGCTATTGC

60

TAAACC

66

(2) INFORMATION FOR SEQ ID NO: 1757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757:

ATTAATCGGA GCACTTGGGT TCGCAATTTA TGCTGAAATG GATCATTCTA CATCATC

57

(2) INFORMATION FOR SEQ ID NO: 1758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758:

CGAACAATAA CTCTAAGTAT CCAACAAATG CTGCAAGTGT ACCTACTGTG ATTGATCCAG

60

AAATAGCAAG ATATGCACCA ACACCGATGA CAATAATTGG TCCAATATCT GTAAGTGTAT

120

TAATTGCGGC AAAGGAATag GCATTCCATC TTGTATGTTT CAACGCACGT GTTAGGAAAT

180

TAGTATTCTT TTTATCAAAG TTTTTCGCTT CATTGTCTTC AATCGCAAAA CTTTTAACGA

240

CTGAAATACC TTGAACACGT TCATGCAAGA ATCCTTGAAC CTCAGCTAAT GCTTGAGATC

300

TTTCaNGTGT CAATTTTCTT AATCTTCCAA AGAAAACGTA CACCGTTAAA ATGTAAAATG

360

(2) INFORMATION FOR SEQ ID NO: 1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759:

DATTATGTCA TGCTAGGTCA CTTGCATCAT CCATTTAGTA TAGAAGACGA CAAAATTAAA 60
 TTATAGTGGG CTCCTTGATT GGCAGTATTC ATTTTCGGGA AGCGGGGTCC AGGCTTAAAG 120
 GGTATTAGAC GTGGTTACC 139

(2) INFORMATION FOR SEQ ID NO: 1760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760:

TCGCCCCTCC AGGCTATTAT TTCATCTATA TCATTGTCAT CAGTTAAATT CAGCCTCGAC 60
 ATTTCCATTT CAATAGACTG TTCATTCAAT TCTAAGTCAT TATTGTAAGT TTCTAGTTGA 120
 TTTTCATAAT GATTTAGATT ATTTTGCTCA ATTAACTTTC TTTGAGACAA TTGCATTAAC 180
 TTATCTTCAA TCTCCTTTGA GAGTTCTTGA TGCTGATTCA CATCTTGAAC ATACTTCTTA 240
 TAATCCACCT CAAAATTAGT GATATTANTA TATnTCGAGA GTGTTTCAAA TTCAGTGATG 300
 AGATCTCGAC ATAAT 315

(2) INFORMATION FOR SEQ ID NO: 1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761:

TAAATCCTCG AGATTCTTAA TAGGGTAGAT ATCTAACGTT TTCGCAAAGC TCTTTTTGAT 60
 TTGTTCTTCT TTTGAATCTC CAATGATCTT ATTATCACCA TCACAAGATG TAACAAAGAT 120

CCATCCTCAT CATTCAATCAT CTTCATCTAC CTTCGCGGCT GGAAATTCAA aGaaTCTATT 240
 ACTGACAAAT CGCTTTTTCC ACCTTTTGAA AAGTCAATTT CCAACTTTTT ATAACCCACA 300
 5 GAACTTCCTT TCAAATTACC ATCAATATGC ATTTTAAATA CCGGTGCTTT ATCAGTAGGA 360
 ATATTATAAC GACTTCTTAA TTGCTTAACA TTTTCATCT 399

(2) INFORMATION FOR SEQ ID NO: 1762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762:

20 GTATAGAAGA CGACAAATT AAATATAGTG GCTCCTTATT GCAGTATTCA TTTTCGGAAG 60
 CGGGTCAAGC TAAAGGGTAT AGACGTGTAC AATTAATGAT GGCATTATTA ACGATGTATT 120
 TATTCCTCTT AAGCCACTTA GACAATTGGn AATTATCTCA GGCGAATATA ATGATGTTAT 180
 25 TAATGAAAAA GTTCATGTGA AAAATAAAGA TAATTATnTA CATT 224

(2) INFORMATION FOR SEQ ID NO: 1763:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763:

AGCAACCAAC GCCAGATAAA GCAGAAGATA ACGCATTTC CCCCATCACC ATAT 54

40 (2) INFORMATION FOR SEQ ID NO: 1764:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764:

50 ATTCCTTAT CGCATTCTGT AAAATGATCT TCATCAGAAA TTGCTTCGAT ACGTTTATG 59

(2) INFORMATION FOR SEQ ID NO: 1765:

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765:

10 GATTCAATTC ATCTGTATAG ACGATATATC CTGATATGAA TTGGAAATGG AATA 54

(2) INFORMATION FOR SEQ ID NO: 1766:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766:

ATCGCATAGA AGCATTAGAC TCAAAC TATT TTCGGTTATG AGAATAACTC TGACATCCAT 60

25

ATGGATACTT AGTTTCCAAG TTAGA 85

(2) INFORMATION FOR SEQ ID NO: 1767:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767:

CAGTACTGCT GAATGATGCT ATTGATTTTC TCATGAGACA TGGCGATAAC ATCG 54

(2) INFORMATION FOR SEQ ID NO: 1768:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768:

50 GnCACTACTA ATCGTATCAG GATCACTAAT TAAGGCATCC AGCATCAGAT ACGAGCGCAC 60

GTCAGACTAA TCTACTGTCA TGATAAGCA GCTGCTAACC TTGTAAGTTC GTGAAA 116

(2) INFORMATION FOR SEQ ID NO: 1769:

55

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769:

10 GTTCTATCCA ATATGGAAAT GAGGACATTA TGCCTGAAAG CTATGGACGA TGGACGATGG 60
TACACGCATG TTGTGTAAGC AG 82

(2) INFORMATION FOR SEQ ID NO: 1770:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770:

25 TATCTGTATT GTAGTAATCC GCTTCTCCCA TCTATATAGG GATCTTTCGT AGATATTCAC 60
TTTATGCCTA GGATCCAAGA TGTGTAAGCA GCACTTTGCA TTATCTAATG CAAAGGGnAC 120
ATGCGGCTGT AAGCCCTGTT CTGATAATCA TA 152

30

(2) INFORMATION FOR SEQ ID NO: 1771:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771:

40 TGGAGGCGAA GTAAATGAAA AGTATTACGT TTGAAGAACA TTATGTCATT G 51

(2) INFORMATION FOR SEQ ID NO: 1772:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772:

50

ngAAACAAAT ATCTGATGAG ATATGCAATG ATGACTATAA GTAACATTAA AATGAAGCCC 60

55

CGTACACCAA TTATATCTTT GTGGnTGTTA TATTAAATCT ATATTATGTT CATTTAACAG 180
 CATATGTTAA AAATTGACAG TTAACACATG TAGCTATTTG ATGTGAATGT GC 232

(2) INFORMATION FOR SEQ ID NO: 1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773:

TAATGTCCCC CAGAATGTAG GCAAATGCAG AACCTGGTTT TAGGGTCAAC TGTTTnTTCT 60
 CCAAGCAGAA ACAAAGTTCT TGTGTCAGTG CACTTTTGGT CCACCATT 108

(2) INFORMATION FOR SEQ ID NO: 1774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774:

CGCAATTGAA GGATACACTA TTTTAAGAGC TGCAAACATG CGGGTGTAA C GTGTGGTATA 60
 CTGCAACTTT GGTnATTGGT TTAGTATAAG ATAAAATCAT CACAATGAAT C 111

(2) INFORMATION FOR SEQ ID NO: 1775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775:

CAGGTTATCA GCTAATAGAT ATGTTGAAGA GGCAGTTGCA GGCCAAATGA AACTGCAGAT 60
 GTAGTTCAGT ACC 73

(2) INFORMATION FOR SEQ ID NO: 1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776:

5 TAGACACAGT GCAAAATCTG GTACAGCTTA TGGAATTAGA CGGGTAAAGC AAATTACTGA 60
GTACCCA 67

(2) INFORMATION FOR SEQ ID NO: 1777:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777:

GTATGCCAGT GTCATTGCTG AAAACATCAA CCATTCCCTG CACCAAAATT TTTTGGTAGA 60
20 GTTTGATGCT GGCCATCCTC CAAGGGACTA AGGGTAATTT TgntTAAAAA GAGCCAAAGG 120
CCCAATG 127

(2) INFORMATION FOR SEQ ID NO: 1778:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778:

GAACCCAAAA ATTAGCAACA GTGGCTACAA TAGTTGGGCA CTGAAAGCCA GCCAAGTGGG 60
35 ATTTTGTAGCC CTTGATTTGA AAGCGGGGTC CCCAGGATTA AAAAATTTAA ATTAGCCTAA 120
TAAGCCCAAAA ATTCCCATTG GGAAGAGGAA ACCTCCTTAA ATTGGGTTGG AAAAAAGnTT 180
40 AAAAAAAAAA AGGCCAGnC CTTGGAATTT TTTGGAATTG GAAAAAGGAA TTAAAA 236

(2) INFORMATION FOR SEQ ID NO: 1779:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779:

(2) INFORMATION FOR SEQ ID NO: 1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780:

GACGACTCGC TTCTATTTTA AAATCCGGCG TACTTgGTTA TATAAATATC ATAATGGTTA 60
 AAATTAAAAA GCAATGTCAG TTCACACTAT TACTGACATT CTTTtagTTA TGTGTATATT 120
 ATTCATTAC AAGCTTTTGG TCTATAAATC GAGTGATTG CTTTGTTTGT ATATAACCAT 180
 CTGCTACATA TTCATCGTTC ATTGTAATTA ATGGATAAAA TAGTTCATCH n 231

(2) INFORMATION FOR SEQ ID NO: 1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781:

GTCTCCCTGC CCCACATTTA ACATTGTAAT TTTGTGATGT GAATTTGTTG GAAACGTTAT 60
 TAATAATGTC AGAATAATTA TAGTCCAAAA CGTAACCAAT ATATATTTAC GTTTAGCCAA 120
 TAACCAAAAT ATGTAATAAA CAGAAATTAT AAATACTATA AATATCCAAT CATTAAACTT 180
 GGGAACAGAA AAATGTGATT GCTTGATT 209

(2) INFORMATION FOR SEQ ID NO: 1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782:

GTTAAACTTA GTTAGATAAA ATGCAAAATCA CATTATTGTA GATAGTCTCT TTTC 54

(2) INFORMATION FOR SEQ ID NO: 1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783:

TCTGGAATGT CTCCTTGTCT CTCTATATAG CTATAGTCCG TCGCAAGCGG ACGTAATGTT 60

10 CATTTCATA ATGATTATAG TATGAAAGCG CTTTCTTGTA TATGTGACAT GTGCGTGTng 120

(2) INFORMATION FOR SEQ ID NO: 1784:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784:

CTACCATTTA CATAAGACC GTCTAATTCT TCAGTTTCAA TGGCATTITG GAGCAAT 57

(2) INFORMATION FOR SEQ ID NO: 1785:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785:

35 TCATAACCAT TACCAAGTAT CCAAGCAGCT TTAAACAAT ATGGCATAAA CATT 54

(2) INFORMATION FOR SEQ ID NO: 1786:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786:

GGATGGGTGA TTTTAGCAGG TTTGGCTATG AGTACCGTAT TTGCATTAGG ACCGATTTC 60

TTTAACAAAA TCATAATTTT GGGC 84

50

(2) INFORMATION FOR SEQ ID NO: 1787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787:

CCGGTTTACC CTAAAAATTA TTTTGGGG GGTTCATTA AACCTTCAA TTCCAATTA 60
10 ACCCCnACCC CCCTGGGTTT TCCTTAAAA CCAAAGGCC CTTTTCCTC CCAACCCAAC 120
CTGGGGGAA TTGG 134

(2) INFORMATION FOR SEQ ID NO: 1788:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788:

TATATCAACT AAAAAGCGCA TCTGCAACCG ACGGTTGAAA ATTTGGACAG GAGACAGATA 60
25 ATGTAATATA 70

(2) INFORMATION FOR SEQ ID NO: 1789:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789:

AATATCCAAT TATACAAGCA GGTATGGCAG GAAGTACGAC ACCGAAATTA 50

40

(2) INFORMATION FOR SEQ ID NO: 1790:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790:

50

TGATTTACTA GCTGAATCCG ACATGCTTGA TGATACACTA TGTGAATTCA 50

(2) INFORMATION FOR SEQ ID NO: 1791:

55

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791:

10 CCGGACGCTT TACTTCCAAC TTTAGGTGGT CAACACAGGT TTAAACATGG CGATGTCA

58

(2) INFORMATION FOR SEQ ID NO: 1792:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792:

CATCATCCTC TAATTTAGTC CAAACTCCTG GATGATATCC AAATGAAGTT CCAATTGA

58

(2) INFORMATION FOR SEQ ID NO: 1793:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793:

35 CACAAGTTTT AGAAGGAAAC CAATAACAAA TGACGAGATT AATTGCCACA AACATTAACG

60

AC

62

(2) INFORMATION FOR SEQ ID NO: 1794:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794:

AAGGCCCGGG GGGTTTAAAA AAAAAGGTTT AAAAAAGGnT TTGGCCCTTT AAACCCAAAG

60

50

GGAAATTTTA ACCCCAAAAA AAAAAACCC CTTTGGGAAA GGG

103

(2) INFORMATION FOR SEQ ID NO: 1795:

55

- (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795:

10 TATCGATCGA TCATGTCGAA TCGATCTGTC GATCGATCGT ATCGATCGAA TCGCGTCGAA 60
 TCGAATnCGT CGAATCGATG CTATCGATCG AATGCTATCT GAGTCGAATC ACGTCGATCT 120
 G 121

15 (2) INFORMATION FOR SEQ ID NO: 1796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796:

25 AATTCATGTT AAAATCCTCC TGATATTAGA TGGCCCATTT TTATTTTTTTT CGTTTCCATA 60
 TA 62

30 (2) INFORMATION FOR SEQ ID NO: 1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797:

40 CATACTCGAC AATTTAGATG GTGAaTACTT ATCATTTAAG TCCTTTGaCA CCTCATCTAA 60
 AATTCTAGGA CTTTTAACAA TTTCTTTATA CGTATTTACA AGTTGAATAT TACTTTGAAC 120
 CTCTTGCGCC ATAAACTGAG GATTGTCACC CTTAGTTTGA TTCACTAAAA TTTGAGTATT 180
 45 AGCTTGATAT TTAGGTGATA AGACGAAAAA TGTAACAATA GCGCTAATAA TTAAAAATAA 240
 TAGCGGTAAA ATAATTAAAA TCTTCAAGTT TTTTGTGAAT ACTTCITTAA TTTTGTAA 300
 TTCTAATGTA CTTTCCATTA TTTACCTCCC TTAAAAATTT TCATTAAAAT TGGTATTATA 360
 50 TATATAGTAT TTACATATTA CATATCGTTT AAACAAT 397

(2) INFORMATION FOR SEQ ID NO: 1798:

55

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798:

10 CGGGTAACAG CGAATGGTGT GTCACCGTAT ATAACCTTTAC TATTTAATAT TTGGCCTGTT 60
GCTTTC 66

(2) INFORMATION FOR SEQ ID NO: 1799:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799:

25 GTTGCTAAGT TTGTATTACA ATTTAAATGA TTTTGTAGCTT GAGTAAGTTT ATTTAAAGAT 60
GCAGTAATTT CGCTAGG 77

(2) INFORMATION FOR SEQ ID NO: 1800:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800:

40 TAATGCTATT TAATTTTCTA CTTCTAAGC TTCCACCCAT AACGAGTAAn ACTTTTTTAT 60
TTTCATTAAA GCCTGTTAAT TGATAACCAT TATGTGCATT ACCATTTTTT AAATCTTCTC 120
GAATTGTTGC TCCAATAAAA TCAGCTTTCT CTTTAGGTAA GTAGTTTAGC GT 172

45

(2) INFORMATION FOR SEQ ID NO: 1801:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801:

55

AGTAAAATTT GTCATCACGA TCAGCAAAAG CTTTGTGATTC TGACGTATCT TCCATAAATG 120

ATCTAAAAAT TGGTAGTTCG 140

(2) INFORMATION FOR SEQ ID NO: 1802:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802:

ATCCCCCGTA CAGACTTCAG CTTACGTAAA CATGCTGAAC ACTCTAGTGA AGATTTCAAA 60

(2) INFORMATION FOR SEQ ID NO: 1803:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803:

CAATTTAAAT GCATCTTTCC CATTAATTTC ATTTGTTGTC GCTTTAGCTG TGTTAATTAA 60

(2) INFORMATION FOR SEQ ID NO: 1804:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804:

ACTTGATCGA AAAGGTTTCA TACCGGTAAA CGATAAGTT GAAACAAATG 50

(2) INFORMATION FOR SEQ ID NO: 1805:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805:

(2) INFORMATION FOR SEQ ID NO: 1806:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806:

AAGAACTGTC TATGAATATT GGATGACGCT TTGATGAGAA CATTAGTAAG CCATTTGTTC 60
AAGGAGTACA 70

(2) INFORMATION FOR SEQ ID NO: 1807:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807:

TAGCATTTCT AATGGAATCC AATCTTACCG AATGACAATT GGAATATAAC TGGTGATAAT 60
GTTGAATGGT CCTGTGA 77

(2) INFORMATION FOR SEQ ID NO: 1808:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808:

CCCGGCCCAA AACCCCTTTT TTGGGTAAAA AATTTTTTTT AAAAAGGGAA AAATTTCCCC 60
TTTTTTGGTT CCCAAATTTT AAATTAGAAA GGGCCCCCCC TTCCCCCCCCA AATnTTTCCC 120
A 121

(2) INFORMATION FOR SEQ ID NO: 1809:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809:

AAGTTTGGTG AAGGAACCAC GTGCATGATG GTGTTCAAAC AATGCGTTAC GATGTTGACG 60

(2) INFORMATION FOR SEQ ID NO: 1810:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810:

TGTTGAGAA AACACAGCGT TAAAGTTGAG GTATTTCAAA AGACAAGTTG GAACATTA 58

(2) INFORMATION FOR SEQ ID NO: 1811:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811:

CTTAAATAGC AAGTGGTTTT ATAACAAC TTGAGTTATCT CAATATAGTT ATCGC 55

(2) INFORMATION FOR SEQ ID NO: 1812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812:

TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT 50

(2) INFORMATION FOR SEQ ID NO: 1813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813:

(2) INFORMATION FOR SEQ ID NO: 1814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814:

TGGTCATGCG	GGAAATACTA	GGACATGAAA	ATTATGCTAA	AGGCATCAAA	GTAAGTGAAG	60
ATAATGGCGT	AGTGGATATA	GATATGTACA	TTATTGTAA	TTACGGTGTG	AAAATATCTG	120
AAGTTGCCAA	TAATGTACAA	TCAACAGTGA	AATATACTTT	GGAAAAATCA	CTTAATGTAT	180
CAGTAAATTC	AATCAATATA	TATGTACAAG	GTGTACGTGT	GAATAATACA	GGCAAGAAAG	240
CTTAGGAGGA	CAACTTGAAA	TGATTAGCAA	AATTAATGGT	AAATTATTTG	CCGATATGAT	300
TATACAAGGG	GCACAAAATT	TATCTAACAA	TGCAGATTTG	GTAGATTCTT	TGAATGtGtA	360
TCCAGTGCCA	GATGGtGATA	CAGGAACAAA	TATGAATCTT	ACTATGACTT	CAGGTGCGGA	420
AGAAGTAGAG	AATAATTTGT	CGAAAAATAT	CGGCGAATTA	GGTAAAACAT	TCTCGAAAGG	480
TTTACTAATG	GGTGCAAGAG	GTAACnCTGG	TGTCATCTTG	ncACAATTAT	TCAGAGGATT	540
TTGTAAAAAT	ATTGAAAGTG	AATCTGAAAT	TAATTCAAAA	TTGTTAGCTG	AAAGTTTnCA	600
AGCTGGTGT	GAAACGGCAT	ATAAAGCTGT	TATGAAACCA	GTTGAAGGTA	CAATACTTAC	660
AGTTGCAAAA	GATGCTGCGC	AAGCTGCAAT	AGAAAAAGCA	AATAATACTG	AAGATTGTAT	720
AGAATTAATG	GAGTACATTA	TTGTAAAAGC	CAATGAATCA	CTTGAAAACA	CACCAAACCT	780
ATTAGCTGTA	CTTAAAGAAG	TTGGTGTGTG	TGATAGTGGC	GGTAAAGGTT	TGTTATGCGT	840
TTACGAAGGA	TTCTTANAAG	CGCTTAAAGG	TGAnAAAGTT	GAAGCCAAAG	TTGCAAAGAT	900
AGATAAAGAT	GAATTTGTAC	ATGATGAACA	TGATTTCCAT	GGTGTAATTA	ATACTGAAGA	960
TATTAATTTA	TGGCTATnGT	ACTGAGATGA	TGGTTCGTTT	TG		1002

(2) INFORMATION FOR SEQ ID NO: 1815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815:

GACAACGCTA TTATTTTTAG TTTTCAATT CTATTATGTC ATAATTATGT CACTCAAAAA 120
 CTGTTTTCCA ACATTGATTT ATTGTTGGAA AATCTCGAAA ATCTAGTCTA TTTCTCCAAC 180
 AATCGAAGAT TTATGCCCTT TTTTCTCCCT TTaATAAGT CATAATACGA GGCATACATG 240
 CAACATTTAC AATAAAATAT GTTCCTACAT CGTATTATAC GAATGCTCAC ACTTATAGTT 300
 GTTTAGTAAA CCCAGATGTA TTGCTAACAT ACCCATnAnc nCTATATAGT T 351

(2) INFORMATION FOR SEQ ID NO: 1816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816:

ATATCGTATC CCATGCGGGA AGGGCTTTAT TTATACTGTG CACGATGAAT GCGCACAACG 60
 GG 62

(2) INFORMATION FOR SEQ ID NO: 1817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817:

AAAGGGGGGA AATTTTTTTT TTTTGGGTTT GGGGGGAAAA TTTTTTTTGG GTTTGGGAAA 60
 TTAAATTAA 70

(2) INFORMATION FOR SEQ ID NO: 1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818:

CAAGTTCGGA ATGCGAACGC GTCTTAATCT ATATACAAGT GATGCACTCC A 51

(2) INFORMATION FOR SEQ ID NO: 1819:

- (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819:

10 TCGCCATACT ATCGACAGCT GCTAAAATTG CGTCTTCTT GTGTCGCAAT CG 52

(2) INFORMATION FOR SEQ ID NO: 1820:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820:

CAAATTGGGG AAATTACTAG AAATGAAGAT ATTTATAAAG ATGACTGGAC GTCAACTT 58

25 (2) INFORMATION FOR SEQ ID NO: 1821:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821:

35 ACTGCTTCAG CACCTGTATT CATTGGGGAA AGCTTTATCG TTGACCGGCC AGTTTACA 58

(2) INFORMATION FOR SEQ ID NO: 1822:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822:

ACCTGTTGCT CGTGTCAATA ATAGGTGACT ATAAATCTCT GTTCAATATA CTTTTCGTTT 60

50 TTCCAATCTT AAAGGTCGAT GTTCGTGAGT AATCTTATCT CTGGnCCAAT TTTAATGTCA 120

TGATATGTTT ATAGTATCAC CCCTTTGTTG TGTAATAATA ATCAGGTGGG TGGTTAGAAC 180

55 GGTGTGAATA 190

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823:

AGCnTTAGCn TATGGTTT TAG ACACAACTGn TAAAGATGCn AAGTTCTTGT

50

(2) INFORMATION FOR SEQ ID NO: 1824:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824:

AAAAATTGGA AAAAAGGGGC CCAAAGGTTA ACCCAAATTG GAAAnAAACC CAAATTTTTT

60

GGAAATTAAC CCAAAAATTG GCCCCCAATT GGAACCCAAA AT

102

(2) INFORMATION FOR SEQ ID NO: 1825:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825:

ACGTACCAAT GTCATAATCA GTCATTTTAC CACTCTTAAT AATCTGCTTC CGGGCAA

57

(2) INFORMATION FOR SEQ ID NO: 1826:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826:

ACCATCTTGT ACAAAGTGGA TGTCATATGC ACCATCTTGT GTTTGAGCT GCATTTAATT

60

G

61

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827:

ACCGTTTCGC CAAGCCGACC TAATTTCTCA GCAATATTTT TTTCTACGCC ACCAAT

56

- (2) INFORMATION FOR SEQ ID NO: 1828:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828:

25

ACTTATAGGG CGCACTTATT TTCGCTTCC ATAGCGAAAC TAGTGTCCT TATACGTATG

60

TG

62

- (2) INFORMATION FOR SEQ ID NO: 1829:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829:

40

GCTACACACG ATTTACCTTT CTTGTCACGT TTTGCGACCA TCATTGTGAT GATA

54

- (2) INFORMATION FOR SEQ ID NO: 1830:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830:

GTAATGACCA TCGCTGATTT ATGACATTGT TAGATCTCAT GTGCCATTTA GTCTGCTGAA

60

TCTTGGG

67

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831:

ATAACTCTTC GACAACTCC TCAACAACT TCTGTGTTC CATCTTCTGG

50

(2) INFORMATION FOR SEQ ID NO: 1832:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832:

AAACGTnAGA ATATTTAATG GAGCCAAGAA TGGTTTACAG ACGGAGAAAT GGGATATGTT
 GAAGCGAGGC GTACGCGGAA AGCGTACTAG GCTAGAACAC T

60

101

(2) INFORMATION FOR SEQ ID NO: 1833:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833:

TCGTCATCAT GTCTGTGTTA CCAACGTTTG ACGATTTANT TCATGCnGAA

50

(2) INFORMATION FOR SEQ ID NO: 1834:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834:

ATAAGTTAAT TGATTTATTG ATAAAGAGAA GCCAGATTTA AATATTATTA AACGT

55

(2) INFORMATION FOR SEQ ID NO: 1835:

- (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835:

10 AAACAAGAAC CCCCATATGG TTAAGCTGCG CGTTTCAACA TACGGGGGGT TTTCATAT 58

(2) INFORMATION FOR SEQ ID NO: 1836:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836:

TACGTTTTAT AAAACAAGA ACTAAAGTAT GCAGTGTGAA TTGTTCACTT TChTGGCGTT 60

25 GGAATTGATT AAAACGAGAT ATGGTGTGT GGAAGTTGTT TGTGTTTGA TATTTTAAAC 120

CGATT 125

(2) INFORMATION FOR SEQ ID NO: 1837:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837:

40 AATCTACAAT CCTGAATCAC TCGTTAAGAT TAAAAGTATC GACAATGAGT ATCTGAACAT 60

GAGCTCATCT GCCGTTTTTA ATGCnAAAAA CCGGCGGCGG GATATTTTTG ACCACGGC 118

(2) INFORMATION FOR SEQ ID NO: 1838:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838:

55 ATTTGGGGTT TTGGGACCCT TACCCAAAAA TTGGGGTTTG GTTATTAAAA AAAAGCCATT 60

GTCCCAAGTTT TTGGGATTGC C

141

(2) INFORMATION FOR SEQ ID NO: 1839:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839:

TCTGGGGACT AAGTATGTCT CAGGCTTTAT GCTGTTATGT TTGAAAATGA AAGG

54

(2) INFORMATION FOR SEQ ID NO: 1840:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840:

ATTAAAAAAC CTTTTTAAAC CGGGAACCCA AGGAAAAATT CCGGGTTTTA ATTAAACCT

60

TTTGTTAATT GGTTCCAAAC CAACCTTTTG GGTTAATTTT AACCAGGAAT TTTGGAAAAC

120

nGTTTTATTT GGA

133

(2) INFORMATION FOR SEQ ID NO: 1841:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841:

AAAGTATGGA TTGATCGTGG AGAAGTTCTT CCTACTAAGA ACACTAGTCG

50

(2) INFORMATION FOR SEQ ID NO: 1842:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CGGTTTTCT GGGATATGTT TGATGAATGG ATGTTGTAAC ATGTTAATAA ATCGTTGGTA

60

(2) INFORMATION FOR SEQ ID NO: 1843:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843:

CTGAGATGAA TATTGTGTTT CGCCATACAT ACTGGGTAAT ATCCCAACCA TTGCTGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 1844:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844:

CATTACCTGT AAAAGGAAGC TAAAGACGAT GAGTATTTAT AGAAACCAAT TGCCGACCAT

60

TTGCAGCCAT TAGGAGGGTA GGAGGGCAAT CGCGnCCAAA GGTTATTAAC CGTCAATTAC

120

CTTGA

125

(2) INFORMATION FOR SEQ ID NO: 1845:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845:

ATCCACCTGG GTTTGTTCTT AATTTAACCT GntAATTAAT TGGGTTGGGT CCGGCAAAAG

60

TCCGGACCTG CAAATCGGAT TTTATCGTTA AATCTTGAAT TCTATTGCCC ATATTAAATC

120

GCAAAT

126

(2) INFORMATION FOR SEQ ID NO: 1846:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846:

5 TTTTGGGAAT AAACCAATTA ATCATGGGCA AAAAATAAGC AATCCAAGTA CTTACTA 57

(2) INFORMATION FOR SEQ ID NO: 1847:

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847:

TGATAAATAT TTCATCTAAA GAGAGGGAGT CATTATGACA CTACTTACTG 50

(2) INFORMATION FOR SEQ ID NO: 1848:

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848:

30 ATCTAGGCAA TGAATGGACG GACTTAATAT TGATGTGCAA CAAGAAGAGG AGAAGCGAAT 60

CAATA 65

(2) INFORMATION FOR SEQ ID NO: 1849:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 244 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849:

45 CGTGTGAAGT CATTACTTTT AATCCCATGA TGATGGTGAT GGATGAGACG ATATCTCTCT 60

GTCTTTAACA GTTAAGTCCA ATTCTTCCAA CGAAACTTTT CCATAGGTTG TTTTATAAGT 120

TGGAATACTT GCACAAATCA TaCCTAATTG CTTATCAATT TTCTCAAGAC TGTCATCAGT 180

50 TATAAGATCA ATTTTATTAA TAATAATCAT GTCACCTAGT TTCAACTGAT CTTCCATCAG 240

GCGA 244

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850:

TTTAAAGGTT CCCGGAAAGG TTTGAAACCA AACCTTTGCC CCGGCCCCCC GGGAAAAAAA 60
AAAnTTGGTT TAACCCCCGG GGGGGGGGGC CCTTAAAAAA ACCCAA 106

(2) INFORMATION FOR SEQ ID NO: 1851:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851:

TTTTTTAAGG CCCTTGGGGG GCCAATTTTC CCCCCCCCCC AACCTTCCAA AGGTTGGGGG 60
GCCTTTTTTT TTAAATTGGG GGGA 84

(2) INFORMATION FOR SEQ ID NO: 1852:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852:

TCATGATTAA AATTCAACAA TTACAACATC ACTTTGGATC ACATAAGAGT AA 52

(2) INFORMATION FOR SEQ ID NO: 1853:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853:

ATAAACATT TCAAGATGCG CTTGTAATTG TATGTGATAC TGCCAATGCT CCACGA 56

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854:

AAAAGATCAT GCGCATAATG ACATGGTGAT GATATGAGTA TGATGGTGGG TACA

54

(2) INFORMATION FOR SEQ ID NO: 1855:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855:

ACAACAAATG GTAATGCATA AACATACAGC CAATAGCTAC AATTGCACGA CG

52

(2) INFORMATION FOR SEQ ID NO: 1856:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856:

ACGGCTGCAC TCATCATGGT CTGTGGCGTG ATTGTTAATG TTTTAGTTGC CCGCTTC

57

(2) INFORMATION FOR SEQ ID NO: 1857:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857:

GCAGATAACT TCCTTGATCC TAACAAAGCA AGTTCTCTAT TATCTTCAGG GTTTTCACCA

60

GACTTCGCTA CAGTTATTAC TATGGATAGA AAAGCATCCA AACAACAAAC AAATATAGAT

120

GTAATAnACG AACGAGTTCTG TGATGACTAC CAATTGCACT GGACTTCAAC AAATTGGAAA

180

(2) INFORMATION FOR SEQ ID NO: 1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858:

CGCTGCACTT CCTGAACGCA GTGAGACCAG AACGTGGTGT CACTTTCGGT CTATTCGGT 60
TAAGTGTTGG TCTCGGA 77

(2) INFORMATION FOR SEQ ID NO: 1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859:

TTTGCGTTC GTGATTTTCT CTAGACGTAG TAACTTTCCC ACTCTTTGCG TCC 53

(2) INFORMATION FOR SEQ ID NO: 1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860:

TTTCTCACTC GCGCATTTCA GTTTGTTTTG ATTTACCGT CTCTTCTATT TGTCTTAAT 59

(2) INFORMATION FOR SEQ ID NO: 1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861:

AATGAATGTA TGCACATTAA CATCATCAAT TAATCCTTTT AATAAATTGA GTTGTAATTT 60

(2) INFORMATION FOR SEQ ID NO: 1862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862:

ATTAATACTG AGCAAATGTG CATAAGACAT CATGAATTAG CACCAATTTA CAGG 54

15

(2) INFORMATION FOR SEQ ID NO: 1863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863:

25

TTTAACCATC ATTCTATGTC AAAGTTTGA AATGATGGTT ATTTTTTATT GCTTAAATTT 60

ATTATTGCTA CTACTATACC AATGAAAGT 89

30

(2) INFORMATION FOR SEQ ID NO: 1864:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864:

40

AAAGCTGGTA CGCCTGCAGG TACCGGTCGG GAATTCCTGG GTCGACCCAC GCGTCCGGAA 60

CCTAAATGTC ATCTGATGGT CTCAAGGGTC GTGTGTTTGA AGTGAGTCTT GCTGATTGTC 120

AGAATGATGA AGTTGCATT AGAAAATTCA AGCTGATTAC TGAAGATGTT CAGGGTAAAA 180

45

ACTGCCTGTA CTAACCTCCA TGGCATGGAT CTTACCCGTG ACAAATGTG TTCCATGGTC 240

AAAAAATGGC AGACAATGAT TGAAGCTCAC GTTGATGTCA AGACTACCGA TGGTTACTTG 300

50

CTTCGTCTGT TCTGTGTTGG TTTTACTGAA AAAACGGCAA CAATCCAGAT ACGGGAGGAC 360

CTCTTTTGCT GCAGCACCAA CAGGTnCCGC CAAATCCGGA 400

(2) INFORMATION FOR SEQ ID NO: 1865:

55

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865:

10

AAATGGCGTA TCTTTATGTA TCAACTAAGT AATCACCAAT TTCTTTCGGA T

51

(2) INFORMATION FOR SEQ ID NO: 1866:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866:

GTGTTGCGGA TAATCCGTCG ACATTAGCGT CTGAAGGTAT CATGAGGCAA CTGCGCAA

58

(2) INFORMATION FOR SEQ ID NO: 1867:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867:

35

ACAGCAACTG ACCCAGTTTA CTACCGTCAC TCAAATCACA CAGGTGGTAT CAAATCAATC

60

(2) INFORMATION FOR SEQ ID NO: 1868:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868:

CAATCTCTTA CCATTTATCT CAGCTGGTGA AAACGGTCCA TTACACTTAG AATAAA

56

(2) INFORMATION FOR SEQ ID NO: 1869:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869:

5 GCTATAGACT AGAGGTACAG CAAATTCATG TGTACASTGA TTAGAAGGCG ATGAGCAAAA 60
GTAAT 65

(2) INFORMATION FOR SEQ ID NO: 1870:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870:

20 GCTACTGGCG GGGGATAGTA ACACCCAATG TTACACGTAT ATACGTACGG CTTCTTGATA 60
AAAAGATGAA GCCnTTACAA GTAGAGAGCG TAAGAACGTG ATCATCTAAA TGGTAAGGGT 120
AGACTATCCC ATGCCATTGT GGGCGGTTGC ATAGGTACCA CGGCACATAG CGG 173

25 (2) INFORMATION FOR SEQ ID NO: 1871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871:

35 GCTGTGGGAT TGTCTTTGG CATGGGGTTA GGGAGAGCGT TTCTAAGGGG CGTTTGAAAG 60
CCATTGATCC GTAAAAGGAC CATTGTTGGA AGCnGCCTTA AGAA 104

(2) INFORMATION FOR SEQ ID NO: 1872:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872:

50 CCATTATCTC AAGAGGTTCT AGTAAGGGGA TGGCATTGTC TTCTTATGAA TTTGACCAGA 60
ATAA 64

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873:

GACAACCTAT TGTTCCTTA CCATACTGTT GTCCGGTTTG ACAAACGGC GTTCCACAAT 60
 CCATACATCG TGCACCTTGG ATAGAGGCAT CTTCTTTAGT AAATCGTTGT TGATATGCTT 120
 TATGATGCTT CAAACGGTCT ACCAGTGATA ATTCACCTAA GTACTGTTTG TCATACTTCA 180
 TAAATCCTTT AAATTCACCC ATCGTATCTC CCCCTTTCCT TAATACACAA CGGCTGGTTT 240
 ATGTTTAGCA TCGATTGTTT TGA CTGTnCA TCGTAAATG CAGCTAACAT CGCTTCATCT 300
 TCCATTGTCA TGTGAAGATT TTGTGGCAAA nGGAATTTTT TGCATCAATG AATnGGTGAA 360
 CCTTTGGGGG TGACCTT 377

(2) INFORMATION FOR SEQ ID NO: 1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874:

ATTATCTGAA TACGCAGCAG TTGCAGCACT TGATGGATCA GCAGTATTTA AAAGAGGTTA 60
 ACACATTACC CAATAGTG 78

(2) INFORMATION FOR SEQ ID NO: 1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875:

CTAAAAGAAG TTAAAGAGTG TGATGGTAGA ATTATATTAT TTATTGATGA AATgCCATAT 60
 GCTTG TAGGT GsTGGTAAAA CAGATGGTGC CATGGATGCa GGCAACATGC TAAACCAAT 120
 GTTAGCACGA GGAGAGTTAC ATTGTATTGG TGCAACAACT TTAAATGAAT ATCGAGAATA 180

TGTGAAGAT ACAATT

256

(2) INFORMATION FOR SEQ ID NO: 1876:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876:

15

AGCGCGAAAT TGAGCAAGCG GAACATGCGA CTGATGAAGA AAAACAAGTT GCTTTAAATC 60

AATTAGCGAA TAATGAAAAA CGTGCATTAC AAAACATCGA TCAAGCAATA GCATAAATG 120

ATGTAACGT GTTGAACAA ATGGCATTGC TACTATAAA GGTGTACAAC CTCATATTGT 180

20

AATTAAGCCT GAAGCACAAC AAGCAATAAA AGCAAGTGCA GAAATCAAG TAGAATCAAT 240

AAAAGATACA CCACATGCAA CAGTTGATGA ATTAGATGAA GCGAAT 286

25

(2) INFORMATION FOR SEQ ID NO: 1877:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877:

35

ACTTCCAAAC ATGATAAAGA CAGACTACTT CACAGGTTTA AGGGAAGCAA CCACATTAGC 60

GGGATTCAAC CTAT 74

40

(2) INFORMATION FOR SEQ ID NO: 1878:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878:

50

TTTCATTAAG TTCAAAAAAT CTCAATAACT TTAAGGATTG GTCCGCATAT TA 52

(2) INFORMATION FOR SEQ ID NO: 1879:

55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879:

ATACCCCTGA GATTAATTAC TTGTCCTTTT TTTAGAACAA CATCTCCTGG CTTTGTTCG 60

10

(2) INFORMATION FOR SEQ ID NO: 1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880:

20

AATATCATTATAATATCAT TGATGCAAGT CCTATTGTGC ACAACTGGGG TGATTGCCTT 60

(2) INFORMATION FOR SEQ ID NO: 1881:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881:

35

ACAATGGCAC ATGGACTTAT GCCTGGGGTG TCCTGTTCGT CGCAGCATCA AAATGA 56

(2) INFORMATION FOR SEQ ID NO: 1882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882:

45

TGCAAAGCAT TGGCACATGG CCAGTCAGTT TTACAACGTC GTGACTGGGA AAACCCGAGA 60

NGCGACGTTG TAAAACGACG GCCAGTGCCA AGCTTGCGATG CCTGCAGTCG ACTCTAGAGG 120

50

A 121

(2) INFORMATION FOR SEQ ID NO: 1883:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 56 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883:

ACATTTAATG TATAACCACT TTCAACATTG CCGATTTAGT GGCAGCAGTT GCAGGA

56

10

(2) INFORMATION FOR SEQ ID NO: 1884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884:

20

TGCATCCATT TGATTGAATT TTATGTTTTG ACCAAAGCCG GTTGCAATGT AC

52

(2) INFORMATION FOR SEQ ID NO: 1885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885:

TGAAAAGTGG TGGAATGGTG TTAAAAGTTG GTGGGTAATT TTAGAGAAGA G

51

35

(2) INFORMATION FOR SEQ ID NO: 1886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886:

45

TACACGAACC ATACTCACCA GGTTCGTCGTC TCATGAGGCG ATATTTTTTG TCATTTTATA

60

TACATTTATC CAAATTCATC TTTTAAATGT TGAGT

95

50

(2) INFORMATION FOR SEQ ID NO: 1887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887:

GCTACCAAAG GCGTTTACC TATTGCTAGT CACTGCAAGT GGCTTAGCTA TGCAGATCAA 60
 CTGGT 65

(2) INFORMATION FOR SEQ ID NO: 1888:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888:

GTGGGACCAA CTGGCCGGTG ACGGTGGTAA AGGTGCTTCA GTCGTATTGA AGTGGGATGA 60

(2) INFORMATION FOR SEQ ID NO: 1889:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889:

TGTTGGAGAA ACAGTTAACG AGGTTTAATG TTAAAAAGC AACGTATCAT GGGTATA 57

(2) INFORMATION FOR SEQ ID NO: 1890:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890:

TGGGATCTGC TTGCAAATAC ACAAACCTT CTGGATTTTA TTACAATTGC AATATAATCA 60
 AACA 64

(2) INFORMATION FOR SEQ ID NO: 1891:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891:

GGCATCCACT CAGATAAAAT AAAGATGTCA AAAAGGCCAA GATGGTGCTA AAAAAACAA

59

(2) INFORMATION FOR SEQ ID NO: 1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892:

GGTATCTCAA CGATCCTTTA GGTAAATTCG GAAATTTCTA CACGTGAGTT AGCA

54

(2) INFORMATION FOR SEQ ID NO: 1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893:

TTGTCTTGGC AATGGCAGAG CAACAGAAGT TTAAAGTGCT TGCTGATCAT AT

52

(2) INFORMATION FOR SEQ ID NO: 1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894:

TAAACCTATA CCCTGTAAAA AGAAAAATCG TGGATCGAAA GAACATGTAT GTGGCATTTA

60

TGATTGATGC TCAAGCAGA

79

(2) INFORMATION FOR SEQ ID NO: 1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895:

TTATAAAGGA GAGAAATCCT TAATTATGAA TAAAGCATCA TTTGATAAAA AAGTTAAAAA 60
 5 GCAATTATGG TTTTGAACA AGAAGGAGAA ACAAGCATTG GATCAACGAT TGTCTTCTAT 120
 ATCTGATGAT GACAGCGTTA ACTTAAATAA GCCTGTTACC TTTGCTAATG CTTACTTAAG 180
 ACAAATGTA TTTGAAATA AAGAAACAAA AAGTTATAGT ATGTTTGTTA CATTAGTAGT 240
 10 GATGATGTTT GCTTATGTTG CTTTATTAGG TTTGTTTATA TTTGGGCTAA TTACAAGTCT 300
 ATCTGGCGTA CAATTTTTCG TTAGTCCTAA GGTAGATTTA TCTACTACTG TTGTTATTTT 360
 15 AACAAATATT GGAGCGA 377

(2) INFORMATION FOR SEQ ID NO: 1896:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896:

TTAGGATCCG TCTTTGCCGC AGCGTGGGTG TTCCGCGAGC GCTTCTTAGA GGTTTTGC 58

(2) INFORMATION FOR SEQ ID NO: 1897:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897:

40 ATCGCTCAAA CCGAAATTGA AAATGCATCT ATTACTTCAT TAAGCCGTTT ACCAGACGTT 60
 ATATTAGCAT TGAAAAGTGG AAAGGTTGAA GGTGCTGTAG TTGAAAACC TGTAGCAGAA 120
 GCATATTTAA AACAAAATCC TAAATTAGGA ATTTCCAATG TGAAATTTAA TGAAGAAGAA 180
 45 AAAGATACAG TGATAGCAGT GCCAAAAGAT TCACCAAAAT TATTGTCACA AATTAATAAA 240
 ACGATTAAGG AGGTTAAAGA TAAAGGATTA ATCGATAAAT ATATGACTAA TGCTGCAAAT 300
 GCGATGAATG ATGACAGTGG TTTTATTCTT AAGTATGGTA GTTTTTTCTT GAAAGGAATT 360
 50 AAGATTACAA TATTAATTTT ACTTATCGGT GTTGCAATAG GTTCTATTTT AGGTGCATTG 420
 GTTGCGTTAA TGAAATTAAG TAAAA 445

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898:

ACCTTTTCAA TGTTGCTTTG ATATAAATTC ACAAAGTTGA CTTTThAATT CTTCAATAGA 60
TTCTCTACTG CGATAGCTGA ATTGCCATCT TTTCTACTAC T 101

(2) INFORMATION FOR SEQ ID NO: 1899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899:

TGCCCTGGAT GCCTTTAACT TGATTCATGA CCTGTGGTTT TATTTC AATT TAGATGAGCT 60
ACCTTCAAGA CCTTC 75

(2) INFORMATION FOR SEQ ID NO: 1900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900:

AGCAATACGG AACTGATGAA CGGAATTGTA ATACGAGAAT ATGAAGCATC AACG 54

(2) INFORMATION FOR SEQ ID NO: 1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901:

AGTACCTGAG TATCGCAGAC CGGCTTCAGG TCGTAGAATT TCTATACGTG GAGCTAGAAG 60

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

GTCTAACTAC AGCATGCCGG CTTATTGTTG CACTTTCTCA ATATTTCCAT A

51

(2) INFORMATION FOR SEQ ID NO: 1903:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903:

GGATTnAAAC GTGCATTAAAC GCGTGTnTTA AATAGTTATG GTTTAAGTAG

50

(2) INFORMATION FOR SEQ ID NO: 1904:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904:

ATCGTATTTA TTTCAGCGAG TAGCGGTAGC CTTCAATACA CAAAGATTTT ACC

53

(2) INFORMATION FOR SEQ ID NO: 1905:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905:

ATAAGACGCT AGATCTGGTC AATTTATTTT CGATTTTTTTC AACACTATTC

50

(2) INFORMATION FOR SEQ ID NO: 1906:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906:

TTCATCTGAA TCGTCGGCTT TCGCGATTAC TTCTTCGTCA GGGTTGCTAT C

51

10

(2) INFORMATION FOR SEQ ID NO: 1907:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907:

CAATTGCTAA TAATCCTTTT AAGTCATTAA TGATTGTATC TTCCGTAATG TTGAA

55

(2) INFORMATION FOR SEQ ID NO: 1908:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908:

TTGCCAAACA GACATGACTT AAATTTCAAT ATCTTCTTTG ACTGCATCGA TAT

53

35

(2) INFORMATION FOR SEQ ID NO: 1909:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909:

TGAATTTCTA TACAATTATG GGGAAGGGTA TTGGTGAATT GGAATGGGCT CCTAAGTTTA

60

CAAGCCCCCA TTCGATGGCC GTTAAAGTTT TTAA

94

50

(2) INFORMATION FOR SEQ ID NO: 1910:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910:

5 AACATGATCG TGGGGGGATG TTATGTTTGT TCATATATTT AGGAAGTCGT TTGTAGTTAT 60
TGTTTG 66

(2) INFORMATION FOR SEQ ID NO: 1911:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911:

20 ATCTTCGCTC CACTTACTGC AATAAGGATT TCGGGAATC CTAAACCGTT TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 1912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912:

AACAATCGTA ACGATACAAC GCAATCTTCG AAAAATAATG CAAGTGCAGA TTTCCGAAA 59

(2) INFORMATION FOR SEQ ID NO: 1913:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913:

45 ACACCACACA CACACACACA ACACCCACA CAACACACAC AAACACACAA A 51

(2) INFORMATION FOR SEQ ID NO: 1914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
50
55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914:

TGTACGACT TGGTCGACCT GGCAAGCGCT TCGCGCACGT TCTGCAGCnT CTCACCTTATT 60

GGTATCGCGA TCGGACGTTA AGAAATTTTCG GAGTTCTGGT CACCTTATGT T 111

(2) INFORMATION FOR SEQ ID NO: 1915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915:

TGGTCCGCTC TCAATCGCAT CTTCAGGTTT TACTTGGCAA AAGAGCGCGG TGCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916:

GCCGACAGTA AAATAAAGGT ACTTGATATA ACATATAACG GAAAGCAACA GTTACTGTCA 60

CA 62

(2) INFORMATION FOR SEQ ID NO: 1917:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917:

ATGATATTTA TTTGATTGAA GAGATGTTGC TTAAACAAGA AGACGTACAA TTGATANAAC 60

GTAAAGATTA TATTCAGCAC CCTAAAGAAA ATGTTACCG CAG 103

(2) INFORMATION FOR SEQ ID NO: 1918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918:

5 CAGTGTAGCG TGTGTCATGC CGTTTTACCA CAATTGAAGA CTGAGCTCTA TCCCTGTGCC 60

(2) INFORMATION FOR SEQ ID NO: 1919:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919:

15 TCAAATTAAC TTCCAACAAA AACAAATGCA AGGTGAAGAA ATTGCTGAAG AAGATTTACA 60

AAAAGCGCAA GAACAAGCGC AAGCAATTGA AAAAGATGAA AACATCTCTn CATTAAAT 117

(2) INFORMATION FOR SEQ ID NO: 1920:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920:

30 TGCCTAATGA AACATTTAAA AATATTTTTTA AATATATCTA TCAACACATC GTTCTATTAA 60

TTGGGATTGT TAGTTTTCTC AAAGGATTTT TAGGATTTTT CATGGAAAAA AATGGAAGTA 120

35 ATTTATATTT TGTTCATTC CCGTTTTAG TAGTCGTTGG ATTCTTTATT GTCTTTTTAT 180

TTATATGGTT TAGTTTTAAA ACAATACAAC TGCAGTGTTC TAACAATTCA AATTGGATAT 240

GGATATTCAC CTATTTAGCA ATCATTCTAC TAATTGTAGG ATTTTTCTAT GTATTCTTTA 300

40 TTCCACAATC ATTACTTGCC TTTGGACCAT ATATTCAGGT AAGCAATTGG GTATTTATTA 360

TATTTTCATT TATAGTTATG CCTATnGGAT TACGCATTGA 400

(2) INFORMATION FOR SEQ ID NO: 1921:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 50

TCACAGTCAT CATTThATTT TCGATTTTCA ATAATTGTAT TTTTAATTTA TCTTGATATT 60
 CATTAGATT TATACAAGCT ATCTTTAACA TTGCCTTATC TTTGATATAT TTCTTGCAAT 120
 5 CG 122

(2) INFORMATION FOR SEQ ID NO: 1922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922:

AGAAGATACC ATACACATTT aATTAGTTAC AGCATAAATC AATTTATACC CTTAATTATT 60
 20 ACATTGTTTA TATTTTAAAT TCGGGGGAGT AATTTTAAGT AATATCTTGT TGCTGCTAAT 120
 TCTATTGTTA ATAAATTGAT ATTAGATGTA GAAATTGAGT GTGAAAGTTA ATAATAGATG 180
 ATTTAGCTAG TAACATAATT AATTCATATA TAGTCAAAAA GTTCTGTAG ATACTGTTCT 240
 25 TGATGAATAT TCTTTGATGT TAGGTGTTAG CTATTCTAGA TGAGTTTCTT AGATGTGGAT 300
 GCCTGTCTTG ATGAAGTTAT CTATGATGTT AATATAATAC TTGATGTTGA TTCTTAGATG 360
 TTAGTGCGAT TTCAAGATGC TGATTCTTTG TTGTTGCACT ATCTTGGTGA 410

(2) INFORMATION FOR SEQ ID NO: 1923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923:

TTTCTATGGT TTATCAGGTG ATTTTACGGA AAACAGTGAA GATTATGGCG TATACCGCTT 60
 TAAACGTGGA TTTAATGTAC AAATCGAAGA ATTAATAGGG GATTCTATA AACCAATTCA 120
 45 TAAAGTGAAA TATTGGTTGT TCACAACATT GGATAAATTA CGTAAAAAAT TAAAGAAATA 180
 GATGTAAATG ATGTTAGGGC TTATAGThAT TGATACTATA GGCTCTTTTT TATATGTTTT 240
 TTAATAAAGC CTCGAATAAT GATATATTAA ATGACAAGTT TAACAAGTGA TTGCAATAAA 300
 50 TATAAATnTG AATTGCACAA CCGATTTGnA AATGATTGAG TTGAGGAA 348

(2) INFORMATION FOR SEQ ID NO: 1924:

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924:

10 AGGGCAGATT TAAGCTAACT TGGAAATGTTT TCGAGTTTTT GAGTTAGTTC TCTATCCATT 60
 TTTTCAGTTA CATGAGTATA TATGCGAATG GTTGTGTTGTT CATCTACATG TCCTACCCCTT 120
 TTCATAATTG CTTTAAAGA AACATTCATT TCTACTAATA AAGTTATGTG TGTATGTCTA 180
 15 AATGTGTGCG TGCTAACTTT CTTATTCATA TTAAAGCTT TTGTACGTTT TCTTAACGCA 240
 CACCGGCCAT TTC 253

(2) INFORMATION FOR SEQ ID NO: 1925:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925:

30 GGTATAGGTG CAAGTCCTAT CTTCCGCTCC ATGGTTTAAT GATAATGCGG GA 52

(2) INFORMATION FOR SEQ ID NO: 1926:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926:

TGGTCACTGT TCCTGATGCT TACGTTAGAA TGTAAGATTC CCGATTTATC AGTTATATAC 60
 TGTTTGCTTC ACTTTGGAGA TCTG 84

45

(2) INFORMATION FOR SEQ ID NO: 1927:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

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CTTTCTAAAT AATTCTAGTA TAGTTTTTAT TCAAATACGC TAGGCTCAGA GCTATT

56

(2) INFORMATION FOR SEQ ID NO: 1928:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928:

GCAAATTGTC ATTAGACGGA GTATTATTTA GAATTTTCGG TGATATCCAC CGGCACAAGA 60
 TCGATGTTGG ACAATATCTA ATATACTGAT ACGCATTAA ATAGAAGAAG GGAATTAGAG 120
 TTTGGTTnTG AATGCAAA 138

(2) INFORMATION FOR SEQ ID NO: 1929:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929:

ACATCTTTAT ATGCTTCAAC ATCAAATACA CCACATATTG GTAAACAACA AA 52

(2) INFORMATION FOR SEQ ID NO: 1930:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930:

TTTAATGTTT ACAACACCGG AATAATAATA ACTAAAGCGC CGCTAATAAA T 51

(2) INFORMATION FOR SEQ ID NO: 1931:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

ACGAAAAATA AATAATCATT TCACCTTTAT AGCCAGTATT TTTAATTAAT ATATTTTCAT 60
 CTATTAGCGC TTCTAAAAAT CTATTGACT TTTGAACATA CTCTTTAGCT ATATTATTAA 120
 5 CAACAGTATA GGATTCCTCA TAATTTAGTT GATTAAATTC TGAGTCGTTT ATTAATTCAA 180
 CTAATCCCTT TATTACTTTT TGTACAACAT TAATATTTTT ATCAAAATCA AATTTATCTT 240
 CCTTAGATAA ATTAATAnnn AAAGTCTTAA GAACATTTGT AAATAGCTCT GCAACACTTA 300
 10 TAGTTTGGnC AAATTCCTTA AATTTATTTA CACAGTACTC ACACATTAGT TTTAAAAATA 360
 ATGGATTGTT GAATTCCTGA TTTAATATAG GTAACCTTAGG 400

(2) INFORMATION FOR SEQ ID NO: 1932:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932:

25 ACTTGCGGAA nGACGCAACG TTTATGTACG TTGGAAGAAA AATTCAGGAC TTACGTTCAA 60
 AACTACCATA GCAATATGCA TTGAAAGATG ACAGTATGCG 100

(2) INFORMATION FOR SEQ ID NO: 1933:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933:

40 CGCTCTGCTT TAAGCGTTGG GACTTTGTCA ACGGTAGTGG ATGGGAAGTG GTTCTGCTTT 60
 G 61

(2) INFORMATION FOR SEQ ID NO: 1934:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934:

(2) INFORMATION FOR SEQ ID NO: 1935:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935:

ATGTATTACG GTTTAATTAA GCCACATACC AACAAGATTG CATTATGGT ATCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1936:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936:

TCGCACCAGA AACAAGGGAT TGTTAAATT GCGTAAATCC TTAAATTTAT TTGTAAATAT 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1937:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937:

ATGAATAATC ATATTTCTAA TCAAAGTAAT AGCATTTATA TTGTGTTTAA A 51

(2) INFORMATION FOR SEQ ID NO: 1938:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938:

TTGCTGAAGA TAGAGGCTTC ATGAAGGTGG AGAAGTTAGC TGATTTCTGG AACAGG 56

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939:

ATCTCAATGT ATTCTCTAG TGTAAGTTCT TCATAAATAA CCGGTGATT C

51

(2) INFORMATION FOR SEQ ID NO: 1940:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940:

CTCAGGTCGA CTCTAGAGGA TCCCCTGTTA AATAAACTT CTTAAGCACA TACTTATTTTC 60
 ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA CTACTCCCTT 120
 ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA CTCGTTAAGA 180
 CAATAGGAAC GCCTGGCACC TGGATGCGTA CTTGCACCTG CAAAATATAW ATCTTTATAA 240
 TCTCGCGATA CATTyTGTGG ACGATAATAA TTACTTTGCG CTAAAGTTGG GCATTAAACC 300
 GAATGCCGAA CCAAATTC 318

(2) INFORMATION FOR SEQ ID NO: 1941:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941:

CCGGGAAAAT TTTTGAATT AAGTGGAAAA AAAATCCCCT TAAATTTCCC CTGGCCA

57

(2) INFORMATION FOR SEQ ID NO: 1942:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942:

5 TGTTCCTCTT TTGAATCTGT TTTATTCGTT TGTTCTCTCT TTTTCTGTTC ATCTTTCATA 60
 TTTCCACATC CCCCAATAAA AATGATTAAA AGTAATACAC TCATGTACAA AGCAATTTTT 120
 TTTATATACT CCATCATTTT ACATCTCTCT GTTTTAATTT TATAAACATT TGAATATTTT 180
 10 ATACAACTTA TAAAATAGT GATTATTCAA CTTTTATGTT ATCAAACAAA ACTAACTTAT 240
 TCAATTTAAT ACATGTAATT CATTTTAACT TTATTATTAA ATGTTCTAAC GTnATTTTTT 300
 ATATTAGTAA TTATATTTAT TTATCCTCGC TTGGATTAAA GTAGATACTA TCTGTGAAGT 360
 15 AnATATTTTC TGCCTTGn 378

(2) INFORMATION FOR SEQ ID NO: 1943:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943:

AAGAAGAAGT CAAAATTCAG CTAAGTAAAA GCTCGAGTTA TAAAAAAGTC TAAATTGATT 60
 30 CAACAGGAGT AGAAAAGGAA ATTAGTCTTG CATATTTTAG AAAATGAATA AAAACAGTTA 120
 CTATATGCAA CTCAAGAATT AAATATTATT TAAGCCACAT ACCTATTAGA GTACAAAATA 180
 TACAAGTTGT ACTTATATCT AGGTATGTGA CTTTTGATTT TAAGCGTAAA GTAAAAGTTT 240
 35 TTATGTTTGT ATTAGTTCTA AATTATTTTG CACTTGGATG ACACGTATTT TTGAGTTTAA 300
 GTGGTGA CTC AAGTTCAATA AAATAAATAT CAGATAGGAT AATTTGAnAA TnATATGAAA 360
 40 GGGTTATCTC CAAAATnATC TCCATATTAT AAGG 394

(2) INFORMATION FOR SEQ ID NO: 1944:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944:

50 TATTCGTGAT GACGATTGTC GGTGACATGA AGTTCTATTT GCTGGCACTG AT 52

(2) INFORMATION FOR SEQ ID NO: 1945:

55

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945:

10 CGTTTAAAAA ATGATATCAA TCTTTATTGT GGATTGCAAC ATCCGTGTGC TCCATAAAAC 60
 GTGTGGCGAG ACTTGGGAAA GG 82

(2) INFORMATION FOR SEQ ID NO: 1946:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946:

25 GTATTATTGA TGAAGAAACA GCTCTCCAGT TGTAGATGCA TGCTACGTTT ACGTTACCAC 60
 TGTATCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1947:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947:

40 TATCACCAGC ACCAAGGATA ATGACATGCT GATCTTTTGC AGTTATGGTA 50

(2) INFORMATION FOR SEQ ID NO: 1948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948:

ATTGTATGAA TCTTTGGGGA ATGAACTTTT AACGAACGGA CATCTTGCAA TGACGCATCA 60
 55 AAATGGTTTT AACACATGTA ATCGGCTCTC GGTACTATTC GTGTGATGTA CACATGG 117

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949:
TTTGATGATT TCGGGATGGA TTGGTATTGT GGTGAATGAA TTTTITAGCT CATCATCAAA 60
TTAG 64

15

(2) INFORMATION FOR SEQ ID NO: 1950:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950:
CTCTAGTGGC CATTCAATTT TGTCGCTGAA TGATGTTGGT ACATCCATTG CTGCTGT 57

(2) INFORMATION FOR SEQ ID NO: 1951:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951:

40

CTGTCCTTCT GAAACTTGGG TATTTAATTA GGAATAGTTA AAAAAATCAT TCACAGAAAC 60
ATTTAATA 68

(2) INFORMATION FOR SEQ ID NO: 1952:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952:

55

TTAAATTAAC CTTAAGGTTG GATTATTTTAA CCCCCAAATT TTTGGGGTGG TTAAATTTCC 60

(2) INFORMATION FOR SEQ ID NO: 1953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953:

GACATTTACA CCTGCTTCAA TCTGGTCCAG TGCAGCATCT AATTCTTCGA

50

(2) INFORMATION FOR SEQ ID NO: 1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954:

ATTGGCCAA CTGTTTCAGCA CGGTATTGGT TCAATGCAAC ACTTTATCAT TGCTTCAGGG

60

CTATATCGGT GGTATGGGTT GTATCACTTC TTAGAACGTG GTATTAA

107

(2) INFORMATION FOR SEQ ID NO: 1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955:

GAAGTGAATA TGAAGCTGCT AAAGACTCCG GAATGCTACC TCAGACAACT GATG

54

(2) INFORMATION FOR SEQ ID NO: 1956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956:

ATGATTATTT TAGTTCCATT TGTGAGTCG ACTGCTAAAG TTCCATTTAA ATGTTGTACA

60

ATAAGCAGTA ATTTATGATT GTTTACAGTT TTTAATTAC CATGAACTTT TGAAGCATTT 180
 GCATGTTTAA TAACATTATT TATCGCTTCA CGCGTAATCA TAACTAACAT AGATTGTTTA 240
 5 GTAGGACTTA ATACTTGCGC TAATTCCTTA TTTTCAAATG TAAATCAAT ATCAGCATCh 300
 nTnAAAACCTT TACGTATACT ATCAATCTCT TCAATAAATG ATGGTAATTT TACATCATCA 360
 ATAAT 365

(2) INFORMATION FOR SEQ ID NO: 1957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957:

AAATAATGTC ACAAAGTTA AAGATACTAA TATTTTCCA TATACTGGTG TAGTTGCTTT 60
 TAAAAGTGCA ACTGGATTG TAGTTGGAAA GAATACTATT TTAACAAATA AACATGTGTC 120
 25 GAAAAATTAC AAAGTGGGCG ATCGTATTAC TGCACATCCA AATAGTGATA AAGGTAATGG 180
 TGGTATTTAT TCGATTAAAA AGATTATTAA TTATCCAGGT AAAGAAGATG TATCAGTCAT 240
 30 TCAAGTTGAA GAGCGTGCAA TAGAACGTGG ACCAAAAGGC TTTAATTTTA ATGATAATGT 300
 AACGCCATTC AAATATGCGG CAGGGGCTAA AGCTGGTGAG CGAATT 346

(2) INFORMATION FOR SEQ ID NO: 1958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958:

TTTCCAGTT AATTTTCCA GTTCACTAAA TACTTTATTG ACTGTACCAG ACCCAATAAT 60
 45 AATTTGGTAT TGTCCCCCAG TAGAAAACGT CCCTTAACT ACATCCATAT TGTTTAGCGC 120
 CTCTTCATTT ACTAACTTT CATCATTTAA AACTAATCGT AGTCTCGTTG CACAATGCGC 180
 50 CATTGCATCT AAATTCTCTT CTCCGCCTAT CGCGTTCAAA ATTTCTTCTG CGGATTGCTT 240
 ATAATTCATA TATTTAGCCT CTAATTAGA ACCGGTTCCA TTTATTCCAC TTTATTGTAA 300
 CCGGTTCCAA AAATATTTGC AACACTCTAT TATCATTTTA TATAAACACC TACACCATTT 360

(2) INFORMATION FOR SEQ ID NO: 1959:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959:

GATTGCATAT AATAGTAAAA ACATTACATC TTGAACAGTA CTCGTTTGT

(2) INFORMATION FOR SEQ ID NO: 1960:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960:

AATTGAACC AGACACTGAT ACAAGTCACA CCCAGAAACT TTTAAGGACG TAAATGT

(2) INFORMATION FOR SEQ ID NO: 1961:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961:

AACGCTATAT TAGCGATATA CAATGATGCC ATTATCAATA nTACAnCTGn

(2) INFORMATION FOR SEQ ID NO: 1962:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962:

TACAACGTCA GTTGGCAGAC ACCAGAAGAA GGATTCATAA GTATATTCAG GAACTTGTTA

(2) INFORMATION FOR SEQ ID NO: 1963:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963:

10 AATTTTTCCTCCTTTTTTAAATTTCCCAAAA AAAAnCCCCC AAnAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 1964:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964:

CAACAAGTAG ATGCATCAGA GAGTAGTGTT CAAACGTTAA TAGATGTGGC ATG 53

25 (2) INFORMATION FOR SEQ ID NO: 1965:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965:

35

AGCAAAGGCA TAACTGCTAA TGACCATGTA AATGAGACGA GTCGATCGTG GCCA 54

(2) INFORMATION FOR SEQ ID NO: 1966:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966:

CTCAAATAAC TGGCTCAACT CAACCGGTCT ATAACACCAT AACACCGCAT GCCACTCTAG 60

50 CATACTCAAT CGCTCTGGTA CCAGCnCTCA AATAACTGGC TCACGCCAAC TGTCTATAAC 120

ACTAACACGC ATGCACTCTA GCCTACTCAG AGCTCTGGTA CAGCACTCAA TAGCTGACTG 180

55 TCACAGTCCA CACACACTCA ATACTGGCTG ACACAGTTCA CACACnGCTT ACTCGCTCTC 240

(2) INFORMATION FOR SEQ ID NO: 1967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967:

CAGTTTAAAC TCGATGTTGT GTACTACTGT GCCAGCTGGA ATGTTTATA ATGGTGATG 59

(2) INFORMATION FOR SEQ ID NO: 1968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968:

GTTACATGGC ATCAGCCAA ACCTGTCTAT AACACCATAA CACGGCATTG CC 52

(2) INFORMATION FOR SEQ ID NO: 1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969:

ACAATTTTAA TTATATACT CCAGGGGCTA CAGTAATACG ATTTCTCCAG ACTCCAAA 58

(2) INFORMATION FOR SEQ ID NO: 1970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970:

TGACGTATAA TGGATGAAAG TCTATTAAGT TTAAGAAGCT AATACTGTGA AATCTTTCT 59

(2) INFORMATION FOR SEQ ID NO: 1971:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971:

10

TATCATGTTA TCTTCAATCG TTCACCAACA GTCATTTGCT GCATCAGTAA CG

52

(2) INFORMATION FOR SEQ ID NO: 1972:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972:

TTGCTGGTGC CATAGACTAC ACTTGTTTGA TATCAGAAAT GGGATCTGTT CCATTACC

58

25

(2) INFORMATION FOR SEQ ID NO: 1973:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973:

35

AGTTAAACCG AGTCCAACCC AAACCTCCAA TCCACCTAAT GGTAAAAATT CCAAACCAAT

60

ACCAGGGAGG GACCAAAAAA CGGAATGGGG CCTATTGGTA GGGTACCTAT CCCATTTAAA

120

40

AATCCATCCA AAAGCCCAaA TTATCGGACC ATTTTCGCCA AAAATAATTT AAGCGGAAAT

180

TGAATACCTT AAAATTCTCh GGGCCCACT

209

(2) INFORMATION FOR SEQ ID NO: 1974:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974:

ATCTGAGTAT TTATAACATA AATCACTAAT ATCGTTATTA CATAGGGATA GGGTAAAAGT

60

55

(2) INFORMATION FOR SEQ ID NO: 1975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975:

TTCTCTGCATC CGAGTCTGAA TCGCTGTGCA ATCACGTGCA GTCGATCGCT ATCAGGTCGA 60
 GTCGCGTCGA ATCGTTCGCT ATCGAGTCGA TCGCGTCGAA TCGAATCAGG TCGAGTCG 118

(2) INFORMATION FOR SEQ ID NO: 1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976:

TTGCAACHTT TGATCTAGAT ACTACCTTAG TTGGATTGTA CTAATTGATT CTAATTACCC 60
 TTTAGTTGGT TTTGTAGCAG GCGTTTTGTC TTTACCTGAC TCACTAGATG CGTCATTTTC 120
 TTTTTCACCA CTTGGTAATT GTTTATTGTC ATCTTTTGG CTGTCTTGT TTTGTGATTC 180
 TTTTTCACCA GGTGATGGTG TTGGTTTGCT AGGCGTACTG GAGTAGCTTC CTTCTTAGCT 240
 GAGTTATCTT GTTGTCTTT TTTGTTAGAT TTATCGGTAT TGGCTTTTGT AAATGCTTCT 300
 TTATCAACGA TTCTGACATG GTATTGTCCA TCATAATCAA TCGTTTTTAC GTGAACITTA 360
 ACGATAGCAT CATATAGAGT TTACCTTCAA CATATGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977:

TAGACAAAGA CAGTAACAGT AAAGTACGCT TCAGAACTGA TGGCTCACTG CGAGTATAAA 60
 AACTTGTAGT GTCC 74

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978:

ACTCAAAAAC TCGGAAAACA TTCCAATTGA GCTTAAATCT GACCCTTTTT TTGACCCTTA 60
 TATTTTTTAC AA 72

(2) INFORMATION FOR SEQ ID NO: 1979:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979:

ATGTCATTGG CTTTGAACCT TATCTTCAAG CACCCAATCG TTTTAACTTT TCAAAATTTG 60
 GCACCATAA 69

(2) INFORMATION FOR SEQ ID NO: 1980:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980:

CAGAGAGTTG TCGCTCATTA AACGCCACCT GATGAGTTTT CGCTTACGAA GTGCCACGCG 60
 GTATGGATAA TTTTCACCTG TTGCTGAGTC TTTGATAAGC CTCGACTGT 109

(2) INFORMATION FOR SEQ ID NO: 1981:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981:

(2) INFORMATION FOR SEQ ID NO: 1982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982:

GAATCTGTTT AAGTTAGAAT TATCCCGGCA TAATGATAAA GGCGAGTAAA TGG 53

(2) INFORMATION FOR SEQ ID NO: 1983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983:

GnCTTTTGAA TAAAGAAAA TTCATCAATA GAAAAACCGT CTTTATCGTC TATTTTTTTTA 60
 ACTAGTAAGT TCGGCGTTCT TAGAGACTCA AATATTGATT TTACGTTTTT CTTTGTTACA 120
 CCACTAACAC TAAATATTCT TCCATCTAAA TCTACTAATT CTGGTACCGC AAAGACATCT 180
 AAACCATGTG TTTTTTCTTT GTATTTATTT TCATCTTTTC CCAATAAAAA CACTTGGAAC 240
 TTTTGATTTh GT 252

(2) INFORMATION FOR SEQ ID NO: 1984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984:

CGTGTTAATC AACTAATTCT TAGTTTTAAC TGTCGTAATA ATCAACTGAA CACTTTCAAT 60
 CTA 63

(2) INFORMATION FOR SEQ ID NO: 1985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985:

5 TCCTAAAATG ACCGCTAATG CCTATGGATT GTTATCACCG ACCGCAGGGA CAGCAGGACC 60
TAC 63

(2) INFORMATION FOR SEQ ID NO: 1986:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986:

GGCATATAAA AATTAGAGAA ATTATTTCAA ATGAACAGAT AGAGGCACAA GATGAATTAG 60
20 TTAAACGATT AAACGATTAT GntTTTAAATG TCACTCAAGC AACTGTTTCT CG 112

(2) INFORMATION FOR SEQ ID NO: 1987:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987:

TTTATCAATT TGTAACGAAC ATGAATTACA TGTTTCAGGA AAATATATTT CATCCCATT 60
35 TTAAAAAGTA TAAGATTTTA TGAAAAATTA AACCAATTNA GTATAA 106

(2) INFORMATION FOR SEQ ID NO: 1988:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988:

45 AATGGCGTAG TTACAGCATT TATGATTGTG TTAATCTTTT CTTCTGATAA ACATAATCTG 60
50 TTTGACCAAA AGTATTTAAG TGTTC AATTA ATTAGTTTTT TTATTTACGT CGTATGGCAA 120
GTTTTATTGA TAATGTTTTA TTATCATTCA AAACCAAAAA ATAATTCATT TTCAAAATTT 180

TGGTTAGGTG GACATCAGAT TCACTTCCAT GAAAGTAAAT TAATTGAATT TGTTGGTTTC 300
 TTAGGAATTT CTTATGTTAC ATTCAAAAGT GTGCAGTTAA TTATGGAAAT TCGTGATGGT 360
 5 TCTATCAAAG AAATTAAAGT ATGGAAATTA ATTCAATTTA 400

(2) INFORMATION FOR SEQ ID NO: 1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989:

TTCAGCTTAC AATAATGAGC AGGTTGGGGT GGGCTCCAAC GCAGAGAATT TCGATAAGAA 60
 20 ATTCCACAAA TAATACAAGT TGGCCCACTC CCATTCTGTA ATAAATATAG GAGGTCATTG 120
 TTATGCAAAT AGAACTTACT GATGCAGCAG TAACTTGGTT TAAAAATGAA CTTGAGTTGC 180
 CTGAAAATAA TAAAGTGCTC GTGTTTTTTT TAAGATATGG TGGCGAATTC CAACTCAAGC 240
 25 AAGGATTTAG TCCTGCTTTT ACAGTTGAAC CAAAGGAAGA TGTTGATATT GGCTATGAAC 300
 AACAAATGA CGATTTAAAT GTTGTCGTAG CGGAAAAGA TTTGTGGTAC TTTGAAGATG 360
 ACCACATTAT GTTAAATGTA GTTGTCACGA AGATGAATTT 400

(2) INFORMATION FOR SEQ ID NO: 1990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990:

CAATTTATTA TGTAATAAT TATAGCATTG ATGAACAAGG CGCTCAACGT AATANTACAA 60
 TTAATGGATT GTTTCACAAG ATGGTAAAGC TAGGATGTCT TTTTATTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 1991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAAACAAATT CATCAATTGT TAGTGGCATA TCCTAATGTA ATTAGAGAGG AGTT

54

(2) INFORMATION FOR SEQ ID NO: 1992:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992:

GAACGATAGA TTGATGAAAA GTTTAAAAAA GTACGTATAT GTTTATTAAAG TTTGAGTTT

59

(2) INFORMATION FOR SEQ ID NO: 1993:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993:

CGAGACCAAA ATATTCGAAC GAATAATTTTC AGTGTTTTGC TCCTTTATTA TAGATTCAAG

60

CTATGGATAA TAG

73

(2) INFORMATION FOR SEQ ID NO: 1994:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994:

ATCCATACAA ATGTAACAAG CACAATTGCh GCCATACTTn GCATGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 1995:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995:

(2) INFORMATION FOR SEQ ID NO: 1996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996:

TCaTTAAaA TTAATGTnCG TTGGGGCTCT AATAAAATTT GTTTACAACG

50

(2) INFORMATION FOR SEQ ID NO: 1997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997:

TCATGATTTG AAATGACTTT CAATGACTTG GGTGGGACAC TTGTTGCACA GCTGGATGTG

60

C

61

(2) INFORMATION FOR SEQ ID NO: 1998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998:

CATGCATTGA TgTCTCAAA GAACATGATG AAACAGGTCA nCACATGnCA

50

(2) INFORMATION FOR SEQ ID NO: 1999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999:

GGTTCGCTAC TGATTGGGTA TACATCTGAT TTAGCAATCT TGCGCACTTG TT

52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000:

ATGTGGTTAG ATATCTGCAC ACTTGAACGT TATTGTGGGA TATACTTGGC CAT

53

(2) INFORMATION FOR SEQ ID NO: 2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001:

ATCTCAGTAA GGGTAAGCGT CAAAGTCTGC ACGGATGCTA ATGTTTACCA GGTT

54

(2) INFORMATION FOR SEQ ID NO: 2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002:

CTAAAGATTG TAATGCTTGA ACAATTGGTT CAGTGAATTT TTGGAAATTG TGGAAACTGT

60

TACCATCATC ATCTGTTATA AACTAAAGT TTAAATTGCC AGTATCATGA TAAACAGCGC

120

CACCACCAGA AATTCTTCTT ACTACATCGA TGTGTGAGC ATCGATATAT GTCTGATTTA

180

CTTCCTCTAT CGTATTTTGA TTCTTTCCAA CAATGATAGA TGGTCTATTT ATGTAAAATA

240

AAAAGTAACT TTCTTCTGCT GGTAATTTT TTAAAACATA TTCTTCCATT GCTAAGTTTA

300

AAGTTGGATC TGTAATATTA TTATTACTAA TGAATTTTCA TACAATCTCT CCCTTATATC

360

TATATATATn CTCTACTTAT TTATGCCTTA ACTTTGCTCA

400

(2) INFORMATION FOR SEQ ID NO: 2003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003:

CCGAAATAGG ACGGGCAGTT GGATTTATTC GAAATGGGTG GCGTTAATAT ATACAGT

57

5 (2) INFORMATION FOR SEQ ID NO: 2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004:

15

TAGTAGTTGA AGGCGACCGC GGTCCACAAG CTGCAACGT TGTTAAACTA TAATTCTTAG

60

ATTTGAATCA TTGATTTTAA CTAACACCTT ACCAAGAAGT AAGGTGTTTT TA

112

20 (2) INFORMATION FOR SEQ ID NO: 2005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005:

30

AAATCTTGAC ATAGGCACAG GAATGTATAT TGATCTCGAT CACTTAAGTC

50

(2) INFORMATION FOR SEQ ID NO: 2006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006:

40

AAGGTGGGTT TAAATTTCCC AAAAAAAAAA GCCTTTTAAC CTTTGGGGG GTCCCTTTTC

60

45

CTTGGAATTG GAAAGGGGCC AAAATTGGAA TAAGGGGnTT GGAAAAACCC AAGCC

115

(2) INFORMATION FOR SEQ ID NO: 2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007:

TGAAGAAATA GCAAATGAAC TCAATATTTTC TATTGAACGT CAATATTTCA ACCAATTATA 60
5 TCGCTTCAAT AATCAAGATT TAAAGCATCT TGAACAAGAN TTTGA 105

(2) INFORMATION FOR SEQ ID NO: 2008:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008:

ATTGGCTACT AAAGTTAAGG ACATGATGGA TTGGATTAGT GGTATGCGCT TTGAAAAGAT 60
20 CAATTAT 67

(2) INFORMATION FOR SEQ ID NO: 2009:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009:

30 TATAAATTAG CGTCCTTCAT ATCACAACGA TGATGCTCTG TCGGAAGATC TGATTTATTT 60
CAATGTGCGC ACG 73

(2) INFORMATION FOR SEQ ID NO: 2010:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010:

45 CTTTGTTTAT GTTTCGTTTA ATTTGTAACC CTCTCTTTGG ATACCGAGGT T 51

(2) INFORMATION FOR SEQ ID NO: 2011:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 88 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011:

TAACGACCAA GCTTAAAGAG ATACGCTCTT ATGCGATTGG ATAGGTCGTT AAAGTTAACT 60

10

ACAATACCTC ATAAGTAGAT TTAGAATC 88

(2) INFORMATION FOR SEQ ID NO: 2012:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012:

GTCAACCCCTT GCCAAGCTTA TATCAGGATA CTGGGATGTG ACTTCCGGTG AATTAC 56

25

(2) INFORMATION FOR SEQ ID NO: 2013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013:

35

AGCTTATAGT ACTTGTGACT TCATAATGGA TGAAGTTGAA GTACCAAAG AATTAACACA 60

ATTACACGAA TAATTAAAT AGAGAGTGTG ATAGTAGGTG GAATTATTAA ATAGTTATAA 120

TTTTGTTTTA TTCGTATTAA CTCAAATGAT ATTAATGTTT ACAATACCAG CTATAATTAG 180

40

TGGTATTAAG TACAGTAAAC TTGATTATTT TTTCATCATA GTAATTTGGA CATTATCGTT 240

ATTTCTATTT AAAATGTTTG ATAGCGCGTC CTTAATCATA TTAACITCAT TTATTATTAT 300

AATGnATTTT GTCAAATCA AATGGnATTC nATTTTGTG ATTATGGCTT CGCAGATTAT 360

45

CCATACTGGT GCCAACTACA TGGATATAGT TATATATGCA 400

(2) INFORMATION FOR SEQ ID NO: 2014:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014:

TCTTTTCGAGG ACAGTAGAGG GTCCACCCTA TTGGACGTGG TACTGTACTA CTTTAAAA

58

(2) INFORMATION FOR SEQ ID NO: 2015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015:

TCTACCTGCA GGCATTCAAG CTTGGCACTT GCCGTCTTTT TACAACGTCG TGA

55

(2) INFORMATION FOR SEQ ID NO: 2016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016:

TACTCTTAAG CTAACAACGG CGGTTATGAG TCCTTTGACA AGGTATCGGA GGAAAGACCG

60

TAAAGC

66

(2) INFORMATION FOR SEQ ID NO: 2017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017:

CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATATAC GGTTAGACCC AATTGTTTCAT

60

GGCGGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC

105

(2) INFORMATION FOR SEQ ID NO: 2018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018:

CCTTCCAATA GTAATTGATT GATGTATGAG TATATTAGGT GTGAAATCAA GAGGATTC

58

5

(2) INFORMATION FOR SEQ ID NO: 2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019:

TTTCCTCGTA GGTGGTTCTT CTCATCTTC GTTGTTTTGT CCGAAGTTTG GA

52

(2) INFORMATION FOR SEQ ID NO: 2020:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020:

30

ATAGTTTAGG TGAGGATGTT GnGGTACGAC AGGAAGAAAG ACGGCAAACA

50

(2) INFORMATION FOR SEQ ID NO: 2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021:

TTGTCACAAT AATTTCTTCA GGATCATAGG AAAAATGATA ACGATTTTTG AAGTATTGAC

60

45

TAATTGCTTC GCGAGTTTCT AATAACCCTT TATTGTGAGA GTATGATGTC TTGTCATTGT

120

TAATAGCATC AATATATGCC TTTTTCACAA CATCAGGCAT CGGGAAGTCT GGTTGGCCAA

180

TAGTTAAATT AACACAATCA TCCAAATTAT TCATACGATT TGAAAATTGG CGATACTTGG

240

50

GTGGCTCCTA AAATAATTAG GAAATGAGGA nTTnAAGGAA GGTTTCCATT TnGTGGACAC

300

(2) INFORMATION FOR SEQ ID NO: 2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022:

	TCATCCAAAT TATTCATACG ATTTGAAAAT TGGCGAATAC TTGGTGCTCT TAAATATTTA	60
10	GAATTAGAAT TTAAGAAAG TTTCAATTTGT GACACCTCAA ATATAAATCA AATATTGTCT	120
	AAAAATTTAG AAATTAATAA TATCATAACA TACTTTTAAA GCAAAAAAGG GTAAATTACT	180
	TAAGCTTTAT TTGAAAAACG AAAAATGTCT AAATACACTG TAGTAACTAC TTTTCAAAAT	240
15	GAATAAAGTG GTTACAGTTA ATGTACTTAG ACAGTATAAA ATTATGAATC TTTAAACTGT	300
	GATGGTCTTT GTAAATTAAT TATTGGATTT GTCCATTAC AAACAAAGTT TGTAGATAAT	360
20	ACATATACGA TGATTACAGA TATACTTATT AAATAAAGAT	400

(2) INFORMATION FOR SEQ ID NO: 2023:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 50 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023:

	TTnAAATATA CCAATCACGT TCATCCACAG TGATCCTAGA CCAATCCAGA	50
--	--	----

(2) INFORMATION FOR SEQ ID NO: 2024:

35

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 66 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024:

45	TTTTTAATGG TTAAAAAATT CCCTAATAAA ATTTTGAAA ACCTAAATTC CAAGGGGTTA	60
	AATTCC	66

(2) INFORMATION FOR SEQ ID NO: 2025:

50

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 64 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
55	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025:

GTAAGAGCAA TGGCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG. 60
5 GACC 64

(2) INFORMATION FOR SEQ ID NO: 2026:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026:

CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 53

20 (2) INFORMATION FOR SEQ ID NO: 2027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027:

30 CATTTCACTA TTATTGGTTT AGGGTTGTTT ACGTTCATCA TGACCGCACC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2028:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028:

CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60
45 AACGGAATCG TCA 73

(2) INFORMATION FOR SEQ ID NO: 2029:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029:

AATAATAATT CTGGAATAGT GTTTAATACT TATTnTCCGT TTAAGATTTC AACTTAATAT 60
 5 GGGTTACAGC GCGTAGCTCG TCTAATTCAT CATCACGTGT AGAGTGCTCT GCCTTATCAG 120
 ATCAGTT 127

(2) INFORMATION FOR SEQ ID NO: 2030:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030:

20 GCAAGTGAAT TGAAGTGACA TGTGGCTGGT GCTTCATGGT AATGATAAAC CAACACCATG 60
 G 61

(2) INFORMATION FOR SEQ ID NO: 2031:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031:

35 ATAAATATCT ATTAGATAT AAGTATTGAT AAGTTGCTTG AATTTATAAA GTGAAGGAGT 60
 AGGTGTCATT AGTATAGT 78

(2) INFORMATION FOR SEQ ID NO: 2032:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032:

50 GAATAGTGTT TATAAAATGT TGACACTGTA GTGGCATATT GTAAATTAAA TATTATTATG 60
 TGATCATTTT GTTTAAATAT TAGTTATAAG AAGTGAAATA nTCATTTTAA AAGGAGACTT 120
 AAAACTTGAA ACGATCAACG AATCAAGAAA AATTTCTTGA TACACTAATT AGACTTAATA 180

(2) INFORMATION FOR SEQ ID NO: 2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033:

TTTTGTCATC TGTATAGGTA TGCGCGCCGG TGTCTTTATT CACTTTGAAC TGTGCGT 57

(2) INFORMATION FOR SEQ ID NO: 2034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034:

AAGGCATTGG ATATAAGACT TGATGTTGCA TGGCAATCAC ACTGCCTAAT CCTTGCATAT 60

AA 62

(2) INFORMATION FOR SEQ ID NO: 2035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035:

ATGGCAAATA CTATACATCG TCCAATTGAT TGAAAAATAT GGTTATTAAA GA 52

(2) INFORMATION FOR SEQ ID NO: 2036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036:

AAGGTGTTTT TATATGCTTA TTACAAATAC TTAACGCGAT GAGTTTCTCA ACCAAATTGA 60

(2) INFORMATION FOR SEQ ID NO: 2037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037:

TACCCACCCC CAAACCCAAG GTTTTAAAAA ACCCCTTCCA AAAGCCCGGA AAAACCAAAA 60
 GGAATTATTT T 71

(2) INFORMATION FOR SEQ ID NO: 2038:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038:

GAATCCCGGA AGTACAATTT GGTACGTGAA GAAAATGGTA GTGGAATTAC 50

(2) INFORMATION FOR SEQ ID NO: 2039:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039:

CAGTATCTCT TGGTATTTTA ATTGGTGCTT TATTAAACGT AATTTTACCT TTATATATCG 60
 ATGGAGCGAA GAGTATTTTC GTATACGTTT ATAGTGCCTC TATTTTACCA GGTATGATTC 120
 CTTGGTTTAT GATTTTATTC AGTCATTTAC GTTTTAGAAA ATTACACCCT GAAGAATTGG 180
 AAGGTCACCC ATTCAAAATG CCTGGTGGCG CAGTAACTAA CTATTTAACA ATCTTATTCT 240
 TAATATTAGT ATTGGTTGGT ATGGTATTTA ATGTTGAAAC TAGAATATCA GTGCTTATTG 300
 GTGTCATCTT CTTAACGATT GTAACGATTT ATTATTTTAT TAGATATAAT AAAAATAATG 360
 TAAAGCAnAA TAGTATGTTA TAAnGAGCGn TACTTATGAC 400

(2) INFORMATION FOR SEQ ID NO: 2040:

- (A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040:

10 AAGCTGATTT TTCTAAATGT TGAAAATCAT AAAGTGCTTA ATAATAAATA ACGAGATCTA 60
AGTAATAGTG CTCCATTAA 79

(2) INFORMATION FOR SEQ ID NO: 2041:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041:

25 AATTGAACGG ATCGTTCCCA ACCGTTATCA ACCCAGACCG GTGTTTGAAC CCAA 54

(2) INFORMATION FOR SEQ ID NO: 2042:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042:

AATGGGATTG GTTCAAAGTG AAATGGGCTG TTAGTCCCTG TAAAACCAAG 50

(2) INFORMATION FOR SEQ ID NO: 2043:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043:

50 ATTGGnATAA TCAAAGCATT GAATCATACA TAGTCACATT GATTGTTTCC TCAGAGTTTC 60
AACACTCTAT AACTCATTTT AGTAATTTCG TGATTGCGCA CTTTCATGTG 109

(2) INFORMATION FOR SEQ ID NO: 2044:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044:

10 TTTTATGGAG GTGATGAAGT GGGTGAAGCT GAAAGGAAGC AAAAGCTTGG 50

(2) INFORMATION FOR SEQ ID NO: 2045:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045:

TTGGCCCCCT TCCAACCCTT GGAAATTTTA AAAGGCCANT TTTGGGGTAA AACCCCTTGGT 60

25 TCCAAGGACC CCCAAAAGTT TTTTAACCTT CCAATTATTA T 101

(2) INFORMATION FOR SEQ ID NO: 2046:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2046:

ACCCCTTTCCA AAAAGCCCAT TTTGAATTCC CCAAAGGGAG CCAAATTTAA GATGGCCGCh 60

40 AAAAAGGACC GGGGGGTCCA TGTTTAAATT TAAGCCGGAC 100

(2) INFORMATION FOR SEQ ID NO: 2047:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047:

GTTAGTTATG AGCAACGTAT TAATGAAATT ATTGAGCAGT AATThACCAG 50

(2) INFORMATION FOR SEQ ID NO: 2048:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048:

10 TACGTATTTT CAAATGACGT TGGTGGACGT CACACTCCAT TCTTCTCAA CTATCG

56

(2) INFORMATION FOR SEQ ID NO: 2049:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2049:

TTTTCCCCC CCCCCCAAA TTGGGGGTTA AAATTTTAAA AAAAGGGGTT AAAGGGAAC

60

25 CCCAATTCCG GTTAACCTTT TG

82

(2) INFORMATION FOR SEQ ID NO: 2050:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050:

TCAGATGGAT GGCAGTTATT TGGTATTCCA TGGGTATAAA GATAGCATAT T

51

(2) INFORMATION FOR SEQ ID NO: 2051:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051:

50 TGAACGGGAG AAAGATGTTG TTGCATGGTG TCTCGGAAAC GTTTGTGTCC ACGTA

55

(2) INFORMATION FOR SEQ ID NO: 2052:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 74 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052:

ATACCTGGAT GCAAAGGCAA AGTCGCAATT TTCCCTGTTC TAATGTGTCT AACTTCTCTT 60

10

CTAAAGTTCA GGTT 74

(2) INFORMATION FOR SEQ ID NO: 2053:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053:

AATCTTGTCT GATGTAATGT TCAGGTCCCT TGACCCTCAT ATGCATGAGG T 51

25

(2) INFORMATION FOR SEQ ID NO: 2054:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054:

35

CATCGACTTA TAGCTTAATT ATTATAAAAA ATTTCTCCAG ATTAACTTT CT 52

(2) INFORMATION FOR SEQ ID NO: 2055:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055:

ACTGACACAT TATATTAGTG AATTATTAAA AAATGATGAG AAAATTAAAA TCATCATGAA 60

50

TGAATTCGGT ACTTTTGATA TTGATAGCAA TAGTATTTCA AATGAAATTG AAGTCCATTC 120

ATTGATTAAT GGTGTGTGTT GTTGCGATCT TAAACAAGAA CTTGTCTATG AACTAAAAGC 180

CATTGCTTTA AAAGGGGACG TTAATCATGT CATCATAGAA GCGACAGGCA TTGCGCATCC 240

55

TTATTTATGG TGTATTAGAT GCGACTCGAT TTTTAGAACG TCATCAATAT ACCGAAAAAT 360

ACAGTTTCGC TGGATGGGGA GGATCCAGTT GGAAACTAAN 400

(2) INFORMATION FOR SEQ ID NO: 2056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056:

TCAAAACTTT GAAGTTGTGC TTGCTTTGCA CCATTTTAA AATGTTTCAGC TGAGAGTATA 60

TCTTCCGCTG TAAAATTAC TTCTCCTGGA CTAAAGATT CAATTAACAA CCAAGCCGAT 120

AACGTATCAT TTAGCAATTG ACTCATGAAA TCCCACCTTG TTCCCTATTT GTTTTTTACT 180

TAATGCTATT TTAACAAATA ATTTAATCAT ATTAGTGTTT TTTCAAAAAT ATTCATATAT 240

TATCATTACC ATATTTATTC AACAAATGTT TGTAAAATCC TCACTAATAA AATTAATCGA 300

TATGACCATA ATTCATTATC CAATAAATGA CTATAAAAAT TTCTnCTATG CCTTCATTG 360

CAACTAAATT TGGACATCAA AAAAGAGCAC TCCTGAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057:

TTGTTGTTGT GATTTCACAT TTTCAAAATT TTGTTGCATG TTGTTAACTT CATAAATTAG 60

TGATTCGACT ACATCATTCA TGAGGACGCC TCCTACATTT TTTAATTTAT CACAATATAC 120

TGTATTCGTC ATGTTTTAAC ACTCTATATA ATTTGATTTA ACTATTTTTT CAAATGTGTT 180

ATCTGTTAAA TCAAGTAAAT CTAAAACTT CCTATATAAA TACAAAATTT TATCGTGTAT 240

GTTGTTATAC GATGAAAATA CTTTTAATCT AATAAAATCA TTTAAATCAA ATACACCTCT 300

GCTGATTAAC AACACATACT TGTACTTGCC TCAAAAATAA AAATTACTAA TCATGATTG 360

ACTTTTATAA CAAAATTCAA AAATATTGTA ATGAGTATTC 400

(2) INFORMATION FOR SEQ ID NO: 2058:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058:

10 TCTTTTTTACT CGCAATTTTA GGAAAAATGG TTGGATCAAT TGATAAAACC GGAAAATTAT 60
TAACAATAAT CAATAAAATA TCAAGCATAA TAATTATTAT TGTGCTCTG ATGATATTAC 120
AAAAACTTAT TCAATTATTA TTCTAAAGCG TTATGTAGTT GTATTTTAAA AGCGTTATAC 180
15 AAAAGACATA CTTGTGTCTA TGTATAACGC TTTATTTTATT ATAAATTTGG ATCAATTAAC 240
TCAACAAATT TAAATGTTCC ATTGTCATAT TCAAATTTCA GGATATTACA ATTACCGATA 300
TTATGCTTTA ATGCTTCATC TAGTTTAAAG CAATATCTTA AAAATACCnC CCTTANTGGT 360
20 CCATGACTCA CGACTAATGC ATTATTCTTT GGTGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 2059:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059:

AAAACAACAC AATCAAAAAT ATTGGATACA ACTGAAAAGT TATCAAAGCT A 51

35

(2) INFORMATION FOR SEQ ID NO: 2060:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060:

TTATCATGTT TAGTAGATTT TAAGAAGCTA GAACATTGTA GATATGATGA 50

(2) INFORMATION FOR SEQ ID NO: 2061:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061:

5 AACGTCGThA TATCAnCTTG CCAAACAAAG ATATTGTCAC CTTTTATCGG 50

(2) INFORMATION FOR SEQ ID NO: 2062:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062:

ACCATGGTGn ATATGGTCAT GATGATCGTT TGTGCCGGGA GCTTGAGCTG 50

(2) INFORMATION FOR SEQ ID NO: 2063:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063:

30 TTTCCCTTGG TTTTGGGAATT TAACCAAATT TGGGAGGGAT TTGGGACCAC CCCAGGATT 60

TTAÀÀÀÀÀÀÀ AAAATCCCAG G 81

(2) INFORMATION FOR SEQ ID NO: 2064:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064:

45 TTTTGGGGAC CTAACTGGG TGGGTCTGGA ACTGTTTCCC TTCAAACAC A 51

(2) INFORMATION FOR SEQ ID NO: 2065:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

ATGATGTATT CAAAAGGTAT CTATAAATA GCTTTAGTTG GAAAAGATGA GA

52

(2) INFORMATION FOR SEQ ID NO: 2066:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066:

15

TTTCATCACT GGCATCTTGT AATTTCTTGG TCTCATATCT GGAATTAATA GGT

53

(2) INFORMATION FOR SEQ ID NO: 2067:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067:

AACCATTAAG AAATTGGATA CACAGAGCAA ATATGGTTAT GATTAGGAAC CATGGCATT

60

30

ACC

63

(2) INFORMATION FOR SEQ ID NO: 2068:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2068:

AAAGGCAGCG ATGTTACTCA TACCGAACCT GGTTATATAT GAGCGATGAT GCAATGTA

58

45

(2) INFORMATION FOR SEQ ID NO: 2069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069:

55

AACAGGA

67

(2) INFORMATION FOR SEQ ID NO: 2070:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070:

15

CATTTAACCC ATCTTCTTTT TTTAATTCTT CTATACTACG GTTTAAAAAC TCTACAATAA

60

CTGCCATTTT ATCATCATCA AAGACT

86

(2) INFORMATION FOR SEQ ID NO: 2071:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071:

30

GTTTCTTCAA AATATGTGTA TTACCTTTTT GTATGGTTAA ATCTTTTAAT TCTATCATTC

60

TTGTCTTACC TCTTTTGGTG TATCCTCTTT TCAACATAT GTGATCGATA TGACATATTG

120

CCCTTTATGC TTTATTTTGA CATACGTTCT ACTAGGTGAA AATCCATTAA ATGTTAATTT

180

35

ATAATCAAGC TTTTCCCCTC TTTCACTATA AGCCGTAATA TTAACATATT GTTGCGTACC

240

TTTTGGCACT TTGGCATAAC TATACTCCGT TTTTAAGAAA GGATTAAAC GATCAAGTAT

300

AGGATGATGT ATGANTGTAA AAGCAATAGT AATGGATAAT ATTAATCCTA ATAATATTGC

360

40

AATGATAAAT TTCATAGTTA A

381

(2) INFORMATION FOR SEQ ID NO: 2072:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072:

ATCCCCGAAT TGCTTCGCAA ATGTATCATC TTCGAGGCTA CGTTACTTAA AT

52

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073:

10

CCAAAAACAG CATCACTGTG ATTATGGTTT TCATCTTCTA TAACTAAGAA TACATGTTTT 60
TTTGTA AAAA TTTTTTTGAT CA 82

15

- (2) INFORMATION FOR SEQ ID NO: 2074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074:

25

TTTATCGCAA TGAGGGAAGA TAAAGGATCC CGAAAGCGCC GTATGGGTTG GCAAACATTG 60
GGGACCAAGA CCGTTCCCCA TA 82

30

- (2) INFORMATION FOR SEQ ID NO: 2075:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075:

40

CTTGTTGCT CTTTATTTAT TTAATTGAGA CCTAGAAATA AGTTATTAAG CACAATCATT 60
CACTTT 66

45

- (2) INFORMATION FOR SEQ ID NO: 2076:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076:

55

(2) INFORMATION FOR SEQ ID NO: 2077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077:

TACGTTCTAT CATAGAGCCT GGAGATGAAA TTATAATACC GGGACCAATT TATGCAGGCT 60
 ACATACCACT CATCGAAGTA CTAGGTGGTA AACCAATTTA TATTGATACA ACAGCAACAC 120
 AATTTAAAT TACACCTGAT GCATTAGAAA GTCATATTTT TCCAAAGACA AGAGCTGTCT 180
 TGTAAATTA TCCGACTAAT CCAACTGGCG TAGTTTTTAA AAGAAATGAA GTTGTATA 240
 TCGTAAATGT ATTAAAAAA TATCCGTTAT TTATTATTAG CGATGAGATT TATGCTGAAA 300
 ATACATTTAG TGGTAAACAT GTATCC 326

(2) INFORMATION FOR SEQ ID NO: 2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078:

ACCCCTTAAT TTAATTGATG TTTTGTATT TTTAAATGA ATAGTTGAAG AAAAAT 56

(2) INFORMATION FOR SEQ ID NO: 2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079:

CACGTACTGC CATGTATGCA CAAGCCGGCA TTCATAAAGC CTTCCATGGC AGTCGTTATC 60
 A 61

(2) INFORMATION FOR SEQ ID NO: 2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080:

TGGGACAGGG CGTACCATT CAAAATGATA GTTCTGAGCT GCTAATTAAT ATGCCTTCGA 60

10 AAAAGATGAG TTAAATTTA GATGATGAGA CTGA 94

(2) INFORMATION FOR SEQ ID NO: 2081:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081:

AAGACGACAT GCAAGACATT GCCTTATCTA ATGACAATGT TAAAGCGAGT 50

25 (2) INFORMATION FOR SEQ ID NO: 2082:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082:

35 TTGTTGGCT AAAAATAAAG TGGCATTGAC GTGACCGCAA GTTGACGTAC 50

(2) INFORMATION FOR SEQ ID NO: 2083:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083:

CTTCCCAACA TTGCGCACTG AATGGCGATG GCGCTGATGC GTATTTCTCC TACGCTCTng 60

50 CGTATTCAAC CGCTATGGGC ATCTCATACA TCTGTGATG CGCTATTAAG CAGCCCGAAC 120

CGCACACCGT GAG 133

(2) INFORMATION FOR SEQ ID NO: 2084:

55

- (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084:

GGTAGGGGCA CTATTTTGTA TGTAAGGTT TTGTCGGGCA GTGTGAAATC AACGACT

57

(2) INFORMATION FOR SEQ ID NO: 2085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085:

CCCCCCCCAA AAACCGCCCC CCCCAATTTG GCCTTTTTC AAGGGGGTG TTTTAA

56

(2) INFORMATION FOR SEQ ID NO: 2086:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086:

35

AATAGCGAGA GCCCGACCAT CGCCTCCAGA TTGCGACTGA ATGGCAATGC GCTGATGCGT

60

ATTTCTCCTA CCATCGTGGT ATTCAACGAT ATGGGCACTC TCATACAATH GCTC

114

(2) INFORMATION FOR SEQ ID NO: 2087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087:

AAGGGGGAAA AGGAACCCAA GGCCCCCTTC CCAAGGAAAT TGGGGGGTTG GAAAAACCA

60

AAAATTTTTT AAAAACCCGG

80

(2) INFORMATION FOR SEQ ID NO: 2088:

55

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088:

10 GGGGTAAGTG GTTGAGACAG GAACTTTACA AGAGGTGTTT CGTCATCCTA GAACGACGCT 60
TGCTCA 66

(2) INFORMATION FOR SEQ ID NO: 2089:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089:

25 ATCAATGTAT TACGTATCGA AGGTGAATTA TATCATACTG CTAAATATGA CGGTTTCACA 60
TC 62

(2) INFORMATION FOR SEQ ID NO: 2090:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090:

40 GAATTCGCTA TCCTGAAATC CTGAGTCGCT GTCCTGAAAT CTGAAATCGC 50

(2) INFORMATION FOR SEQ ID NO: 2091:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091:

CGGGGTTCCC CCGTTCAATT CCCTTTGAGT TTTCAACCTT GCGGGTCGTA ATTCCCCAGG 60
CCGGAATTGC TTAA 74

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092:

ATTGTTGGGT ACGGTGGTGG GTTAATAATC CAAACACGTT AACTACCCG TTTTAGATAT 60
ACCTATACAA 70

(2) INFORMATION FOR SEQ ID NO: 2093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093:

GTTTTGGGTC TTGGGTATTA GTTTAATCTC CATCATGGTT AATTGGTATG GTATTGGTAT 60
TAGTAATCAT GTATGATGGG CTGGGCGG 88

(2) INFORMATION FOR SEQ ID NO: 2094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094:

TGGCCATTGA GGCGCATTAC GTACTACGGC TTGTCGTAGG GACAATTATT AT 52

(2) INFORMATION FOR SEQ ID NO: 2095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095:

AGTTGATGCA ATGAGTGATG CAAGGCGACT GAAAAGTTGG TATGAATGAC AAAACTTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096:

ACTTAAATC TAATACGGTA TTTTCAAAAA CGAATAAAAG TTACCTCTTG TCT

53

(2) INFORMATION FOR SEQ ID NO: 2097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097:

AACTTAATAT TGCTACGATA TGAACGGCAT NAACATACTT AGCGnTGnTC

50

(2) INFORMATION FOR SEQ ID NO: 2098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098:

CAAAATAAGA AATTAATTAA GAAAATGCCA AGATGCCAGA TGCCATCGGC GGAAAGGAAA
TTGCACGTAC GG

60

72

(2) INFORMATION FOR SEQ ID NO: 2099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099:

CCACCCAAAC CCAAAAAATA AAGCCCAAAA AATTGCCAAG GAAGGAAAAG GAAAATTGTT

60

(2) INFORMATION FOR SEQ ID NO: 2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100:

CACCAATTTTCTGGGCT GGATCTCGAC CTAAGTCCTG TAATAATTGA CGTTGAACAC 60
 GAATTAATTT ATTAATTGTT TCTACCATAT GCACAGGGAT ACGAATCGTA CGTGCTTGGT 120
 CAGCAATTGC ACGAGTGATT GCTTGTCTAA TCCACCATGT TGCATATGTT GAAAACTTAA 180
 ATCCTTTGTT AAAGTCAAAT TTTCAAC 208

(2) INFORMATION FOR SEQ ID NO: 2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101:

TAATGAAATT AAGTAAAATA AAAATTATTT CATGGATTGC TTCTATCTAT ATCGAAATAT 60
 TAAGAGGAAC ACCAATGTTA GTTCAAGTAT TTATCGTATT CTTTGGTATA ACTGCTGCAT 120
 TAGGACTAGA CATTTTCAGCT CTTGTTTGTG GAACAATTGC ATTAGTTATT AATTCCTCAG 180
 CTTACATTGC TGAAATTATT CGTGCAGGTA TAAATGCTGT TGATAAAGGC CAAATGGAAG 240
 CCGCACGTAG TCTAGGTTTG AATTATAGAC AAACGATGAA AAGTGTAATT ATGCCACAAG 300
 CAATTAAAAA TATTTTACCA GCTTTAGGTA ATGAATTTGT CACTTTAATT AAAGAATCAT 360
 CTATTGTGTC AACAATTGGA GTTGGCGAAA TTATGTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102:

(2) INFORMATION FOR SEQ ID NO: 2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103:

TTTAAGGAGA AAGGTCATTG GTATAATCTT GAGAAAGAGT GGCAAGAGTT CTTAAACTCT 60
 GGGAAAGAGG TGAAAAATAT TAAAATGGAA GTAAAATATA GCGGTAATAG TCAAAGACCG 120
 ACTATATTTA AAGTTGAATA TGAAATTAAT GGTGAAAGAA ATATTAGAAG AATATTAAAT 180
 AAGTAGAGGT GCCAACATGA CATTTGAAGA GAAGCTTAGC AAAATATACA ATGAAATTGC 240
 GAATGAGATT AGCAGTATGA TACCGGTAGA GTGGGAAAAA GTATATACAA TGGCTTATAT 300
 AGATGATGGA GGAGGTGAAG TATTCTnTAA TTATACTAAA CCAGGnAGTG ATGACTTGAA 360
 TTATTACACC AATATACCTA AGGGTATAAC ATTCCGGTGC 400

(2) INFORMATION FOR SEQ ID NO: 2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104:

AACCATCATA AAATGTTATT AAACCGTCAT GGACCGCGTC ACCATTTAGT CCT 53

(2) INFORMATION FOR SEQ ID NO: 2105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105:

AAGCACAAAT TAGCAGAGTG TTTTAATTTA AATGAACAAG TACCTTTACA ATTTTGGAT 60
 AATGTAAAAG TTGGTAAAAA TAATATTTAT GnTGCTTTGG AAGAGTTTGC CAACAA 116

(2) INFORMATION FOR SEQ ID NO: 2106:

- (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106:

10 AATTTGCAAA AGAATCATGG ACAATTGAAA GCAAAAAGGA TCATCATTAA AATTGAACTG 60
 C 61

(2) INFORMATION FOR SEQ ID NO: 2107:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107:

25 GAACCAATGT TAAGCTAATT AATGGAATCC TAACAGCGTT AATCTATTTA AAAA ACTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108:

ATTTGAAAT GAATCTGTGG AACATTTTGC TAATCATGAG GATAAAATCA TATGATGTTG 60
 40 AAAGCGAGAA TGGGATTACG TTAAACGTGG GCGCTGCTAA TTAAAGCACC TTATTTAGTG 120
 GAAGAT 126

(2) INFORMATION FOR SEQ ID NO: 2109:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109:

55 ATAATGTTAA AAAACGGCA ACTAATCTTT TCATACTAAC AATGATTATA TGTACAATAA 60

CGTTAATAAT GCTAGATAAT TTTAAAAAAA TGAAAAACCG TGAATATCAA AAAGAAATAG 180
 5 CAGAAAAAAA TAGACATATT AATACATTAA TTGCTGAACA AGAGCGACAT AGAATTGGTC 240
 AAGACTTACA TGATACGTTA GGGCATGTGT TTGCAAGTTT ATCATTAAAA TCAGAATTAG 300
 CTTATAAACT AATAGATGCT GATGTAGANA AAGTAAAAGC TGAATTATTA GCAATTATA 360
 10 AATTATCTCG TGAATCATTG AACAAAAGTC GAGAAATTAN 400

(2) INFORMATION FOR SEQ ID NO: 2110:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110:

AAGATTTAAT ATCGGGGGTA ATGTTGATTT TCAAATATCG CGATGTGCTT GTACCACCAT 60
 25 T 61

(2) INFORMATION FOR SEQ ID NO: 2111:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111:

TATACTAAAT TATGGCAACT TGGCTCATAT AGGTCGAGTT ACCAGACATA TTCGG 55

(2) INFORMATION FOR SEQ ID NO: 2112:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112:

50 CGAATAAGTT CTGGGCCTTT TGTTGTTTAT TAGCTTGTTT CTGTTTTGAT TGTCTGCCA 60
 TTTGAACTAC ACCAACCTTT TAAATTTATT CTAGTGACAG GATAACTAAA ATATATTTCT 120
 55 TATGCAATAA TTCCTATTG ATAAGCATTT TCAGATTTTA GTTGTAATT TTGCCCTAAT 180

AATTTATAAA GAATAAATTC GTCTCCTCTT TGACCTATAA TATATTGAnC ATTATAAGCC 300
 ATGCGATTCA TTCCAGACAC AGCCATAAAC TCTTGTATTAT CTATCATTTT AAATACCATT 360
 5 TTTAATTGGG CTTAATGGGA CATTCCGTAT TAAATCATT 400

(2) INFORMATION FOR SEQ ID NO: 2113:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113:

TGTTTTCAAA GCATGGTATA AATGCTTTGT AACATAGGTT TTGCCTACAT CAGTATTCGT 60
 20 ACTTGTAATA AAAATCCTCA TAAAAAT 87

(2) INFORMATION FOR SEQ ID NO: 2114:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114:

TTTACAAGTT AATATAnCA CTAAAAATTT TTAAGTCAAT AAGAATATAT 50

35 (2) INFORMATION FOR SEQ ID NO: 2115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115:

45 TGTGCATAAA ATCCTTTTAC TTTTGTGAAT TGATTGTTAT CTTTAACAAT TA 52

(2) INFORMATION FOR SEQ ID NO: 2116:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116:

ATTTAnAACC CAATTCCCCA TTATTTTTTA AAACGGATTC CATGGGTGGA CCATTGGAAA 60
 TTTTAAAAAA ACCATGGCCC CATTCCAAAA AGTTAGGATG GCCAAAAAGC CTT 113

(2) INFORMATION FOR SEQ ID NO: 2117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117:

GATTTATCAA CTATTTCCGT ATTTTGATTA TCTCATACA ATTTCCAATC CTCTGGCTTA 60
 TCAATAAATA ATGATAATGG CTTATCTTTC GAT 93

(2) INFORMATION FOR SEQ ID NO: 2118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118:

TGATTACCTT GAnACATGAC TTTnCTGAn TGGTAAATAT TTACAGTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119:

AGATATAAAA TATAAAAAAT TATTAAAAGC TATATCCAAT CAAGACTTTA AAGGGTTAGT 60
 TCCAATATC AATCAGAATG ATAATTATn TGAAATATAT ATAATTAACA ATACTAAAAA 120
 CTTAATATAT CATTTATATG ATGATAGAGG TCTATGGCTA GCTTTTAATA ATAATGAAGA 180
 TTATGCAAGA TATnCTGAAA AATATAATGA TTTAATA 217

(2) INFORMATION FOR SEQ ID NO: 2120:

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120:

10 AGACTTAGTA AAGTTAGATC ATCTAAAGAT GAGCGTAAAA TTTATATTTA TTAAATAAT 60
GGATGATATA TCTAA 75

(2) INFORMATION FOR SEQ ID NO: 2121:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121:

25 CACCACCTAC ATTTACTATA TAAATGTAG GAATGGTAGA TTGATTAGA TAACTGGAC 60
GTATCACTTT AAGTGCTTTT TCAAAGA 87

(2) INFORMATION FOR SEQ ID NO: 2122:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122:

40 TGTTCCTTAG CTAAAGCTTT AGCTTCTTCA TCACTTTTAA CTTCAATAAAA ATCTACACCA 60
GTAGCTTCTT 70

(2) INFORMATION FOR SEQ ID NO: 2123:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123:

55 TAAATCTAAA AGGAGAAATG CTGAAGATGA GAGAGGTATT TTTGAAATGT 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124:

10

TTAAAGGGTA ATTGTTTAA AAAAAGATTA AACCGAGGAC TTTTAATTGT TAAAACCATC
CCT

60

63

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(2) INFORMATION FOR SEQ ID NO: 2125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125:

25

TGTAAACGAC TATTACATGA TCACAATCCA TTCAGCGCCA TTATATAAAG GTACTTAATA
TAGGACATCA TTCGCAGC

60

78

30

(2) INFORMATION FOR SEQ ID NO: 2126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126:

40

TTTGGTCGTG TGCAAGACAG AAGTCGACAT ACTCCAATGA AACATCATGT

50

(2) INFORMATION FOR SEQ ID NO: 2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127:

TTTGTGTCGA TCGCCTTTTT CACTTCTTCT GAATGCTCGA AATCATTCGT

50

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128:

TGTCTGAAAT GATCATTAGG ATTGCTCCAG CTCAATGTCA GTnGnAATGA

(2) INFORMATION FOR SEQ ID NO: 2129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129:

TCCAATTACC TACAAAGTGA GTGCTTTCTT GACCAAGTCA AAACGAACTT TTATATTTGT

CCAAC

(2) INFORMATION FOR SEQ ID NO: 2130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130:

TTCCAAGGTG TCGCTGACTT TCAACACACT GAATATATAC CTGCCAGTCG GCTGGTCATG

C

(2) INFORMATION FOR SEQ ID NO: 2131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131:

AGTTCTTCAG TCCAAATGCG GCATGTTGAC CCACCATAGG CGAGGGCATT TTCACCACGG

(2) INFORMATION FOR SEQ ID NO: 2132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132:

CCCCTCGAGT TTTTTTTTTT TTTTTTTTTTA CTGGAGCAAA ATGAATTTTT TTTATTGTAC 60
TTCAGGGCAA CAAGTCAACA GCTGCAGGAA AACAAAACCA GGTCCAATCT ATGATCTAAG 120
AGGAAGTCAG GAAAGGCTTG GAAGAGAGAT CCAAAGGCCA TCCTGGCAAG GGAATCCCA 180
CATGAGAATT CCTGGGAGAG AGCAGGCCCC AGGCAGCAAG GTCATCTTGC CTGCTTCTCT 240
GTAAGTTAAT CCTTCACAGG GAGCCAAGGC TTCTCTTGAC TGCTTGACA AGAGGGTAAG 300
GGCCCTGGTT GCAGGATTTG CCAGTGAAGT CATCCATGTC AATAGACCAG ATCATGGCTC 360
CTCCCAGGTT AAATTCCTTA AGAACTGAAC CTTGnCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 2133:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133:

TTCATCATAC AACATTACAC TTTGTATGAC TAAACCCAAA TTAACGATAT 50

(2) INFORMATION FOR SEQ ID NO: 2134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134:

GTGGCAAGCT TTTTAAAGT CTGACTGCCA TCGACGGATC TATGTTAACA GGTGGATCT 59

(2) INFORMATION FOR SEQ ID NO: 2135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135:

ATCAAAGTCA TCTnCATGGT CnATCACACC ACGCTTTATA TGGTAATTCT

50

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(2) INFORMATION FOR SEQ ID NO: 2136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136:

20

CGGGATCTGA GGTGCTATC TGCAATCTGC AATCGCTATC TGCAATCTGG AG

52

(2) INFORMATION FOR SEQ ID NO: 2137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137:

nCTCAACCAC CCACACAACA ACACAACAAG CAGCACCCAC ACACCACACA

50

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(2) INFORMATION FOR SEQ ID NO: 2138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138:

45

TGTATTGTCA TTGTAGACGT GTGTAGCCAA ATCATAAGGG CATGTGATT ACGCATCCAC

60

CTTCTCGGTT TGTACCGCAG TACTTAG

87

50

(2) INFORMATION FOR SEQ ID NO: 2139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139:

TTCACCGTTG CGCAACGTTT AAGTTTGAAG TTCGTTTGGC ATGTTGAAAT AAGCACCAGT 60
 5 TACACCAAAA CGCCAG 77

(2) INFORMATION FOR SEQ ID NO: 2140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140:

ATCTTCTAAC ATTCACCTTAG TAGCGTnATT TTTCGCTTAT AATGAAATGT TAAGCATATG 60
 20 CGGGATTTTAT ATTTTAAAGA GACCTTTAGA TACCATATAT ACCTAGGTTA TTGAAATAT 120
 GGATACCTTA TATAAGTGAT TTGCAATA 148

(2) INFORMATION FOR SEQ ID NO: 2141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141:

GCTGGCACAT AGATGATCGT CAAGTCGATC TCGCCAGTCT GAAGTCAAGA 50
 35

(2) INFORMATION FOR SEQ ID NO: 2142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142:

TTGTTGTAAA TACTATCACT GTACATGGGT GCTATCAAAA TATTGTCAGT TCGTAAAATA 60
 45

(2) INFORMATION FOR SEQ ID NO: 2143:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143:

GTAGTATATC TTATTAATTG TATCATGAAG CAATTTAAAT ATCATGACAA TTTAGTTTGA 60
10 AAAACACACT TTGTGTTGAC GTTGTGTTTT ATGGGATATA GnATAGTAAG GAATGTAAAA 120
TGAAGGAGTG AATGC 135

(2) INFORMATION FOR SEQ ID NO: 2144:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144:

25 TTTTAAGGTT TGAAGAAAAA AAGTTTTTAAA AATTCAAGGA AACATTAAAT TAATTTA 57

(2) INFORMATION FOR SEQ ID NO: 2145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145:

TTTCGAAAGT TTGATAGTCC ACCTTACATT CTCCTACTAT TTTCTGATGT CCCAATACTT 60
TATATTATTT AAAGTAATAT AAAAGCAATC TCTTTTGAAG ACATGTTAAC CTAAATATTT 120
40 TTATATATAA TATATATATA AAATATA 148

(2) INFORMATION FOR SEQ ID NO: 2146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146:

55 GTTAATACAA TACGGTTAAC AGCACCTTTA CGnTAGTTGC TTTnCTGCAn 50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147:

AATCCCCTCT TTTCTCTATT TCCTAAATCA TAGAACTTTT AACAGTAAAA TTCAATCATT 60
AATACATG 68

(2) INFORMATION FOR SEQ ID NO: 2148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148:

AGGTCCATTT GTAATTTATA ATGTTGACTA ATAACATCTA CAGAATTTAA CGTTCCCAT 60
CCTCGCCACT GATTGTAAAT AAACAAACCA TA 92

(2) INFORMATION FOR SEQ ID NO: 2149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149:

ACCATCCATT AAATCAGGAT CTTCACTAAT AAGTGCTAAA TTAGCAGCGC CACGTTTAA 60
GTAATCCAT 69

(2) INFORMATION FOR SEQ ID NO: 2150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150:

TCAAAATATA TACGATCACC TTTCTGTAAA ATCACACTAT TTTTATTTGC CGCTTCTGGA 120
 TGTGTGTTTAA AAAATTGTTG GCCAACTTCA CCTTTTAACG TGGCAAATTG ATAATTTCTT 180
 5 GGTAGGTCAT GTTGAATTAA CCAAATGACA TAGTTATAAC AATATATACA GTTTCATCA 240
 TAATATACGA TTGGCATAAT TTATTCGCTC CTTTAATAGT ACTTATAGTC ATTTTTCCTA 300
 10 ATTTAAAAAC ATTTAAACAA GGTGTGCTACT TGATAAGTCC TCGCGACACG AAATTGCCAT 360
 AAAATTTATT TTTCAGnTTh ATAT 384

(2) INFORMATION FOR SEQ ID NO: 2151:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151:

TGTGTGTTTAT CACTATATTT TAAAAATAGT CTATAAGGCT TATCAGATGA AGTAGCTGCT 60
 25 GCGGTAACAC CACCACTAAA TGT 83

(2) INFORMATION FOR SEQ ID NO: 2152:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152:

GTATTCGTAC ATTTTTCAGC AATTAACCAA GATGGTTACA AATCATTAGA AGAAGGTCAA 60
 40 GCTGTTGAGT TTA 73

(2) INFORMATION FOR SEQ ID NO: 2153:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153:

CCCCCCTCCC CCCTCCCCnC CCCCCCCCCC CCCCCCCCCC GCCCCCCCCC 50
 55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154:

TATTTTAGGC TTAGCATTGA TGATGTTGCT CATTTTCAAT AATATAGGAA TTATT

55

(2) INFORMATION FOR SEQ ID NO: 2155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155:

ATGCTTGCTG ATATAATGTA ATAGCGTCGT GATAACGTTG CTGGCTTATA ATATACATT

60

GCGAGATT

68

(2) INFORMATION FOR SEQ ID NO: 2156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156:

TAATCTTTGT CGTCGAAATA CAACTAACT TTTGAGTTTA ATGATGAAGG TACGCATTGT

60

GTATCACT

68

(2) INFORMATION FOR SEQ ID NO: 2157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157:

TCATTCATT TCCTCTTTTC TTTTATTTAA AATGTTTCATG GTTGTTCCTC TTAATTCTGT

60

AGATGCTAAA TGGTCAAATT GAATAATTGT TTCTAGACTC ATTCATAAA TTTCGAAAAA 180
 TAATTCTTCG GGATTACGTT TTGTATTTTC TCCAAATGTT TCATAAAGCA AATCAATTTT 240
 5 ATCAGCAACT GAAAGTATTT GGCCTTCTAA TGAATCATCT TTACCTTCTT GCAGTCGTTG 300
 CTTATAAACA TCTCTATATT GTAATGGAAT TTCTTCTTCA ATAAAGGTCT CTACCATTTC 360
 10 TTCTTCAACT TGCGAAAATA ATTTTnnTAA TTCACTACTC 400

(2) INFORMATION FOR SEQ ID NO: 2158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158:

TATTTTTTTC TTCTAGGCAG TGTTAATACT GCITCAATTT GTTTTTTACT AAATTGATAT 60
 TTCTCTATGA TTGAATTAAT CAATTGATTG TCCATTTACT TAACCCACAC TTTTCTTAA 120
 25 ATTTACTCAT TTATTTTAAAC ATATTCTAAA ATACTTCTAT TAAGATATGA TACTTAATGT 180
 AATTTTCACT TCCAAAACAT TTAAAACGAA TGATTAGGnC ATACTATATT nT 232

(2) INFORMATION FOR SEQ ID NO: 2159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159:

CCGTTTTTTC AAAAAGTTGA TCATAAACCC GCTCCTTTTT TCATCATAAC AAAATAAGAA 60

(2) INFORMATION FOR SEQ ID NO: 2160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160:

CGATTTACTG CACGACACAT TGCCACATCC TGGATGGGCA ATCTTTTCTC TTACCCGTCT 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161:

ATTAGTTGAA GTTTTGTAGC AATTGAAAGA TATTCAGGGT CAAATAAAAA CGACAAAAAA 60
 AGAATATCAA CAGACCAACA AAGAACTTTC TGCTGTAGAT AAAGAAATTA GAAATATAGA 120
 AAAAGACCTC AATGATACAA AAAAAGCACA AAATGAATAC GAAGAGAAAT TGTATCAAGC 180
 ATATCGATAT ACCGAAAAAA TGAAACACG TATTGATAGT TTGGCAACGC AAGAGGAAGA 240
 ATATACTTAT TTTTTCATG GCGTCAAACA TATTTTGAAA GCTAAAAATA AAGAATTAAA 300
 GGGTATTTAT GGTGCAGTTG CGGAAATTAT TGATGTGCCA TCTAAATTAA CTCAGGCAAT 360
 TGAAACAGCA TTAGGTGCTT CATTACnACA TGTCATTGnA 400

(2) INFORMATION FOR SEQ ID NO: 2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162:

GTGCGTACCA TTGTAATCTT CGTAACTGG GTAATTATTT TGTCTTTCTT CATCATAAAG 60
 TAATAA 66

(2) INFORMATION FOR SEQ ID NO: 2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163:

AGAATGGTAA CATGGTAATA ATAAATATA AACAGAATAC TAGTTAATAC ACTTTATACT 60
 AGAAAAAGAT AT 72

(2) INFORMATION FOR SEQ ID NO: 2164:

(A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164:

10 CGATAATCTG TTTTTTTAAA TCTGTTGCTG TTAGATTTAG CACCGATTCTG TTAACTTCA 60
 AATAATTTTT ATTACCTTTG GAAGAAAGTG GAACTATTGT AACTGTTTCT TTTCCTTTAT 120
 TGCTTTTGTT ATCTAATATT ACACAAAAAT GATTACCAGA AAACCTCACTT CCAATATTAC 180
 15 TCCCTAGTTT TACATATACC ACTGTTCTCT TACATATGA TTTATAATAT CTTTnTTTAT 240
 TGCTTGTAAC ATCGCTATGT ATAGCAATTG GAATAAACT CTAGCCAATG AGGCATGTnT 300
 ATAACTTTCA TGTTTTTACT GTCGG 325

20

(2) INFORMATION FOR SEQ ID NO: 2165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165:

TAAACCCCTT TTGGGTAAAA AAGTTTGGA AAATTTCCCC GGGGGGAAAG GCCCCAAAA 60
 AATTGTGCCC CTCnCGGGG GAAAATTAAA ATTTCCCCC TTTTAAAAGG GTTTCCTT 120
 35 T 121

(2) INFORMATION FOR SEQ ID NO: 2166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166:

CGGACAGTTA AATGAACTGT TCAATGAGCC CAGGATGTTG TAAATGGTTC GG 52

50

(2) INFORMATION FOR SEQ ID NO: 2167:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167:

ATTACAGTAA AAAATGGATT AACATTACAA GCGTGTCTTG CTAGAGCAGC CAA

53

(2) INFORMATION FOR SEQ ID NO: 2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168:

AAAGATTATT TATTTGCACT CATTAAATTGT GATTTAATAC GGTCAGCTTT GTTTGAATGT

60

ATTAAATTAC nTTGAGCAGC TTTGTCTACT AACTTAACTG CTAAGCTTAC TAAT

114

(2) INFORMATION FOR SEQ ID NO: 2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169:

AAGGAACCCC CCCCCCTTAA AATTTTTGGT GGTTTTAAAA AATTCCTTTG GATTATTAC

60

CTTTATTCTCT ATnATTTTCC GTTTGGATT TCTGGATTA AATTTCCCCA TTAAGCCATT

120

TCCGCTTCCC TTATTTTATn ATTTTCCAAA ATTTCCAAAG GTTCCATTTG GGATTTTGGC

180

AATCCTTTTT TATTAAAATG GCCTAAAAAT TTTTT

215

(2) INFORMATION FOR SEQ ID NO: 2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170:

TATCGTTTTT AGAAATGGAT GTTCTCTCCA AAGATGATGG TATCTAACAT TATCTTATTG

60

GTATCATTAT GCAACnTTA CAAACATTT ACGCAAGATG ATACATTATC CAAC

114

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171:

ATCACAGATG AGATAACAGA TCCACTGTAA CTTTACAATA AATAAATGGT ATCATAATTA 60
ACACGTAAAT GGTTTC 76

(2) INFORMATION FOR SEQ ID NO: 2172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172:

ATTATCACAA AATGTTGACA CGCAAAAAGT TGGTCAGTTA TCAATATGGT ATATAAATCT 60
GAGA 64

(2) INFORMATION FOR SEQ ID NO: 2173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173:

AAAGGCCAAC CAACCAAAGG CCAAATTA CCGGCCAATT CCAAGGGGTT AATTAAACCC 60
G 61

(2) INFORMATION FOR SEQ ID NO: 2174:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174:

CACCCCGCAC TCTCCCATCT TTTACCTACT GGCTTCTTTG CATTGCCCTG GCACCTCCGT 120
 CCTCAGCCTC CCAGGCTGTA TTCATTCAAT CCCTTACTGA GCACGCACCA TACACCAAGC 180
 5 ACCATTCAAG GTGAACCACT CAAATGAAGG CCTGGCTCAT TTTAATGGGG GACAATGAGC 240
 ATTTTTGTGA CAATTTTCATG GAGTGATGAG TGCTGTGAAG AACTAAACAG GTCAGGTGTA 300
 10 AGTGGCTCAT GCCTGTAAATC TCAGCACTTT GGGAnGCCGA AGCAAGTGA TCATTTAAGC 360
 CCAAGAGTCA AGACCAGCCT GGGGnnACAT AGTGAGAnTC 400

(2) INFORMATION FOR SEQ ID NO: 2175:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175:

ATATCGTTTA AACCATCAAC AAGATTTTAT AGATGCAACT TTTACTGCGC TGAATCAGA 60
 25 TAGAGCACGT TTAAGAAG TGCCAGTTCA TGTTGAACTT ATAAGTTATA TTTCTAAATC 120
 AAAATAAACT GCTATCTAAA ACGCAAAGTT GATCAAATA TCGATTTTGT GTTTTTTATT 180
 30 GAGAAATTAT ATAGGAGTGT CAATCGATGA TTTATTGTGA ACAGAGCGTT TAATATTAAG 240
 AGACTGGCAT GAAGATGATC TGTTACCTTT TCAAAAAATG AATGCGAATT ATGACGTAGC 300
 TAAATATTTT CCAAGTTTAT TGAGTTAnCG nCGTTCAGAA TTAGATATGA GACCTATGGA 360
 35 TCGGTTATn AAAGATTATG GCCATTGGGA TTATTGCCnG 400

(2) INFORMATION FOR SEQ ID NO: 2176:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176:

TAAATCAAGG AAAGACATTT TAAGGTACGA AGGTTGATAA CAAAAACCA ACAGATTTAG 60
 GGGTATCAGA G 71

(2) INFORMATION FOR SEQ ID NO: 2177:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177:

GTTGAATTAG GCAGCACGAT TATTGATGCT GAACTGTTAG AGTCAGATAA G

51

10

(2) INFORMATION FOR SEQ ID NO: 2178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178:

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TTAATTAATG GTATTTACAT ATTCATAACC AAAGGATAAA ATAATTGTGA AATTATTCAC

60

A

61

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(2) INFORMATION FOR SEQ ID NO: 2179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179:

35

CATTTTACCA TGCAGCAAAT AATACAGGTG GTGCCGTTAA CAAACGTGA

50

(2) INFORMATION FOR SEQ ID NO: 2180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180:

GCCGAACGAA TCAAATACCA TACCTAATTG ACTGCAGGCA TGTCCATATA GTGCAGTTAA

60

50

CTGTCTACAA GGC

73

(2) INFORMATION FOR SEQ ID NO: 2181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181:

	TACTTTTGGC GATATTCGGT ATCGTTATTA CAGTTATTTT ATATGCAATT AAATTGCCGG	60
10	GTTCTATCTT TATCGGTATG ATCATCACAG CAATCGTTGG TATGTTCACT GGATTGATTC	120
	AAATGCCATC TGGTATTGTG GGTAAGATTC CAAGTATTGA ACCAACGTTT GGTGCTGCAT	180
	TTGAAGCGTT TAAAGACCCA AGTCAATTAT TAACGATACA GTTCTTAATT GTTATTTTAA	240
15	CGTTCTTATT TATTGATTTT TTTGATACAG CTGGAACATT AGAAGCGGTT GCAnCnCAnG	300
	C	301

(2) INFORMATION FOR SEQ ID NO: 2182:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182:

30	TTGATTTCGCC TTGGCCAGAA TTACTTTTGT TTTGGGCGTC ATTGCAAGTT TCTA	54
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(2) INFORMATION FOR SEQ ID NO: 2183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183:

	TTAGTnACAT TGGGACATTT AACTGATCCA CCAGTACTTT TGGCGATATT CGGTATCGTT	60
45	ATTACGTTAT TATTGCATAA TGCGGTCACT ACGAGACACC GCACTGAGTC CGATATCA	118

(2) INFORMATION FOR SEQ ID NO: 2184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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AGATAGTTAT ATAAAGATTT CATCTTCTGT ATTACATTGA TATTTT TAGG TCCCTGTATA 60
 TAAAAATCAT ATGCCTCATC AACACATCA CTTTTATTTT TGATTGCAAT TTGATGTAAT 120
 5 ATCTTTTGAC TAAAAACACG ATTAATCATA TTTCTATTAT CCATAGCTAC GCACCTCCTT 180
 CAACATACAT TTAATGCTTA TCCTGTTAAT ATTATAAnCh ATTTTAAATG CCTATAGACA 240
 10 TTATTTCTAT ACACATACGA TTATnAAATT GTATTGAAAC CAAATGATGG TTGCCAAACA 300
 CAT 303

(2) INFORMATION FOR SEQ ID NO: 2185:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185:

CCGGGGTTTT GGTAAACCC TCCCAAnATT TTTTTTAAGC CCAAACCTTG GAAAAACCCA 60
 25 GGCCACCCGT TGGAATTTTT AAGCCTTGGA TTAATCCGGT TTGGTTAACC 110

(2) INFORMATION FOR SEQ ID NO: 2186:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186:

CCTATATTGT CACCCAATT CATTACGGCA CCTTTACCGA AAGATTTCTC CATATTTTTA 60
 40 ATTACTGTAT CTAAAGCTTT TTGACG 86

(2) INFORMATION FOR SEQ ID NO: 2187:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187:

TTTGCTAGAA AACATACCAC ATTTGCCAAT TATATTATTT ATTCTGATGT TTATTTTCGG 60
 55

TATTTAGAGG TGATAAAATT TGTCAACTAT TACAAAGACT AAAATAAAAA TCTTTATTAA 180
 TTATTTTATT GGTATATTAG CCTTGGCGTT TGCTGCTTAT ATATTATTTA AATAAAGGTT 240
 5 AGAGTGAAAC GTGTTTATGA ACTAGACGTT CTAGTATAGT TACTACAGCT TTAGTCAGAA 300
 GGTATCATTG ATAAGATCAT ATTAAATCAA AGAGGCATTG ATATACACTA AAAAGAGGCA 360
 AGATTACCTG CCTCTTTTTA GTnATTAAAT ATACGTGTTA 400

10 (2) INFORMATION FOR SEQ ID NO: 2188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188:

TTTTATAAAA TATCAGACAT TTTTGnTCAA CATACTCTC TTTGATGTT TCTAATACTT 60
 TATCATTAA CATTACACCT TAAAGTTATG ATGTGGCATG TTTTCTTATA TTCATAACAT 120
 25 CAATTTTATC A 131

(2) INFORMATION FOR SEQ ID NO: 2189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189:

CGTAAATAT TTTGATTTAA AATGGAGGGT ATTAATATGA AAAGGTTTCAT GTAAAATCTA 60
 40 GGGGTATTCC AATATTATAA GGCAC 85

(2) INFORMATION FOR SEQ ID NO: 2190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190:

CCCGAGGAAT ACATGGCATT AAATACACGT TTAATATTTA TAAAGGTGAC TTAATTTTGT 60

ATAATTGTTT ATCAGTGATA AAATATTTGC AATAAGAAGA GAATGACTAA ATAATCTTAA 180
 TTTTCAGAnA AGTAATTGTA ACCTTACTGG TCTTATGGTA ATAn 224

(2) INFORMATION FOR SEQ ID NO: 2191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191:

AGCTTTTGTA GTTTTCTTAA GCACACCGGC GATTTGATTA TTACATAAAG GATTCCCTTT 60
 TTTTGTTGTG AATATGAACC CTCTGTCAAC ATAGCTCGAA TTCCATCTTT TCAACATTTT 120
 GTTTTCCAGT ATTATCTTTT TAAAAATTC TACGGTTCTA GAATTGATGC TGATACTTCT 180
 TTTTGAACCT ATAGTCTTTG TAGTGTCTTT GTATCCGAAT CCTTTCTCGT ATTTAATGCG 240
 GTGAATTGTA CCTGTTATAT TGATAGTnTT GTTTAATAAA TCTATATCTT TTTCTGCAG 300
 TGCTTGTAGT TCTCCTATGC GCATACCACT TAAAGCCTGT ACTTCTAAGA TGCTGGCAAT 360
 TAAAATGCCA TTTGCTTTT GTAACCTATT ATCATTTAGT 400

(2) INFORMATION FOR SEQ ID NO: 2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192:

GACGACTGAG AGGCCGTTGA ATTTGACGTT GCCATATnTT CAAATTTAAC 50

(2) INFORMATION FOR SEQ ID NO: 2193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193:

GTTGTTTTCA TATCAAAACA CCGTAGAATA AACAATGAAT GGAATTACTT TTGCAATGAT 60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194:

CCAGTCACTG ACTACGTCTT CCTCGGTGCT GGCGGTGGAG CCATTCCCTT ATTACC

56

(2) INFORMATION FOR SEQ ID NO: 2195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195:

GTAGGGAAAG GAAAAACTGC TTCCATTGGG AAATGTTAAA CCTTGTTCTT TGGTGATGCC

60

ATTGGATTT

69

(2) INFORMATION FOR SEQ ID NO: 2196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196:

ATATGACACT ATATTTTATA AACATACATT TAATGATTCA TTATACAATT GCCAA

55

(2) INFORMATION FOR SEQ ID NO: 2197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197:

GCCCTAGTTC AATCATATAA CCATCTTTAC GATACGATTG AATCTTTCCC CCCGGACGAT

60

TCGATGCTTC A

71

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198:

AGTAGCACAA CAGCCATGCG GAGACAGAGA ATCGTTAGAG ATTAATGGAG ATCA

54

(2) INFORMATION FOR SEQ ID NO: 2199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199:

GGCGGTTTTA TATTTATCGT TGCAGTTATG CAAATTGTAC TTGGTAGAAG TATAGATTCT 60
 CGTGATTCGA AAAAAGTACT TTAAACGGGA TTGGGAATAG TAATCATATC TAGCTTTATT 120
 TGTGCAGTGA CACATAACTT TATATTATTT GCTATATCAA GGTATTTC AAGCAATTGGT 180
 TGCAGGAATTA TTCCTCTCGT GACTTTAACT TTATTAGCCA AACTAAGTAC AGATAATGGT 240
 AGAGCTCAAG CTATGGCGAA CTATCAAATA TTTTATCAT GTGCACCAGC TTTGGCACCA 300
 ATCTTAGGGA GTACTTTAGG TGGCAAGATG GGGATATATT GGTATTTTAG TTTTGGGCT 360
 CGTTATATCT ATCGGTATTA TTTTGGGATA nCTnTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200:

GGATATGCGA TGGATGACGC ATTGCTATAT CGGCAATTGn GAAGCTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 2201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201:

ATCGAATATC ACTACTATCT CTTTtAAAGT ATCTACAATC TCTCCAATCT

50

(2) INFORMATION FOR SEQ ID NO: 2202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202:

TCGACAATCC TAATGCAATT GCTTCATGTG GtTGTGGTAG TTCATATTAG AACTGCAAAA 60

GTTGCAGGTG ATCCTGAAAA TTGCTAATAA AATAAGTTTT TAATGGTTAA CCCAATTTTT 120

GGGATACAAA TTGATATCAA TAACGATTAA GGACATATTT GATTATGTCC TATTTTTGCG 180

TAAAGATATT TTGTTTTATT AAAAAGCTTA TTGAAAATTA AGAATCTGAC TATAAATAGT 240

ATTTTAAATG ATCGTGATAG CGGATACATT TTTAATCGAA ATCAGGCTAC GAAAAAATTA 300

ATTAATTTTT TCACAATCTG ACTGAATCTT GCTTGAAAAT ATAACATAAA AGCTATAGAA 360

TTAGTATTGG ATTAAAAATG TCTTTTTTGT GAACATCACA 400

(2) INFORMATION FOR SEQ ID NO: 2203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203:

GCGTTGTCCT TTTCGTGACA TGAAACAATG TGGAAAACAT AATTAAATnn AGGGAAAGTG 60

TGAATAGTTA AAAAATTAGT ATTGTGTTAT AAAAAATAAT TAATACTGTT AGGATTTTCAT 120

TAACCTAATT AACGTTGGTT CAAAAATAGT TAAAAAGAGG TTAATTCATA GCGCAGTATC 180

TCACTTATAT AATGATAGTA GATTGTTTCG ATTACGTAAT TGAATTAATC ATATAAAAAT 240

ATATTAAGAC AAATTTATAA ATAGATTGGG AGAnTAGTAC TGTGAAATTA AAAACGTTAG 300

CTAAAGCAAC ATTGGCATTa GGCTTATTAA CTACTGGTGT GATTACATCA GAAGGCCAAG 360

CAGTTCAAGC AAAAGAAAAG CAAGAGGGng TACCACCATT 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204:

10 GTTATTTTGT ATGGTTAGTC TTTAAAATAn ATATAGATAT TAAATATTTA TTTTACGAAT 60
 TGTTAAGTAA AGAAAAAATA TTAATCAATC CGGGTTACAT TTATGGCAGT AAAGAAAAGA 120
 15 GTATAAGGCT ATCTTT 136

(2) INFORMATION FOR SEQ ID NO: 2205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205:

25 TTTTATTTTT TCGCAATGAA AAACAATCTT TCTGCATCTT CATTATGTTT ATCTATATT 60
 AAATCAGTAA ATGTTTCAAC ATGTTTAAAA CCAACTTGAG CTAACCAAGA CAAATATGTC 120
 30 TTTTCATCAA ATGTTCTCTG AAAATGAGAC TCATCAAATC TTGAATATGT TTCATCTTCA 180
 TGTCGAATGA AAAATGTCTAT ATCATGATAA ACACCTTAAAG GTAAATCTCC TTGCACAGCA 240
 35 TCCCATGCTA AAAAAATGTC CCCTTTATCA TCAATATAAC TTTGATTATT AAACAAAGTC 300
 ATCATTTTTAT AAACAGTATG TACATCAGAA ATAAATACAC CTGAATCAGT CAGATGATGA 360
 TAAACATTGA TGAATGTTTC AATCACTGCA GTTTCATCTT 400

(2) INFORMATION FOR SEQ ID NO: 2206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206:

50 TTGAATATCA TATAAAAACA TCAGGTTCAA AGTTGACTAC TCTTAATAAT ATAAAAATAA 60
 GAATTAAAAA CATTAAACGA TACTGCTCTG AGAACTTGCT TTAAACAAA CTTGATACAA 120

GTCAACTCGG AGATATGAAA GGAGCnATTA AATATGCAGT TAAATTTTAC AATTATCCAA 240
 ATGAATATTT GTTAACTAAT GTCAAAATTC CTAAAAGAAG AnAAACAATA GAGGATATCG 300
 5 AAAAAGATGA ATCTAAATG GTACCACTAT TTAGAAATGG AACCAAGTCC TACnGATACG 360
 TGATCATATA CTAATGGAT 379

(2) INFORMATION FOR SEQ ID NO: 2207:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207:

20 CATCTTGGGA CGTTTTAAAA AGTAACGTAG CGAAGACTAT TGGACAACA ATGAGAACCA 60
 ATGCTAGAAG GATCAAAAAG TATTTTAAAA ATTTATTCAT GATTGATGCT CCTATATTAA 120
 ATTTnTGTTA AATCATA 137

25 (2) INFORMATION FOR SEQ ID NO: 2208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208:

35 GCGCCGCTCT GTTCATTTTA CCTAAATCCA ACGTTTCAGG AATAGATGTT TTCAAACCAC 60
 TTTGAAATGG AT 72

40 (2) INFORMATION FOR SEQ ID NO: 2209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209:

50 ATGTAGCAAC TAAAGATGAT AGTGGATAGC GACACGGTCA ATAAACTGCC TA 52

(2) INFORMATION FOR SEQ ID NO: 2210:

(A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210:

10 TTTTTTATGT TCTTTTTTAA TAAGAGGGAA GTGAAGTTGT ATAAAAATGT ATTAAATATG 60
 CACTTTTTAT ACATTAACGA TTCATATATG TCTATTATGT ACCAAATTTA TAATTTGTAT 120
 AATTTTCGAA CTGGTTAAAT TCGAAAAATA TCACTAATAT ATnTAGATCG ATGTGTAACA 180
 15 TTACGTTCTA nTAATTTAAT GTTGCA 206

(2) INFORMATION FOR SEQ ID NO: 2211:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211:

ACGATGTATT TTGATATCGT TACCAAAGTC TTTTAATAAC TCATTTTCAT CTAAATAAAT 60

(2) INFORMATION FOR SEQ ID NO: 2212:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212:

40 TGATAAGGTT TGTCCCATCG CTATTTGAAA TGATGCATTG TAAAAAACTA TCATTTGTTG 60
 GTAATATCTT AGTTCGATGA CTTTCTTTCC AATCTTTCCG TGTCTAGAG ACAAGATTTT 120
 TTGTAGCTAT CTTAGTTGCT TCTTGAATGT TCATTTGTTA TTCTCCTTT TAAGATGTTT 180
 45 GTnTTTCTTT AAATGCTAAA ATAATTGATT TCTTTTTATC ATTCGTGAAT ACGAAATTTT 240
 CGTATTCATT ACCTAAAAAA ATATCATCAT ATTTAACATT AAAAGCACTC ATATACTTAG 300
 50 AAAGTAACT AACnTTAATG GntGTAGAGT C 331

(2) INFORMATION FOR SEQ ID NO: 2213:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213:

AGCATAAACC AAAAGATGCG GATATACTTG AACGCGTCAA AGATATACTT AATAAAAAAG 60

10

A 61

(2) INFORMATION FOR SEQ ID NO: 2214:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214:

TCTATTTGAG TTTACATTG ATTAATGAA TGACAATTAT ATGAACCTGA CTGGT 56

(2) INFORMATION FOR SEQ ID NO: 2215:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215:

35 ATACCACTAC TATACAGTTA AATTAATATA CGTTAAACT TTAATCCGAT ACATTGGTTA 60

AAATGATGTT CCTCGCTGGT GGATCGAGAC ATACTTCGCT CTGACTTCTT TAGTCAGTTT 120

TTTTTCAGCT TTTTAGGTGT AATCACTGAC TTTGTTACAT CACGTCAAAT TTACAGTCGC 180

40 TATTATCTTA ACTTATCnAC GCTTATCACA CATCAATTCA GATATTATAT TGCATTGGCG 240

nCTATCACTT TGAACCTGCT GTGACTGGAA CTACTGGCTG TCAnGAGCGA GGGCTGATAA 300

TGAGCATAAA GCAACATATA AGTAATACGG CCGAATATGT AAATTCGGCA GCTTTAGGCA 360

45

ATGCTGCCCCG GGCATGACTA GnACATTCAc AAGAAGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2216:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216:

TTTTTAAAAA AGGGGTTAAC CAAAGTTTTG GAACCCCAAA AAATTCCGGA GTTAAAAAAA 60
 5 CCCCCAAAAA TTAAATTAAC CGGTTATTCC GTTCCAGGAG CCAAATTTT ATGGTTCCAA 120
 TTnCCAAAGT GGG 133

(2) INFORMATION FOR SEQ ID NO: 2217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217:

TACTCGTACC ATTAACCACT CTGATTAACC ACAATACTAA GGTATTCAAT ACATCACTGA 60
 CATC 64

(2) INFORMATION FOR SEQ ID NO: 2218:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218:

TATTCTATAG AATATGGATA ACGTTTAACA TGATGTAGAG TATTCATCAT TGTAACACGT 60
 35 CAATTGATA TGTGAGATTA AC 82

(2) INFORMATION FOR SEQ ID NO: 2219:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219:

TTTGACGCAA TGATTAGCT GTAAATATGC AATCTAAAGG AAAGTACCAC TTATGAGATG 60
 50 TATTAAAACG 70

(2) INFORMATION FOR SEQ ID NO: 2220:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220:

10 AAAAATTACC CCAAAGAATT GAAAATTTGT TGTTCGGTT ACCGGGTTTA AGATTAATCC 60
GGTTGA 66

(2) INFORMATION FOR SEQ ID NO: 2221:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221:

GATCGCAACC AAAATAATGG TCTTCCTGGA TTATTACTTT ACCAGCTGGC ATAC 54

25

(2) INFORMATION FOR SEQ ID NO: 2222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222:

35

GTGTTGCTAC AGCTAaCATT TCATATTTAA CGnGTTGTGG TATTTCTAAA 50

(2) INFORMATION FOR SEQ ID NO: 2223:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223:

AATGGGGGnA CCCAGCnTGA GTTATGTCAT CATATCGGTA TGTGATACAT 50

50

(2) INFORMATION FOR SEQ ID NO: 2224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224:

G TAGATGCGC CCTCATATGG ACAAAGATAA AGTATCAGCA GATTGGACGC TTTA

54

10

(2) INFORMATION FOR SEQ ID NO: 2225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225:

20

C GAGACTTCA CTTTGACTAA ACGCGTTAAG AATTTAGATT ATGCTTACGA TGAAGAAGAA

60

TTA

63

(2) INFORMATION FOR SEQ ID NO: 2226:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226:

35

TGGCCATTTT TAATGGGGGG AAACCTTAAA AAGGGGTTTT TAATTTTAAA CCAAG

55

(2) INFORMATION FOR SEQ ID NO: 2227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs

40

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227:

TCCATTTGGT TGCCTTCTTT AAATAAACCT TGGATTATGC CTTTCCTCCG GTTAATTAAT

60

GGGACCAGGG GCCAAAAATA CCCCCTTTTA AATATATATT CCCAAATCC ATAGTTAAAT

120

50

AATCCATTTG C

131

(2) INFORMATION FOR SEQ ID NO: 2228:

55

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228:

10 CCATCTGTGC TTCGTTAGGC GCTTTCGGCA TCACGGTGAT GGTTCGCGAC AGATCCGCCA 60
 TCCGGCTGAA TGGGAAGCCC GCGTTAaAAA GCGCGGTAGA TCCGGCATCG GGATGAAGTG 120
 GTAATACTTC GAGAAGTCGA TGGTGGAGTC GTCACCAATC ACCACATGAT TCTGCACCGG 180
 15 CTGGAAGGTA ATACAGTTAT CCACCGAACC GCCCGGCATC GGGTTCATAT ACTCAAAGTC 240
 GAAGCGCACT GGnTTTGGTC GCGCCCAGTT TCAGCGCCGG AATAGAGACA TCTGTTTTGC 300
 CATCCAGCAA ACCTTGTAAT ACCGGAnTCC GCAGCAGCAG GCGGTTTCGC 350

20

(2) INFORMATION FOR SEQ ID NO: 2229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229:

AACTAAAAAT ACTATATAAA AAAGGTTGTT ATAATTTAAT GGATATAAAT AAAAACGA 58

(2) INFORMATION FOR SEQ ID NO: 2230:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230:

45 GGGCGAAAGC TGGACGGAGC CAACGTCGCG TGAGTGGATG GAAGGTTCTT 50

(2) INFORMATION FOR SEQ ID NO: 2231:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

55

AGCCATACGT GGTAAGCACA TGCTAAATTT GCCAGCCTGA AAATGTTTAG

50

(2) INFORMATION FOR SEQ ID NO: 2232:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232:

15 TGTATCATTT TGGCAAAATC ATAATCTTTA TCGTCGAATA CAACTACTTT TAAGTTTAAT 60
 GATGAAGGTA CGCATTGTGT AATCACTTCA TCTAACTTTT TTAAATCAGG TGTCATAGTT 120
 GAACTTGGnG GT 132

20 (2) INFORMATION FOR SEQ ID NO: 2233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233:

30 GATCTTGAAG CAGTTGAAAC ATATGTATCA GATGCATTAA GACAAGTACA CTTACAATCA 60
 GACATTTTTG CTGTATCA 78

(2) INFORMATION FOR SEQ ID NO: 2234:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234:

45 TTTAGGCACA GACGGTAATA AGCTACAATT TTCATAAAAT CATCTCCTTn 50

(2) INFORMATION FOR SEQ ID NO: 2235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235:

ATCCTGGAAA ATCTGGTAAG ATATCTTGGA AATAACTAAT ACCAATTCCT AAAA

54

(2) INFORMATION FOR SEQ ID NO: 2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236:

GGGTGATGGT CATTGACAAA GTCAACTTGT GATAAGCCAT GGATATTTTT CGTT

54

(2) INFORMATION FOR SEQ ID NO: 2237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237:

TTATTTACTT TAAATTTCTC AATCTACAGT GTAATCTTAT TTCTTATTAT

50

(2) INFORMATION FOR SEQ ID NO: 2238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238:

CCTTAATGGG TTTTGGGGGG GGGCCCCCCC GGCCCAAAC CTTTGGCCCA ATTGGTTCCT

60

GGGTTAAGGA AAAA

74

(2) INFORMATION FOR SEQ ID NO: 2239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CCACCCATGG CGCTTGACAA AATATGGATG GAACATAACC ACACCGTCCA AGTTCACTGT 60
TAGCACCGTG T 71

5 (2) INFORMATION FOR SEQ ID NO: 2240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240:

CAGCTAGGTA GTTAGGGATT CGACTCGTAA AACGGATTAA TAGGTTTTAT AAGAAGGGGG 60
TTTG 64

20 (2) INFORMATION FOR SEQ ID NO: 2241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241:

CTTGACACGT ACATCTAATA CGACAGTCTG TCGGTTTAAA ACCTTTTGGG TCAAAC TG 58

(2) INFORMATION FOR SEQ ID NO: 2242:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242:

GACTCATCAC CGnTTGTTAA GAnATACAAT TTATTACCCA GCAnTTAACA 50

45

(2) INFORMATION FOR SEQ ID NO: 2243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAATTTGGAT TGGTTGGAAA TTTACAGTTA AAATTTAAAG GGTGGATGGA AAAATTTTAG 60
GAACTTCTAA G 71

5

(2) INFORMATION FOR SEQ ID NO: 2244:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244:

GGGGGCCCCCT TGGGGGTTTG GGTTTTGGGG GGCCCCCCTT TTAAAAAantT 50

(2) INFORMATION FOR SEQ ID NO: 2245:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245:

30

TTATAATTTT TGAAAATAGA AGAGGGAAGC CTTAAATTAC CAAATGGATT TA 52

(2) INFORMATION FOR SEQ ID NO: 2246:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246:

ATTAGTTGAA AAGTACAATA TTCCGCAAGT TACCAATCGA TACAGGTATT ACAAG 55

(2) INFORMATION FOR SEQ ID NO: 2247:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247:

55

(2) INFORMATION FOR SEQ ID NO: 2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248:

GGGAAGGTAA AACTTCCTGC TTTTTTTATA AGTATTCATA CTCTATTGCT ATATTAGTAG 60
 AAACCGTAAA ATCAGTCATT CACATACATT nTGAAACATC TAAATAG 107

(2) INFORMATION FOR SEQ ID NO: 2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249:

GTTGGATACC TGnAACTAAA TAACTATTCT TTAAAAGTTA AAAACCAACC ACTAGTGGCC 60
 ATTGGGGATT AAAATTCCAA CCTGGGCCGG TCCATCCCCA TGGTGGGTAA AATGGGGGAG 120
 GGAAAATCCT TATTAGCCAA AGGATTCCTT ACCTAATAAT AGGGGGAA 168

(2) INFORMATION FOR SEQ ID NO: 2250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250:

TTTAGTTGTG ACATACTGAG AACTGTAGTA CTTAGTGcna TACCAAAGGG 50

(2) INFORMATION FOR SEQ ID NO: 2251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCAGAACATA CCACGTGTCG CTGATTACCA ATACAGTAGA TCAAGATGGA CTCGATTGC

59

(2) INFORMATION FOR SEQ ID NO: 2252:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252:

15

GTTTGTGTTT TAATTTTAAG GGGAAGGGAT TTTTITACCA AATGGGAATT TT

52

(2) INFORMATION FOR SEQ ID NO: 2253:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253:

AGTGTAATTA GAAAGGCAAG TACACCTGTT TAAAGTTTAT CTTCTAAGAT TTGTTTACTT

60

30

TAGAACTATA GCAGTTAATC

80

(2) INFORMATION FOR SEQ ID NO: 2254:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254:

GTAAATGACA GAGGAAATAT AACAATGATT AATAATGTGA CAGCATTTAC TGCAAATATC

60

45

TACTAT

66

(2) INFORMATION FOR SEQ ID NO: 2255:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

ACATGTGTTA ACTCTTTGGC AATATATCCT GTTCTTCTT CTAATTCACG

50

(2) INFORMATION FOR SEQ ID NO: 2256:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256:

15

AATCTTTTAT AGGAAAGAAA GAAGAAGATG TTATCAGTTG CGATTATCGG CCCAGGCGCT

60

GTCGGTACA

69

(2) INFORMATION FOR SEQ ID NO: 2257:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257:

30

TAGCGGGAGA TAGAAAAACC ATTCCGCATT AGCTTTGGTC AAGTTGGGAA TGGGTAAAAA

60

AATA

64

(2) INFORMATION FOR SEQ ID NO: 2258:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258:

45

GGTTAAGGTA TGGCGAAATA TCTCCAACAA CACTTCAAAA GGTTCAGAA AATAGAAGTC

60

GACTGAACAA TGTCATTAC ATGTGTGCGT CATGCACACC NTATGT

106

(2) INFORMATION FOR SEQ ID NO: 2259:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259:

CGGAATAACT GACTATGTAT CATTGTATGT TATTAACATC AATATTTTTG GTTAAATGAT 60
 5 ATGCTAGAAA TAAAGCATA 79

(2) INFORMATION FOR SEQ ID NO: 2260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260:

GCTGGnTGTT AntGGCAGAG CATGTGAGCT GGATAATCAG TTGGAGAGGC 50

(2) INFORMATION FOR SEQ ID NO: 2261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261:

nCCATTAATG ACCGAGATTA GTGAGCATGC ACAAATTGTT ATGGTAGGAT 50

(2) INFORMATION FOR SEQ ID NO: 2262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262:

AATGAACCAC ATAATGACAA CTTGAATGAC AATATGAATA TGATGTCAAC A 51

(2) INFORMATION FOR SEQ ID NO: 2263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CATTAGGTGC TTATATAAAT TACTTTGTGG TGGCTCCAAA ACTTCGGGTT AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264:

TTTCnTCCCC CCCCCGGGGT TTTTGGTCC CTTTTTTTTT TTAAATTTC

50

(2) INFORMATION FOR SEQ ID NO: 2265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

TCATTCATAG AGGTGTAAAG ACATAAGGGG AGCTTAACTG CGAGGACCTA CA

52

(2) INFORMATION FOR SEQ ID NO: 2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266:

AGATGATGCA ATAATGGTGC AGTATAGAAG TACTGAGCAA TGCAAATTTT AGACG

55

(2) INFORMATION FOR SEQ ID NO: 2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267:

GTTTCATCACA TTTATTACAT TCAGCGTTGG AATCAGTACT GGGTTATCAT G

51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268:

CTGTTGACAA CAAATTAAAA ATGACAACAT GTCGTAGTTA TAGTTAATTG ATTG 54

(2) INFORMATION FOR SEQ ID NO: 2269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269:

AACCAAAAAG AAAGCAAGGT CAAGGAAATT TCAGCGnGAC GTATCTTTAG TTTTGAATAA 60
 GCATATTAAT ATGGTGATAA TATGCAAGAn AACCTGTTTA TTCGATTCAA TGAAATTATA 120
 TTATTAATAT ACTTAATCAG TATCATTTGC TATTTTTATG ATTTTGTACA AAAAAGTCAT 180
 AAGATTAGAA GTTTAGGCAT ATATTTATTG GGGATTGTTT GGGTTTTACA AACAATCTCT 240
 TTATCTATTT TTATTATACA AACTAGACAT ATTCCATTAG GGnCTATTTC AGATGTATTC 300
 TATACTTTAA GT 312

(2) INFORMATION FOR SEQ ID NO: 2270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270:

GTTGATGGAT TCTCTTGGTT TGGTGTAGTC ACAATTTCTG AACTGGCCCT TGTTTACG 58

(2) INFORMATION FOR SEQ ID NO: 2271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271:

CGTTCAGACG CTAAATCAGG CACCAGGTTG TACAATTGTC CTGGTTCTTC

50

(2) INFORMATION FOR SEQ ID NO: 2272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272:

CAGGTGTTGG TAAAACATTT GAGATGCTTT CAAATGCCAT TGAATATTT CAAAGTAA

58

(2) INFORMATION FOR SEQ ID NO: 2273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273:

TTATAAATTG GTGTAACAAT TTCATACACA TGATCATTCT TTGATTGAGG TAAAAATGAT

60

TCTACTAAAC GTACACGTTT ATGCTTCTTA TATTCTTTCA TCAATAAATA TCTATGATTA

120

GCTAATGATA AATTTAGTAG AAGCTTGTTA TCTCCATAAA CTAAATTCAC GATATTAGGT

180

ATATTGAATT GTTCTTGATA TTTCAAAAAT TGTGTATCCC ATTCTTCATT TTTAGGTAAA

240

GGTAATACCA TCTCGTTAAT TTTCCAATAT GCTGGTTTAA GAATGACATT TTTATATCTG

300

ATTCGTGGTG AATAACTAAA TGAATCAATA CTCACATCAT TCATAGGTTC AATGCATTTC

360

ACAGATTCCA TTGAAATTTT TCGTAACAAT CGATATnaAT

400

(2) INFORMATION FOR SEQ ID NO: 2274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274:

GGGTACAAAT TTGThGATGA TAGAAAAGTT CGTATCGCTA GAAAGTCTGG

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275:

TGATTTACCA GTTGATTACG ACAAAGAAGA ATTTTCAAGA ATTGTTGAAG CATCAAAACG 60
 CATTA 65

(2) INFORMATION FOR SEQ ID NO: 2276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276:

ATGGCGTTCC ACCAGCAGTC AATAATCCTG TTGGGATAAA TGCCAATACT GTCGA 55

(2) INFORMATION FOR SEQ ID NO: 2277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277:

TAATAAATCA CGTGCATTTA CGCTCACTAG CTTTCATCTC CTCATTTTTC CTTTCAAAT 60
 TTATTAAGTA TGAATA 76

(2) INFORMATION FOR SEQ ID NO: 2278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278:

GTGGCTTTGT CTGTGTTATT GTAGTTTGT TTCGCTGCGT CCAGCTTTGC TGCTTTTCCC 60

(2) INFORMATION FOR SEQ ID NO: 2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279:

TTAAGTGCCA AAGTCCTTGG TAGCCAGAAT GAACCACCAA CCTCCATTTT TCCAAAAATG 60
GTCTTACCT 69

(2) INFORMATION FOR SEQ ID NO: 2280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280:

GGATGGAATT GGGTTAAGAA TAAAAAGGT AATAATTGAG TTTATGATAA TAATAATAAT 60
ATTGAGA 67

(2) INFORMATION FOR SEQ ID NO: 2281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281:

TTGTTACTTC GGCACGGATA AATCCACGTT CAAAATCAGT ATGAATGATA CCAGCACATT 60
GAGGTGCAGT CATACC 76

(2) INFORMATION FOR SEQ ID NO: 2282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AACCCAGAAG ACTTATTATT AGAATCTTAA TCCACAACAC AAAATAGTTT ACTATTCCTA 60
 AAAGCGGGAT TAAATCAATA ACAAACAGCA GTAAGATTAT TTCCTAGTCG AAATATCTTA 120
 CTGCTGTACT TTATTn 137

(2) INFORMATION FOR SEQ ID NO: 2283:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283:

ACAAAGATT ACTATTTAAC TAATTTATAT GAAGAATAGC TTTCCCTAAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284:

ACTCCTGCAT ATCACAATA GATTAAATAT ACATCAAACA GATATAGTAA A 51

(2) INFORMATION FOR SEQ ID NO: 2285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285:

CTAACATGTG TGAACGATAT GCAAATTCAA TATCTCATTC ACGCTTTGCA CTTTATTACT 60

ACAATCAACG TAACTAT 77

(2) INFORMATION FOR SEQ ID NO: 2286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286:

AAACCTGTAT TTTTAATAAA CAATCGCTTG GACCTATTCA CTGCAGCTCT TCTGGGAC 58

5

(2) INFORMATION FOR SEQ ID NO: 2287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287:

AATTCATAAA ACCAATAAAT AAGAATTTTA TAGTAAAAGG AAATGGANTA GAGTTGGCAG 60

ACTTATACAA TATTAAAAAC AAAGAGCTTT TCACGATTAA AAGAGGAATT AATACATCTT 120

20

TATCTCTTTA TAGTCTAGAA CAGGAATATA ATAACAATTA ACGCCTTAAA ATATCCAGAA 180

TCATATAATT TTGAAGAATT AATA 204

25

(2) INFORMATION FOR SEQ ID NO: 2288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288:

GCTCGTAAGG CGTCAACTGT GGCCTTGGGT GCTACATGTA AAGGTTACTT 50

35

(2) INFORMATION FOR SEQ ID NO: 2289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289:

TCGCTTCGGT GGTAAAAATG TCGTGGAGGT CCCGTTGCAG ATGGTTTTAA ACG 53

50

(2) INFORMATION FOR SEQ ID NO: 2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290:

5 TTGGAGGTCA ATGTTCCGGC TAATCTTCAA TGTTTCCGTA CACAATTGCT GCGGTTGACA 60
CACATACG 68

(2) INFORMATION FOR SEQ ID NO: 2291:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291:

TTCGACGAAT TAAACAAAT CCTTTATAT GTTGAAGTGT ATTCGAGATT AAA 53

20 (2) INFORMATION FOR SEQ ID NO: 2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292:

30 ATCAATTGTC AACATCTAAT ATTCACTACC AATTATATCG CCACATGTTT TTTAGCAGTA 60
ACA 63

35 (2) INFORMATION FOR SEQ ID NO: 2293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293:

45 CGACTCAGGT CCATCAAGAG AGACACATTT CGACTACAGG TTATTACTTC TTTGA 55

(2) INFORMATION FOR SEQ ID NO: 2294:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294:

AAATTTTGGT TAATTTTAAA ACCAAAAAAC CTTGGAAGGA AATGGCCCTT TTCCCAATTT 60
 T 61

(2) INFORMATION FOR SEQ ID NO: 2295:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295:

AATCTTAAAA CCTATGGCGT CTATTACATT CCCAAAACCT ATTTTCAGnA ATGTTACCAA 60
 TTAAACTTGC CGGGGTATGG ACCAGGTAC CAGGCTAAAA ACTGGAAGAA AGGAAGGAAT 120
 TTTAGAAAAT AATTTATTAA CATGGACCAG GTAACATA 158

(2) INFORMATION FOR SEQ ID NO: 2296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296:

TGTTCCAACG ATGAATGTTT GCATGCTTTG TTGCACTGAA ATTGATGAGT TGCTACTTGC 60
 AATCCTAG 68

(2) INFORMATION FOR SEQ ID NO: 2297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297:

GTAGGGATTT TTTTAAACCG GGATAGCCCA ACCAAAATTT AATTAATTTT GGGTTTTTGG 60
 ATTGAAGGAA TT 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2298:

AAAAATTTTA CCAGGTGAAA AATTATTTTG GTAGGATTTA AATnTAATGG TTAAATGGT 60
 GGTTTATTAC CTAATTTAAA AATGGTTAAA AGGGCCTTTA CCATTTTTAA AATTTAATCC 120
 GCCTTTTGGG AGGGGGATT TAGGGATGGT CCAGTTAGGA CCCCATTACC ACTGGAAACC 180
 AACTTAAAT TTAGCCAAAT TTCCTGGAAA AAA 213

(2) INFORMATION FOR SEQ ID NO: 2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2299:

TATTTTAAA GGAGGGTAAT AATCTTAATT TAAGTTCATT ATTTTACTT TCATTATAAA 60
 TATTTAATGT TACTTTCTTA TTTAGATAAC AATAAAAAA TATAATCTCT nAAAACCCAA 120
 TGAAACAGCT GCTCCAAACA ATTAGTTCTT CTAATTGAA 159

(2) INFORMATION FOR SEQ ID NO: 2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2300:

ACAAGGTCAT TCGGATTGA CTTTGTTTCA ATTGTAAAT TTTGCTCCAT CAATTGTCTA 60
 ATTCT 65

(2) INFORMATION FOR SEQ ID NO: 2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2301:

5 TTTATTCTTA TTTAAAAACC CANTGAAAGT AntCTTTnCA TTantAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2302:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2302:

GAGATATATG CATGAGCTCT ACGACTTCCT TAGGTTTCAT GCGACTATC CTGGCAGGGA 60
20 TG 62

(2) INFORMATION FOR SEQ ID NO: 2303:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2303:

ACCAATCCCG TTGTTTGGT TTTTAAAAA AAGGAAATTC CAAAAATCCC CCATT 56

(2) INFORMATION FOR SEQ ID NO: 2304:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2304:

45 TTTAAAACCC AACGGGTTTG GTTAAAATGG CCTGGGCTTT TCCAAAACCTT GGC 53

(2) INFORMATION FOR SEQ ID NO: 2305:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2305:

CGAACAGGTT GCCACTGTAA GATCTGGTGG CATTTAATGG CAATCGTATT TTATTTGGAG 60

5 (2) INFORMATION FOR SEQ ID NO: 2306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2306:

CTTTATAATG GCGGCGCACT TGGCATCTCT GCATTCAGTT ACACGCGGTG GCAACACAAA 60

ATTTAGGGAA TTCT 74

20 (2) INFORMATION FOR SEQ ID NO: 2307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2307:

30 TGTCCATGCA CAGCTTTATT GGAATTTACC TTTTACAGG CAACCGCTAA AGA 53

(2) INFORMATION FOR SEQ ID NO: 2308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2308:

TAAATGATTA TGGGAATATC CAAAATTATC GAGATCTAAT ATGAAGTGAC TGCACACATA 60

45 TCAGCTCTGA ATGAAT 76

(2) INFORMATION FOR SEQ ID NO: 2309:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2309:

TCCTCAAAAT GTGAGTTAAT AGTCGAGTGG AAGCTGTGAC TTGAGCGACG ATACATCATC 60

5 AACTATCAA TAATGTTTGC ACATCACTTT TACTACTATC ATTTGATGTA TAAATAC 117

(2) INFORMATION FOR SEQ ID NO: 2310:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2310:

AAACTCATAT CGCTTCCGAT AACCAACCCT GCTGCTGTTG GTACAAATTG TC 52

20 (2) INFORMATION FOR SEQ ID NO: 2311:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2311:

AACACTGGAG TCCTAATGTC ATCAAACATC TACCTATAAG ACCTTATATA ATCGTC 56

(2) INFORMATION FOR SEQ ID NO: 2312:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2312:

GATAACATCA TAGGCCATAA CTTCCATTTA GGCCATCAGT TATAGCATGC GGACGACATA 60

45 CTGTGCCATA TG 72

(2) INFORMATION FOR SEQ ID NO: 2313:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2313:

CATCTAATGG GAACGTGTCG ATCCTAGTCA GTATAGTCAT CGGCAGGTAC GA

52

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(2) INFORMATION FOR SEQ ID NO: 2314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2314:

15

TAAACTGAAA TTTAATTTTC GGATGGTATT GTTATTAAGA AATAGACATA ATTTGTGCTG

60

GATA

64

20

(2) INFORMATION FOR SEQ ID NO: 2315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2315:

30

CTAGTTTAAA TTTCTTAAAC TTCTACATCA GTAAAAGGCC GCTCTGGGAC CATACAATC

59

(2) INFORMATION FOR SEQ ID NO: 2316:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2316:

GCATAGTAAC TTAATTGATA GGAGATGAAA ATCCGCAAAG TCATTGGAAG GATT

54

45

(2) INFORMATION FOR SEQ ID NO: 2317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

GTATATGCTG GAAAGATAAA GTATGGANAA TGCATGGCGA ACATTTTGTA AGCAGAATGA 60
 GCTATAAGCG TTGAATGGGT TTGAACGTAA ACAATCGAAC AATGATATGT CAGACATACT 120
 5 TGCTTTAGAG CACATTTAGA GAGCGACATG 150

(2) INFORMATION FOR SEQ ID NO: 2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2318:

AAATCATCGA TGTAAATAA TTTAATGACA AGGATTAATG AAAGACGGAT TG 52

(2) INFORMATION FOR SEQ ID NO: 2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2319:

TTAAGGAAAC CTTGGCCAAG GTTAAGGAAA ACCGGGGGTT CCAAGGTTTT TA 52

(2) INFORMATION FOR SEQ ID NO: 2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2320:

ATGAAGTTGA TTTAGGATGA AAATTAATCT TGGGATATTT AATACTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CTAACGCTAA GGGCGACGGA TGGTGGTnAT GTCAAAGAGA CAAATAGGAT

50

(2) INFORMATION FOR SEQ ID NO: 2322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2322:

CGTGGTGATT AATTTTTCGT CGCGTTTTGT TTCCTTTCCC CAGTCATGTT TTATCATTGT 60

GGGCATCATT GCACCTGGGT TCCATATTAT GACGTCATTT TTTAnAAT 108

(2) INFORMATION FOR SEQ ID NO: 2323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2323:

GTCACCGAAT TTCGATTTAT ATTATCACTC AATTTATTAT CTTGAAGCAC GCGTTAAATC 60

GTCTTTAAAT TGnAACAGTT GCTACTTTAT TGTCTTTACC ATTGATCTGA ATTTGATCCG 120

CTTTAAGTCC ACTATCTTTT ACAACTTGCh CTACCTTTTG TTAGTAATT GCTTGTTTAG 180

ATTGGAAATC TACGCGTGTA CCACTTGAAA AA 212

(2) INFORMATION FOR SEQ ID NO: 2324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2324:

TCATTTGTTT TTAATACGTT GTCAAAATTA CCAACAAATG ACAAATTAAA TTTTGCAATA 60

CATATCAAGG TGTTATTTTT TTCCTATTTT AATTATGTAT AACGCATTAA AAGTGACGTh 120

AATATTCAAA GGA 133

(2) INFORMATION FOR SEQ ID NO: 2325:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2325:

10 ATGAACGACC GTGGACAGAC AATATTTAAA GCATTTAAAA ACAGCGTTCC CAGAAAGACA 60
 ATATATAACC AATATTAACA AAAGCAATGC ACATTACTTC ACAAATGAAA TCAAAGCAAC 120
 ACACATATAC AATGCAATAA GCGGGCAACA ACAAACAGAT TTCAACACGC CTGTCATACA 180
 15 GCAATATCGT TAACAAATGA CAnCCGCCnT TTAGGC 216

(2) INFORMATION FOR SEQ ID NO: 2326:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2326:

TGACCATATG ATTGAGGAAG GTTTTATTGA TCCTAAGTAT CGTGCTCTTG CACCGTTATG 60
 CGACACTAAG GAATCATTAA TTGAATCAAT ATTAAATTTn AAACCTCTGG GTACTCGTTC 120
 30 ATACGATTAA TCATTCTAAG G 141

(2) INFORMATION FOR SEQ ID NO: 2327:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2327:

TGAAACTGCA GCGTGGCCGA GTGGGGGTTG TGCCAGGTGA CCCCAGATGG GCGTG 55

45

(2) INFORMATION FOR SEQ ID NO: 2328:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

GAAGCCAGCC TAATTGGATA CCACCGGAAG TAACTTTTGA CCAGGGCCGT CGCA

54

(2) INFORMATION FOR SEQ ID NO: 2329:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2329:

15 GTTCCCGGGT CCAGGCCGTT GTCTTGTCGCC GGGGTGTTTG GTCCTTGGTT GTGT

54

(2) INFORMATION FOR SEQ ID NO: 2330:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2330:

TATATTATAT ATTTAACTGC TGTGATGTAT TCTGAAAAA TAGTAGTATT GCCTATAATC

60

ATCTATGCCA TTGTGTTTGT AATAATTGGT ATCACTTATA TCTTTATAGG CGACAGCTAT

120

30 GATCAATTAA CAAATTTCAA TGTGATTTTG TATATGGGGA GTTTGTtTTA TGCATGGATG

180

GCTATTAGAA

190

(2) INFORMATION FOR SEQ ID NO: 2331:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2331:

45 TTTTCACCTC GTGTTTTTAA TTCAATTGAA TCTAAACTAA AAGTACCTTT AAGT

54

(2) INFORMATION FOR SEQ ID NO: 2332:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2332:

5 TTCTAAAAAT ATTAACGAAT TATACAACTT TAAGAGTTTT TAGTATGTAA ATATTCTTTT 60
 CATATTAATA CAATACACCC CTATATATGC TCACTTGTTT GAATTAATAA ACTTTAGCAT 120
 TCTGCAAATA ATATTTTAAA AATAACTATA CTTTTTATTT ACCTATTGAA AAATAGTGTT 180
 10 ATCATATTTA TTAAGAAGCT ATTTTATAC TAGTAGGTGT CAGTCATGAA TAACATTTTG 240
 TTAAAT 246

(2) INFORMATION FOR SEQ ID NO: 2333:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2333:

25 CCTTCTAACA TCTTTTACC ACTCATTGAA ACATGTGATC CTAATAACAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2334:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2334:

AGAAAAGAGA CTGAAACAAC AAATTCAGGC AACTTTTGAA CAACAGAGAC ATCGATTAAT 60

(2) INFORMATION FOR SEQ ID NO: 2335:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2335:

50 CCTCAATCAG CTCCTAAAGA ACAAATAGC GACTCGATTG ATGAGGAAAC AGTAACGAAA 60
 AAAGAACGAA AAAGTAAAGT AACACAATTA AAGCCATTAA CACTTGAAGA AAAGCGGAAG 120
 TTAAGACGTA AGCGACAAA GCGAATCCAA TACAGTGTTA TTACAATTTT GGTATTGTTG 180

55

(2) INFORMATION FOR SEQ ID NO: 2336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2336:

CCTACAGTCC CAACACTGTC AGTACACTGC CGATACCCAA CCTCTGGCCG GTCCGGCA 58

(2) INFORMATION FOR SEQ ID NO: 2337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2337:

ATATTTTThA TTTAATGGTT TTACTACTGC TACAACTATC ATAGGTGGCA 50

(2) INFORMATION FOR SEQ ID NO: 2338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2338:

CTCCTGTAGA TTAAAATCT CCTAAATAAC AAACGAATAA TCGGCCATCT TTATGTATTT 60
 TGATTGCTGC AGGATTCGCT TTGTGACTTA CAAAAGGTCG TTTGATTTC TCGTTTCAG 120
 GATTGATTTT GAAAATATTG CCTTCGAATA CATCCAATAA AAAGAGTTGT CCCTGCCGAT 180
 CAAAGTTCAA TCCTTCTAGT TGCAATCCTT TTTTGGAAAT TTCAAGCCAT GGTTCAGCTG 240
 TAATTGTTTG TAATTCACCT TCAGATATAA TTGGAACAGC ACTATTGGAC TTCCCGChAT 300
 AAAATAATGG AGGGnAAAnC TGGTGGGGAC ATCCATGAGC CATTCTTTC CATTCCATTC 360
 GGTTTTAACT AACCAATT 378

(2) INFORMATION FOR SEQ ID NO: 2339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2339:

ATGAAAATAA ACTGTGTCTC CnGATGTATA CGTCCCTTCA AGCAGACTTC

50

10

(2) INFORMATION FOR SEQ ID NO: 2340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2340:

20

TATCCATATG TGAAAAATGT CATATATGAG TCTAGTTTTG TATAAATGGA GACTCGAAC

59

(2) INFORMATION FOR SEQ ID NO: 2341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2341:

ATTGATAAAA TATGATTAAG CGTTGTTGCA AATGACATTT TCTCAAAAAG CGCTTCACTA

60

35

TCAATTGGTA CTTGTGTGTn AATTCAGCC AGTCGCTTCG ATAAATATAG TTCATCTAAA

120

TTGTCATTAA TCTTATTACG TTGCCAGCT GATAATGCAT CAATGTTTTC AACCACATTT

180

TCAACGCTT

189

40

(2) INFORMATION FOR SEQ ID NO: 2342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2342:

50

ATCAATTAAA ACAAAGCATA CAACAATTTG TTGATGTTGA ATCTAAATCA ATTTTAGAAC

60

AACAAATGAT TCATCAGCTT CAACAAATGG ATCGTTCTTA TGTAGAGATG ATTACAGAAT

120

55

(2) INFORMATION FOR SEQ ID NO: 2343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2343:

CTTAACCCCC CTTTTTCCC AATTTTAATG GGGAAAATT GTAATTAACC TGGGC

55

(2) INFORMATION FOR SEQ ID NO: 2344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2344:

GACAAATAAA CATGACCTGG ACAAAGAAGA ACAATAAACA AGCCTGGCAA

50

(2) INFORMATION FOR SEQ ID NO: 2345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2345:

GTATTGCGAT GATGCATACG GGTATTGTTT TGATTAAATA ATATTCATA TTTAATGTTG

60

ATAAATGTTG AATAAACAAT CCGCAAAGnG CACTTGATGA TAGTGCTAAG A

111

(2) INFORMATION FOR SEQ ID NO: 2346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2346:

GCAAACAGTT TCCGTGTCCG TTTTCCAATT AAGTTAAGGA ACCCAAAGAG A

51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2347:
 TCGTAGGTGC CATAACACAC GTTACCTGGG ACTCATATGA AGTATTATGT CGAGACGACC 60

(2) INFORMATION FOR SEQ ID NO: 2348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2348:
 GTTTTAAATA GGCTCTTTAC GTATCTAAAA ATAATTGCAT TATTGGTGTG CCTTGATGTA 60
 ATTGAATTAA AGTACCGTTT GGTGTGAACG TTTCAGGTAT ATCATTITTC AChATAAC 118

(2) INFORMATION FOR SEQ ID NO: 2349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2349:
 ATGACAGAAA GCAAAATCCC AATGTTGATA TACCGTTTTT GACACCACTT GATTATCATT 60
 AITTTTTTCTT TAGCGATGGA TTTTATATTA CGATTTCAT TCTTACTATC GTTGCATTAT 120
 TGTCAATCAA ACTGTATCGT TTTTACTTtt ATAGACTTTT CGCAATAGTA ACATGG 176

(2) INFORMATION FOR SEQ ID NO: 2350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2350:

CTACGACTGA CATTAACTGT GCAGATGTAC CTGGATTCTA TTTTTTCAAG AACAAATTGT 120
 AATAATTGAT AGTTATATGG TGCAATGTCA CCTTCATCCA TTGAGCGCTC AATAATTTCA 180
 5 GCTGChAGAG CGGCnTGACT G 201

(2) INFORMATION FOR SEQ ID NO: 2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2351:

ATCGCTATAA CCTATCAGTG ATAATATTTG ATTGCATGGT GCACCATTTG AnATTTCACT 60
 20 TAGAATGGTG GTACCTAATT GCTTATTTTT ATATGTCATT TGAAGATTTA AAAATTAAAA 120
 ACTTTGATAC AGAGTGAAAC CATATTTCAA CAAATTAC 158

(2) INFORMATION FOR SEQ ID NO: 2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2352:

TCGTAATCAA AACATTTTGA ACAGGATTAT AGTAAGGGAA TTTTGGATT TTAAGTTGTG 60
 TTTGTTTCATT TTTTAATAAG AGTCGAGCTA AGTCTTGCAA CATCATTACT TGCTTGGCAT 120
 40 CTAAGTGTTC GTCATTAAAT TTTATGAAAC GATCACTCAT GTTTTATCCC TCTTTAAAAG 180
 TTTAGTTCTA CAGCATTATA TATTGCTTGT TGTTACGTT CATCTTCCAA TTTATCAATA 240
 ATTGTACGTT TAATTGCACG TTCAACTGGC ATTACAGTGA TTAAATCACA CAAGTCTAAT 300
 45 AATGCACGGG ATACTAGCGG CTTCTTCAGA AATTTGTCCC TGCTTAGACA TAGTACGTAA 360
 ATCTTCATTG AACTTNaAT AATTGGTTT GATTGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2353:

ATTAATGGGG TTAAATAACA TTTTGACTGC GAAAGATTTA TTCTTTTCAG GTAAATCATT 60
 5 GATAGATGTA TATAGTCAAT TTGCTGGATT AGCTGAAATG ATAAATGTnT TTGCGAATGC 120
 ACCATTT 127

(2) INFORMATION FOR SEQ ID NO: 2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2354:

20 ATCTCGCTGT TTTTATGAAA GAAAACTACA TTTTCGAGAG AATAAAAAGA TTTTCTGAA 60
 ATTTAATCTA TCAATTACAT TGATTTACTA ATATAATTAG AAAGTAAATT TTATTTGATC 120
 25 AAAGTAAATG GGGGAAGTAC TGTGATAGAA AATAAGAAAA CAGTTGAAGA TACATATTCA 180
 ACAGGCGCAA TTGTTGATTC AATATCATCT TCAGTnCAAA Tn 223

(2) INFORMATION FOR SEQ ID NO: 2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2355:

40 ACACTTGTTT AAACACTCAC AATGATAAAG CATATTATCA GTATTGTAGT GTGTGGAAAA 60
 TGACAGCCAT CTAAGGAGAA AAATGATGAA AAGAATATTG GTAGTATTTT TAATGTTAGC 120
 AATTATATTG GCAGGTTGTT CTAATAAAGG TGAAAAGTAT CAAAAGATA TTGATAAAGT 180
 45 GTACAAAGAA CAGAATCAAA TGAATAAAAT TGCCTCGAAA GTACAAAACA CTATTAAAC 240
 AGACATTAAA CAAGAAGACA GTAATACACA TGTTTATAAA GATGGTAAAG TCATTGTTAT 300
 TGGTATTCAA TTATATAAAG nTCGTGAAAA AATGTATTTA TTTCGCATAT GAAnTAAAG 360
 50 GTGGTTAAGG CCAGAGGATT TAATCAGnGG AAAnTAGACC 400

(2) INFORMATION FOR SEQ ID NO: 2356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2356:

	AATTTACTTT GTGCCACAAG GTTATCAATG TCTTTTGAAC CACCAAACAT TCTAGCGATT	60
10	AAGTGACCTC CATCATCGTC TGGTAATCTA TCCTCTCCCC CCACAGTTCT TTGTGCATGG	120
	CTATTACGAT CCCCATCTTT TAGAGAGAGA TTGTCTACAT AAACCTCTTT TATGCGACCT	180
	TTATGATCGG TTCGATATAT GTGACCAGTA GGTGTTGTGT ATTCAATATT CGCCTTTAGT	240
15	TTCTTAGGTh CTAAGTCTTG GCATAGTGTT CTCCGAATTC nAACCTTGGT GTTAGTTTGG	300
	TGATTCAACA TACTTTTGAT GGAATTCATT ThCATGGGCT ACTT	344

(2) INFORMATION FOR SEQ ID NO: 2357:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2357:

30	TATGCGCCCC TGCTTGATCT TTCATTTGCG TCCACTCAAT TAGTTGTTTG CGC	53
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(2) INFORMATION FOR SEQ ID NO: 2358:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2358:

	ATTTTTTCAC CTTCTGAAAT TGATAAATCT AGGTTATCGA ATATAGTCTT ATCGGCATAA	60
45	GATTTATTIA AATGTTCAAT TTTATATGCT TCCATACCCA TCTTCCTTCT TCTGTTGAAA	120
	TCTCTACGTA CTAAATCAG TTCTATACAT TATACACCTT TTTGAAATCA AAAGAAATCG	180
	ATACCGTTAA GTGTCATAAT TTAATATATT GTTGCTTCAA CTATAAATAA AACTTGTTAA	240
50	GGCTTTGATG ACTATGCTAA TGATCTTTAT AATATACCTT TTTATCAACA CATATAATGT	300
	AAAACATAAT ATAnAAGAAC ATAATAAAAA CCCGGATTGA TATTTTATCA ATCCGAGTTC	360
55	GTGTTTAGAT ATTATTTTTT AGAGTTTGCT TTAGGTCCTG	400

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2359:

TTAATGTCGC CATT TTTTGT TAGGTAGACG TATAAATCTG GACCTTTTGA TGATTGTAG 60
TTAGTAAGCA TTAATTTACC ATTTTAAATC TCAGCTTTAC CTTCAACAGT TTCACCGTTT 120
TTAGAACTGA nTGACCTGT TAGGTGTTTT GTTT 154

(2) INFORMATION FOR SEQ ID NO: 2360:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2360:

ATATGTCTTG TGATTTTTC A GGTGTAAGTT AGTATGCAAG TGATTATGAT TGATAGT 57

(2) INFORMATION FOR SEQ ID NO: 2361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2361:

GGCATCAAAT TAGTAGCGAC TCACACGTGA TGCATCCTGT GTTTTGGATC TCATTCT 58

(2) INFORMATION FOR SEQ ID NO: 2362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2362:

TGTTATTATC GnAGAGGCTT TTCGCTTTGG AATAAGGTAT TACGTGAATG 50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2363:

CTCTTCTGGT CCCTGACATA CATAGGAGAA ATAGCnCCAT GTACAACGTG

50

(2) INFORMATION FOR SEQ ID NO: 2364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2364:

ATTGCCAATG TCGTTAGTTC GTGAGGCTGT TGGTGAAAGT TGTGTTTGAA

50

(2) INFORMATION FOR SEQ ID NO: 2365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2365:

CCATGATTTA AATCATTGAT TAATGGTGCT TGTTCTACAT CTGTGTAAAA TTCATACAAT

60

TCTTTAGCAT CGTCGAATAG TTCATCACGA CGTTGGnTAA ATTCTTCTTC T

111

(2) INFORMATION FOR SEQ ID NO: 2366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2366:

TAATGCTGAG CGTGTTACTT TAGTTGGATC AACGATACCT TCTTCTAACA TATTAACCCA

60

CTCnTTTGTA GCAGCGTTAA AACCAACACC CGGCTCTGCG TTTTCAAAC GTTCTACAAT

120

(2) INFORMATION FOR SEQ ID NO: 2367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2367:

CCTGATTGCA AAGTACAGCA AGCACTACAG ACGCCTAAnC ACTnACACTA

50

(2) INFORMATION FOR SEQ ID NO: 2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2368:

AAAATGGTAT TGCAATTAGT AATGTTACAA CAAGTGTGT AATAGCTGCA TAAAT

55

(2) INFORMATION FOR SEQ ID NO: 2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2369:

TATAGGATGA AAATCCTGCC AAAAGATTAA GGGGTGGCCT AATGAACCAT G

51

(2) INFORMATION FOR SEQ ID NO: 2370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2370:

TTGCTCGAGG TGGTAAATAC GCAAAGTTTA TTTGGTTGTG CTAAGAGAGA AA

52

(2) INFORMATION FOR SEQ ID NO: 2371:

(A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2371:

10 TAATTTGAAT AAGGTGGAAG TGATAACAG TGCTTTGCGA ATCTAGAGTC ATTAATCAAA 60
 ACCCTA 66

(2) INFORMATION FOR SEQ ID NO: 2372:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2372:

25 AGACAGGTAC TGTCCTACGG TATGGAGCAG AAGCGGGAAA GCTGCCCAGA GCCAACTGTA 60
 GACAA 65

(2) INFORMATION FOR SEQ ID NO: 2373:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2373:

40 TTGCAGTGAC GGCTTATAAT CATTCCAAGC GAACAATTAG ACATTCCATA TAAATATAC 60
 AGATGGCTTT CAGTAGAGTA GTGGATTCGG ATTCACGAAC TATACTGGAA GCTTTTATT 120
 ATAAATGAAG AGAAGTTATA TTTTTCAGCAT GTATAGTTGA ATACTGGGTT AAAATACCAT 180
 45 ATTAATAATG AAGTAAAGGT ATGAGTGATT ATGAAAGTGT TTTGAATGAA ATATATTTAA 240
 TTGGTGATGC TTTTAATTGA AAAGATTAAC AGGATTCAAC TTGGTAAATT GTATTAAATG 300
 TGAGAAAATA AAAGTATATT CATTGAGAGA TATATGAGTC AATGATCGTT TTAAACAAGA 360
 50 TAAGTGTATT TTAATATGTA AAAGTTATGT AATAAATATT 400

(2) INFORMATION FOR SEQ ID NO: 2374:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2374:

CCTATCATGC CTCTCTCTCA CTGAATCCTT TAGATCCCCT TCCCTCCCTC TCCCCCCTCT 60
TTTCCCCCTCC 70

10

(2) INFORMATION FOR SEQ ID NO: 2375:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2375:

CCAAGTCAGA GCAGCAGTTC AGTTCGTCAG CnGTTcAGTT CAGAGCnGTC 50

25

(2) INFORMATION FOR SEQ ID NO: 2376:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2376:

GTTGGTGAAG CTGTTGCCGA nGGAGAAGCG GGTATGGATC CTGACGGTGn 50

(2) INFORMATION FOR SEQ ID NO: 2377:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2377:

AATTGCAGGA CAGGTCAAAG GCAAATGCAC GTATTCAGGT CATGCTCATG TGCATGTTG 59

50

(2) INFORMATION FOR SEQ ID NO: 2378:

55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2378:

5 TTTATCATCG TATAAATCTA TATCTAATTG ATTAACTTC GGGTGCTTAA CTAACCTCTCT 60
 CAATACACTT ACACCAGCAG TTCCCATGCC TATTATTGCT ACACGCATAT ATCATCCATC 120
 CTTTTGTAAT TCAAAATATT ATATTTAAAC TATTACCTAT AATTATAGCA ATTTGGTATT 180
 10 TCCAATAAAA TTTATnAAGG TAAGCnATTA TTTCACTTTC ACAACCATT 229

(2) INFORMATION FOR SEQ ID NO: 2379:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2379:

AGTTTTTTGT TTGACGTATT TAATTTACTA TTTGCTTGAT TGATATTTTT AGACATTAAA 60
 25 TAGTGTCTC CTAATCAATT TATTCTCTT TATnTCAGCA TTATTCGCAC TGACAT 116

(2) INFORMATION FOR SEQ ID NO: 2380:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2380:

CAAATCTTAG CGGATGATTG GCATGTATAT TCTGCTGGTA TCGAAnCACC CGGTGTTAAT 60
 40 CCCAAAGCGA TAGAAGCTAT GAACAGAAGT CGGCGTTGAT ATGTCGAATC GTACGTCAGA 120
 TTAAATCGAT AATAAT 136

(2) INFORMATION FOR SEQ ID NO: 2381:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2381:

TTAATTGATA GCTTTTATCT GTAGGAAAAG CTATTTTAAA GATTCTAGT GTATCTATAA 120
 CTTTTTTGGG ACGATATTGA ATATTACAAT CTTTAAATGC CTTTTTAATA AAATTCAAAT 180
 5 CAAAATCTAC ATTATGAGCT ACAAATAATGC AATCTTTTAT CTTATCGTAG ATTTCTGTG 240
 CAACTTGATT AAAATATGGC GCTTGTGTGA GCATATTTTC TTCAATGGAT GTTAACGCTT 300
 GAATGAACGG CGGAATCTCT AAATTTGTTC TAATCATAGA ATGATATGTA TCAATAATTT 360
 10 GGTTATTGCG CACAAACGTT ATACCAATTT GAATGATATC 400

(2) INFORMATION FOR SEQ ID NO: 2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2382:

TATTTTGTTA ATAAAGTTAA TATATGTTTG TTGTACAGAT AGTTCAGGAT ACA 53

(2) INFORMATION FOR SEQ ID NO: 2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2383:

CCCGAGCTTG CCCTCCTTCC CCCCTCTTCG CCTCCAGACG AAGTGCCCTT CTGTCCTTG 59

(2) INFORMATION FOR SEQ ID NO: 2384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2384:

AGCCAACATC CCnGATGGTA CTTGCATTAA TGCATAACCT AGAGAGAAGA ATGATGCCAA 60

50 TAAACCAAAT TGTGGTTTTG TCATCCCTAA ATCATCCATC ATTTGCTTAG 110

(2) INFORMATION FOR SEQ ID NO: 2385:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2385:

10 TGAAAGTTCT TTTAnGCATC AATTTTAAnA CTACGAGCGG ACnCTAATAT 50

(2) INFORMATION FOR SEQ ID NO: 2386:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2386:

GGCAATTTAT TGACACAATG CTTGAGCnAT TGATAGCAGG ACAAGAAAGA ATACTTGATG 60
 25 AGTTAATACC AAAAATGGAT GCGACTGAAA AATTAACGCT TTATTAACT AGTCATTATA 120
 AACAGATAGA TTATGAATTT TTGTATCTCC TTTCAATGGA TAAATTGTTT GGAAATAAAA 180
 GAAATAGATT AACATTAATT GATTTAGAAA ACATATTGGG AGTAGGAAGA GTAAAAATTA 240
 30 GTnGT 245

(2) INFORMATION FOR SEQ ID NO: 2387:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2387:

CACAAAATTC GAAATCGTCA TCGGTGATAT GTTTAATACT TGGGAAAATA TAAAACGCGC 60
 45 CTTCAGGTTG AGCGGTAATC TCAAAACCTA ATTTAGTTAA TTCAGATACT AAATAATTC 120
 TTCGTTChAC ATAAGCTTCG 140

(2) INFORMATION FOR SEQ ID NO: 2388:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2388:

ATATAACATT GTAGGGCCTA ATAATTTATT TTATGTCTCA GACTCATACA ATGGTTATTT 60
5 AACTTATTTA CCACAAATTG AGCACTAAGA CTCACTATTA TCGATTCTTC TATTGAACAn 120

(2) INFORMATION FOR SEQ ID NO: 2389:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2389:

TCTAAATCCA GCATGATCTA CATCAAAGCT GAATTCACCT TTTTCATCGA CTTGCAAATC 60
20 AGGGAATTCT TGACCTTCAC CTAGT 85

(2) INFORMATION FOR SEQ ID NO: 2390:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2390:

GGTGTTTATA AAGCAGGGGC TGAGCCTCGG TCAGGACTGG ATACACAGGC AGTACGGGTG 60
35 A 61

(2) INFORMATION FOR SEQ ID NO: 2391:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2391:

TAAAGTAACC ACTTTAGATG ACATTTTGA AGTTATGGGC CGAATGCAAA C 51

(2) INFORMATION FOR SEQ ID NO: 2392:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2392:

5 GGTCGGATTC CCGGGTCGAC CCACGCGTCC GCATCAACCT AGnAGAAGCn 50

(2) INFORMATION FOR SEQ ID NO: 2393:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2393:

ATTTCCAAAC GAATTGAAAA ACGGACGTAA ATTCTTAACT AAAGGCGATA AATGT 55

20 (2) INFORMATION FOR SEQ ID NO: 2394:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2394:

ATAGGTTGCT ACTATTTATA TCGACTCATT TTCACCTACA AATATGACAT TGTCTCTAGA 60
 ACACnAAAAT TAATTTGCGT CATATCTGCT ACAGTTTTGA GTGTGTTATC AAGTGTATTT 120

35 (2) INFORMATION FOR SEQ ID NO: 2395:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2395:

TGGACCATAG TAAAGCATT ACGTCGGTTT ATTATTTTCT AAGGAAGTAT GTTTATATAA 60
 ATCTATGCTC ATTTGTTTTT TAGCGTCTGT TTGACCTATT ATTTTAGAAC CAGCCATCTG 120
 50 CTCTTTATAA AAATTTATTA CATCATCTTT TTTTAATGTT GTATATTCAT AGTTTATTTT 180
 TATTATnTCA GAATCGTGAA AACTATTTAG TGATTGANAT ACTCTTTTGG GAGGATTCTG 240
 AATATAGATT TTCTTAATAT T 261

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2396:

GTTTTGAATA TAGGGGCTTT TATCACTCTC CGAAGTCTnT TCTAAGTTAG ATTTGGAAAA 60
 TAACACTTTT TTAGTTTCAT TCAAGCGAGT CGAGTGA CTC CAGA 104

(2) INFORMATION FOR SEQ ID NO: 2397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2397:

GATTATCCAT CACAGTATGA TTTACGTAGC AATTTCTGGT ACATATACGC CTAT 54

(2) INFORMATION FOR SEQ ID NO: 2398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2398:

GCTTCACCTT GAACTAGCAA ATAAGGATAA AACAAGCATT CTTTACATGT TTCTTTTAAA 60
 TACGTTTGAT ATTTTAATAA TACTTTTTTCG ATTTTACTCA TATAAGTTTG AAGTTCTAAT 120
 TTTTCATTCT CACTTATTTT GTATATATTA CATTCAATTAT GTTCTGTCAG AAAAATATAA 180
 GGGTCAATAT TAATTTTCGTC TATCAATTCA TAAATTTTAC TTAAGTATTT nTnCT 235

(2) INFORMATION FOR SEQ ID NO: 2399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTTGATGCAC TTATTTGTGT AATGACATCT TTACAGTCTT TTCCTTCCTC CATCATTTTA 60
 ATAATTCCAT TTAGTTGCCC TTGTATTCTA TTAATACGAT TAATCATTTT n 111

(2) INFORMATION FOR SEQ ID NO: 2400:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2400:

AAATGCTGGC TGAGTTTTGG GCCACCCGCA AAGGCACTGG ACCGGTGCGA AACC 54

(2) INFORMATION FOR SEQ ID NO: 2401:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2401:

AACCACTCAT CACTACTAAA ATGATACTTA AAAACAAAGT CTTAATACAC TTTTTCATAA 60
 TATCAACTTC TTTCTATATT TAATACATTA ATTATACATC TTTnTnAAAT AAAAATATGT 120
 GTAAATTTT AAAACTTATT TAATTGATGT TTTAATAATG TATTATAGAA ATTATTGACA 180
 TATGATTAAA AACCCTTAGG ATAGT 205

(2) INFORMATION FOR SEQ ID NO: 2402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2402:

AGATAATCAT AGAGAAAGTC CACAGTCGGT AGAGGTGGTA GCTGAAAACA ACATACTATT 60
 AATTATGAAG TGCTTTGTAA CTTGTCGAGA CGTTTGCCGC GAATCTATCA TGATGGTGAT 120
 CAACGTTTTG TnACAAATGA 140

(2) INFORMATION FOR SEQ ID NO: 2403:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2403:

10 ATTTAACCAC TCCTCCAATG ATAAGATTGA AAGGCAAGAT GACCTTCCAA TCTTATTT 58

(2) INFORMATION FOR SEQ ID NO: 2404:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2404:

CAGCTTCTAC AATACGGCGT GCTATAGCAA GCATTAATGT AAATCCTAAT TCTGCAGTTG 60

25

T 61

(2) INFORMATION FOR SEQ ID NO: 2405:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2405:

AATAATCATT TTAATACGGT CTTCAAGGAAT TGAAGTGTCT ACAGGTACAT ATCCACATCC 60

40

TGCTTTAATG GGCACCAATC ATCCCAACAA TCATATATGG TGACATGTGA CCGANTAAAA 120

TCATCGGGTT TCTTACTACC TTGTAATCGA TGTGGCTAAT TTACTAGACT CATCCATTAA 180

CTGTTGATAA GTTAATTCCA TCAGTTGTGT GTCTAAC 217

45

(2) INFORMATION FOR SEQ ID NO: 2406:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2406:

55

GTAGTATCCA ACGTATTTTCG GATTGCATCG AGTTGATTTT TATTATTTTC TTCAATGCTA 120
TCAAGCGCAN CTGTATTACG TCTTACTTTA GGTTTTATTT GCTCTATTGC CTGATTGTT 180
5 TGATnTCTAA CATCAGTAAC AGCAGCATCT TGATTTGTAT TGTCTATT 228

(2) INFORMATION FOR SEQ ID NO: 2407:

(i) SEQUENCE CHARACTERISTICS:

- 10' (A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2407:

15 CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG 60
20 AGACGGTCAC AGCTTGTCTG TAAAGCGGAT GCCGGGnAGC AGACAGCGAT 110

(2) INFORMATION FOR SEQ ID NO: 2408:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2408:

30 GGAGACCCCA AAAATTTTGT CGTTGAAGAT GCCTTTTTTTT AAGCGTTATT TGGCTATATC 60
35 AGTTTCTAAC TGT 73

(2) INFORMATION FOR SEQ ID NO: 2409:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2409:

45 AAATCATTAG AGAGGAATAG TTCCCTTTGT TACGCCAAAG ATTCGATATT GAC 53

(2) INFORMATION FOR SEQ ID NO: 2410:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
- 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2410:

CCATATGATT GTATAGGATC CATGACGTCT CCACTGACCC CTGACTCTAG TATC

54

(2) INFORMATION FOR SEQ ID NO: 2411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2411:

GTTCTCTTC AATTGTTATA TGTATATCAC AAAAATTATT TCATTATTTT ACCATTATTA

60

TTTTACAAAT ATTATCCCAA GAATACAATT CAAGAAATGA TTAACCTTTAC TTTAGAATTG

120

TACCTTATTA CATTATTTAT GAAAGTACTC TCTCAATTAT AACNAAAAAG AAGGTGTTCA

180

ATACATnCAT ATTTAGTCTT ATAT

204

(2) INFORMATION FOR SEQ ID NO: 2412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2412:

CAGTGGCGCA GAAACATAAC GCTCAGGGAA GCACAGCACC TCATTATGCC AAAGCT

56

(2) INFORMATION FOR SEQ ID NO: 2413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2413:

TCGCTGGCGG GTCCGCGCG CCTAGCGTGC TCATGTGCGG TGTTCTAGGT GTTGGGGTTG

60

CAGTCA

66

(2) INFORMATION FOR SEQ ID NO: 2414:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2414:

GGATAGAAAT GGAATCCAC CCATCGGTGG GGGTACCAGG CTCTTCATAT GGCCTTGTGG 60
 ACTTC 65

(2) INFORMATION FOR SEQ ID NO: 2415:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2415:

TTAAATAGAT AGAATAGAAT TAAAGAGACG ATGATAGGTG CTGCTATCGT CTTAAAAACG 60
 ATGATAAAAG GATCAAAAAC ATATGATACT TTTTCGAAAA TAAAAATAAC AATACCCAAC 120
 AATACTAGCG CTATTAATGA GAAGACTAAA TCATTCCCAC CAACAAACTT CATATACCGT 180
 GATTCGGTAA ATTTTnnAAA ATTCTTTCTT ATATTCTTTT CATTTTCATT CAATTATAGA 240
 TTCACCACCA CTTAAAATAT TCATAAG 267

35

(2) INFORMATION FOR SEQ ID NO: 2416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2416:

TTAAACAAAT GAATATAGTA GTTCCATTAT CCTCACTTTT AATCGTTTAT 50

45

(2) INFORMATION FOR SEQ ID NO: 2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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TTTGCTGGGA GTTGCAATTA GAAAATATAC ACATTTACTT GACATTCAAC TTGATAAAAA 60
 ATTAGTTATT GCCATATGTT GCATCACATT TATAGGGATT TTAATATTTT ATGTACGCCT 120
 5 AATTAAAAAA TCATCTTTAA ATATTTATAA TACTAAAAAT AAAAGGTCAA AAATnTT 177

(2) INFORMATION FOR SEQ ID NO: 2418:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2418:

AAAATGAAGC GGTGCGAAAA TATAATGACG TGAAAGCATT TTATACTCAT GGACATTTAT 60
 20 ATCAAGTCAA TCGAACAAGA GATTTATTAG CTGAAAAAGG ACTTGAATTA GGTGTTTGT 120
 TTGCATTTTA TGGACATACA CATGTGGCAA AATATGAGTA TATTAATGGT GTTCATGTTA 180
 TTAATCCTGG AAGTATATCT CAATCTAGAA GTTCAATGGA AGAAACATAT GCTGAAGTTA 240
 25 TTATTGATGA TCAAACCTTA CATGGCACCA TCAATTTCAA AAATCGACAT CACGAAACAA 300
 TCAATCATACT TACTTTTTAA ATAGAANTAG CTATGGCTTT TTTTAGTTTA TAGACTGATT 360
 TAACTAGGAG GTCGTGTCAT CCAATGTTTG TTAAAAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 2419:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2419:

AGGGTGCCGA GTTAACCAAG AAAGGCCGTT GGTGCCCCG GGTATTTTCC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2420:

(2) INFORMATION FOR SEQ ID NO: 2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2421:

ACCAGAAGAC AATAAGTGTA ATGATGCCTG TTCTAATACA GAATCTTTAC TTTTATTGCG 60
 CTTTCAAGT CGTTGTTCCA CTTTCTTAAT TTCATTGTC ATGTTTAACT TTGCCAGTT 120
 AATCACCTTT GGTATTATCT TTTTCTTTAT AG 152

(2) INFORMATION FOR SEQ ID NO: 2422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2422:

GTACGTTTT ATTAGTTGTT ATATTTCCAT CTGATAATT TTTTAAATCT TTAAATCAG 60
 CATACTGACT AAAAAATTTA AAATTTTCAA TTTTGTGTT AAGTTTTTGT CTTCTACATT 120
 ATCCAAAAGA ACAATCTTAT TATTTTTTAG TTCAACACGA TATTTTTTCT CATTATGATT 180
 TTTGCTAATA TCATCATAAA CTTTATTAC AAAATAATAA CCTGTTGCCT TTTTGGTATT 240
 TCTATTAAGA TATAACACCA TGCCTTCATC ATCTAATACT CCTGGTTTGT TACTTTTTGA 300
 AAAACCh 307

(2) INFORMATION FOR SEQ ID NO: 2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2423:

ATTGTGTTGT ATTTTAGACA AGACCTTCAA TTTTGGAGAT TTCACGATT ACCACC 56

(2) INFORMATION FOR SEQ ID NO: 2424:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2424:

10 AGTCCTTTGG ATCGTCAAGA TTTCACACAT TTACanTTAT TanCTCGTGA

50

(2) INFORMATION FOR SEQ ID NO: 2425:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2425:

ATGTAATATT ACAATTCAAT TAGnAAAGAA CTTTATCTTT AATTGCTTTT CGATTTCATT

60

25

CATGTCATCT TCTGAAATTA TTATCGTTCC AGTAGGATCA GAATCAITTA TTTTGCTTAT

120

ACGTCCTTTG CTTATTGTTG TAATTGCTGA TATATTAACG TATGTATCTT TCCCTTTGTG

180

CTTGAATAA ACACCTATCA CTCTATACAG TTCATTAGCT TTTTGanTTA AGTTAGACAA

240

30

AAGCTTTT

248

(2) INFORMATION FOR SEQ ID NO: 2426:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2426:

CCTTATTATA TGACAGGTTG CCTAAACAAG TGCCTAGAGA AAAAAGTAGC CCC

53

(2) INFORMATION FOR SEQ ID NO: 2427:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2427:

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TATCCACTAA AATGATTGTC GCGTATTGTA ATATTAAATCG TTCTACTTTT TATGATTATT 120

ACAGGGAGCA ATTTGATTTA TTGGATACCA TCAACTCnAA GCATAGGTGG AGG 173

(2) INFORMATION FOR SEQ ID NO: 2428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2428:

TACTTATGTT TATGTCGCAA TAATTAATGT TCGANTTAGT GGAATTGAAC 50

(2) INFORMATION FOR SEQ ID NO: 2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2429:

AGTCATCATA TTATCAATAA TACGCCGCGT TAAATCTGAT AAATTCATAT AGTCTGTATC 60

TAACTCTG 68

(2) INFORMATION FOR SEQ ID NO: 2430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2430:

TGAATTGAAA ACGGTCGGTG AAGCGCTAAA AGGTAGACGT GAAAGGTTAG GAATGACTTT 60

AACAGAATTA GAGCAACGTA CTGGAATTAA ACGTGAAATG CTAGTGCATA TTGAAAATAA 120

TGAATTCGAT CAACTACCGA ATAAAAATTA CAGCGAAGGA TTTATTAGAA AATATGCAAG 180

CGTAGTAAAT ATTGAACCTA ACCAATTAAT TCAAGCTCAT CAAGATGAAA TTCCATCGAA 240

CCAAGCCGAA TGGGACGAAG TAATTACAGT TTTCTATAAT AATAAAGACT TAGATTATAA 300

GAGTAAATCC AAAGAGCCAA TACnATTATT AGTAATCATG GGnATTACAG TTTTAATAAC 360

(2) INFORMATION FOR SEQ ID NO: 2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2431:

TGACTTCGTC CAAGTACAAC TGCAGTCAGT ACCTACGAAA TCAAGATCAG CATGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2432:

ATTCTTAATC GCATCATAAT TAATTAACGG ACGCATAACA AATCCGATAA TACTATTATC 60
 TTTCCAAGTC ACTGACACTC CAAATTGATT TGCTTCnTCT ATCCATATTT GCTCAATAGT 120
 ACCATCATTT TGAGTACACA CTTTAAATTC ATGTACATCA GACTGCCTTG TATAAGATTT 180
 GAAAAGTTTC CTAAACTGCC AATAACTGnA CTCTCGCTTC AAATT 225

(2) INFORMATION FOR SEQ ID NO: 2433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2433:

CGGCCTGACG TTACATTTCT TCAACTTCAC GTCAAAATTG CTTCGCAATA ACCAGGA 57

(2) INFORMATION FOR SEQ ID NO: 2434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAACGTGT CTTTAATGTG GAAGTTGAAA TATTAGTCCG TAAAAAATG AAACTTAAAA 60
 AAAAATAATA TTTATATTTG TCGTACAAAG ATGAAAGCGA nAGA 104

(2) INFORMATION FOR SEQ ID NO: 2435:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2435:

TTTGCTAATC GTTTCACGGA TTGTGGGGAT GGGTAAAGAC TTTGCTAGTG G 51

(2) INFORMATION FOR SEQ ID NO: 2436:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2436:

AAAnTTAATT TTTGGGGGGC CCTTTTTTAA CCGGAAAATC CAATCGGGGC TTTTAAGGAA 60
 TGGTTTTGGT TAACAGGCTT TGGAATTGG TTTGGCAAAA CAATCCTTG TTTGGGGTTT 120
 CGGTCCGGAG GGTCTAATT 140

(2) INFORMATION FOR SEQ ID NO: 2437:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2437:

GAAGCGGAAC CACCGTTGTT TTTCTTTTCA GGTCCAATTG AATAAATGTT ATGAATAGAA 60
 TGGATAAAAA TATAATTATT TAAGTGTTAA AGTAAACCAA ATCATGATTT AAGATTATAA 120
 GAAAGAAAAA TTGACTAATG TTAAAACCAA CAATCATATG GGTTGTAACG TTTATACAAT 180
 CATCGTAAAA CTCAATATGC TTAATTTATT CAAAATGTTC GTCAATAAGT ACAATGAAAA 240
 GGAGATTGAT TTTTGAATAA AAAATATCTT ATGATTGTAA TTATAATTTT AATATGATTC 300

AAGATACGAT TTTGAGACCA TGTGAAGGGA TTAAATATAG

400

(2) INFORMATION FOR SEQ ID NO: 2438:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2438:

TCTGTTTTGA AAGTTGCAGT TTGGACAGCA CCCGATGATT AGGTGAGTCT TTTGGTTTA

59

(2) INFORMATION FOR SEQ ID NO: 2439:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2439:

TTGGTnAAAC CGTTACAGTT GCAAGTTTTG AAGTGAGITA TTTTTTGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2440:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2440:

ATTAAAAATA AATTAAAGT TCCAGAACCA GTTAACCAGA ATATTTACGA

50

(2) INFORMATION FOR SEQ ID NO: 2441:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2441:

TGCTGTTTTG GCGGTTTTTC TCCGTTTGGT TGAGTATGTG GTGTACCTTT TGTC

54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2442:

5 GTTGTTGGGT GTGTGGTTTT GGGTGTGTGT GGTGGGGT CTGGGTTTCGT TGGTGG 56

(2) INFORMATION FOR SEQ ID NO: 2443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2443:

20 GAGACAACT AGTCGTCCAG AACGGAATTT AAGTAATCAT AATAATTACG GAAGTGCACT 60

25 TTTGTTTTTG ATTTATCATT GATGGAAATT AGAACAATTT ATCGAATGAT ATTAAAATTA 120

CATAACATCA TGTGAATGT GAAATTAGGA TTGAACATTA CCTGTTTATT TGAAAAACCT 180

30 TCAGTTTTTA AATCACTAGT ATCACAAATA AAGCGACTTA AATTCGATTC GTTAATAATA 240

GATAATGCAA ATTTAAGTAG CCCT 264

(2) INFORMATION FOR SEQ ID NO: 2444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2444:

35 CCGTCTTTAG TACGTACGTT GTTTGCGGGG CTTGGGGTGC TTCTGGGTG TTGGTCATTG 60

45 TATTGGG 67

(2) INFORMATION FOR SEQ ID NO: 2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2445:

AGCTGCATTT CTCGTGCAGG CTATCAGCAT CGATATCTGT ACCATTTAGT GATCATGC

58

5 (2) INFORMATION FOR SEQ ID NO: 2446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2446:

15

AACCAAAACA AACATTTGTT CGTTAAATA TTGACACAGA ACATAAGTTC TGA

53

(2) INFORMATION FOR SEQ ID NO: 2447:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2447:

CACAAATTAC ACCCATTGTT AntACTAATA CTnCCtntt CATTTGTTTA

50

30 (2) INFORMATION FOR SEQ ID NO: 2448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2448:

40

GCACAAACCA AACGCACCTT AACTGCTTTA AATGGCTGGA CGGGGGGTCA ACTGGCCTTA

60

ATGACACTTG AATCG

75

45 (2) INFORMATION FOR SEQ ID NO: 2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

55

GCAGCCTTCA AGTGTGTTGCT ATTTGCTTTG GTGTCACAAG CCATTATCTA CGGTCCCGCA 60
 ATTTAGCCCG C 71

(2) INFORMATION FOR SEQ ID NO: 2450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2450:

TGGCGTGAGG AAAAATATCA TGTATTGTTA CACAGTCAAC AGTCTTACCA AATGATAAGG 60
 AATGCTTTAA AAACGGATTT ATCACTTCAT CAAGTTCAAC AAATGATTGA TGTGCTTTG 120
 TTAATTGAAC CGGTATAGG AAGTGATGT AATGCTTTTG ATCATATGTG GGGATATTTA 180
 AAAAAATGTG CGAATGAAGA AGGAAAGACA ACAATCAAAA CTACTTAAAA GCTGATTTTA 240
 TTTAATGGnA AAAATCGACA CCCCACTTT ATTAGATTTT TTAGCAGAAC TTGCCTAATA 300
 AATATGGAnG TCAATATTTA CTACAAAGCC GnGTTTTTAA ACCCCAAAAA G 351

(2) INFORMATION FOR SEQ ID NO: 2451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2451:

GTGTACCGCC TCGGCTGGCG TTCGCGGTGG GTGGTGCGGT CGGTGCGTGT CTGG 54

(2) INFORMATION FOR SEQ ID NO: 2452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2452:

TGCCATTCCA ATGTTACCAT CGTCTTGTA CTACTATATA CTGCGGCTAT 50

(2) INFORMATION FOR SEQ ID NO: 2453:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2453:

10 AGACGTGTTT CCACGGTATG GGATAAATGA AGCACCGACT GATAAATCAA TATAGCCTCG 60
 TGTTTTTAGT TTACCCGAAC TATCCCTTGA TAATGATTGT GACATCTGCG GATAATATTT 120
 CATTTTCTTA GATATCGTCG AAATATCACC GATTACTTGA AGTCCATCTG TCGTAAACAA 180
 15 TTCAATTCTG CTTTGTGTTGT TTTTACTTGG GGCATATGTC ACTTCGGCAA TATATCGTCT 240
 AACTTCAGGT GTCATTTTCAG ATAACGCCTT AATCATATCA TCTTCTTTTG TACCTTTGAA 300
 ACCATCCATG ACAGGTGCAT CATTAAATTT GACATCATTT GAACCTTTAA GCAATTTACC 360
 20 ATTTTCTAAT AAAGGTAAAT ATTTACCTTT ATATTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 2454:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2454:

AGAAAGAAAT ACCATTTGGA GATAGAGACT CGTGTATTTT CTTAGCGATG GGAGATTTT 60
 35 ATAATAAAGA AGATAGnAAG AAAATTATCA AAGGTTATGA AAATAATTAT GGTAGAGGTA 120
 TTAATATTCC TCGAGCACAT AGTATATATT TATATG 156

(2) INFORMATION FOR SEQ ID NO: 2455:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2455:

ACTTAGGTGA TATGAAATGT GGTCCGCGAC GATCGTCAGT AACAAAATAA CAGGCAGTCA 60
 50 TTGGATTATG TTTAACG 77

(2) INFORMATION FOR SEQ ID NO: 2456:

55

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2456:

10 AGTGAAATCG CTAAAGAAAA AGATGGAACC TCGGTATCTA ATACACAACT TCTTGAACGT 60
TTTTA 65

(2) INFORMATION FOR SEQ ID NO: 2457:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2457:

25 TATCAATAAT TGCCACTTGC AATGACTGAT TAATTTGAGG TGCACATAAG CCAG 54

(2) INFORMATION FOR SEQ ID NO: 2458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2458:

AATTTTATTT CGAGATTCTT CAATATAGAT GTTCTTCAT TAATTTGATT CTCTAACTCT 60
TGCTTACTAC CTAATAGTTT ATCTAATTCA GCTTTAGCTT TTTCATTTTC TTTAATTATA 120
TTAATTTTCAT TATTTATGTT CGTnATCGTA TTATTTAGTT CGATAA 166

40

(2) INFORMATION FOR SEQ ID NO: 2459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2459:

55 CCAATGATTA AGCAATACAA TCGTCACTAA AATTACACCG ATAATCTGAA TCATCGTCAT 60

(2) INFORMATION FOR SEQ ID NO: 2460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2460:

AAATCAAAAA AATGTATAAT GAAAAGAAAA AGAAATTTGG AAAAAATTGG GAAGACGCTC 60

AAAAAGCTGG AAAAGCTGTA GGTGAAGATT TGAGTGThAA TGG 103

(2) INFORMATION FOR SEQ ID NO: 2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2461:

TTTATATCAG AATAGAATAG TAACTAAGG CATTTGGAGA ACTTATTCCA TG 52

(2) INFORMATION FOR SEQ ID NO: 2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2462:

CAGCAGCGAA TTTTGTGACGT CCAGTGTAGA ATGGATGTGA ATCAGATGAA ATATCTAAAC 60

GAATAACTGG GTATTCTTTT CCATCTTCCC ACTCCATCAT TTCTGAAGAn GTT 113

(2) INFORMATION FOR SEQ ID NO: 2463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2463:

CTAACATAAT TGTTAACACT AAAATATTTA CTA CTTT TAG AACTGTGCGA TTAAATACAA 120
TTGTCAGTAT TGTATGACT AGGCTAACGA TACATAAAAT AAAGAAACCG TTAAAGACTA 180
5 AAATTAAGCG ATCGATTCTT TGTGTAAAT CATTGATATT ACCCAAATTA ATATTTAATT 240
GGATGCATTT nCCAA 255

(2) INFORMATION FOR SEQ ID NO: 2464:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2464:

20 TATGCGACAA TTCGAAACAT TTTATATGCA AAAGGTTATA CAACAGAGAA TGTTGATT 58

(2) INFORMATION FOR SEQ ID NO: 2465:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2465:

30 TGAATTTTCAT TACCACATAT CGGACATTGA TCTCCAATAT TTACAGCAGA TTTAATTTCA 60
35 CTTAT 65

(2) INFORMATION FOR SEQ ID NO: 2466:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2466:

45 CGTGACCTTC AAAGACCGAA CGAGAGAGTT GAAGAGCATT TGCGAAGGCC A 51

(2) INFORMATION FOR SEQ ID NO: 2467:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2467:

AGTTTGTTAA GTTTGTAGTTT ACTAAGTTT CCATTAGATA TTATTAATGA AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2468:

TTGTTGGTAA GGCACCTTCTT AAATATCAAC AACGCGATGA TATTTTCATT GGTACAAAAG

60

TAGGCAATCG TTAAAC

76

(2) INFORMATION FOR SEQ ID NO: 2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2469:

CTTCTATAAT AAAACCATCT GCAATTAAGT CTTCAATAGA CGATGGATTT CTATTATGTA

60

TCAATGCATA C

71

(2) INFORMATION FOR SEQ ID NO: 2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2470:

CTTCGTCATT GTATTCGAGC GCCTGTATAG CTTGCTCAAA TGATGCATAA AT

52

(2) INFORMATION FOR SEQ ID NO: 2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2471:

AGAGGTTATG TTGATGTGCT TTATTTTCAT CAATGTCATT AACACAATCA TATTTCTTCT 60
 5 GTTAATGCAC TGTATTATAT TCAAACGCGC TATCGACAAT TAATTTGn 108

(2) INFORMATION FOR SEQ ID NO: 2472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2472:

GTCCCCAGTT GATATAGGAT CACAGTTTAA TATACTTGGT GAGATAGTAA TACTATTATT 60
 20 AATTCAAATA GGTGGTCTGG GTATCGTGAC CGTAACCCTA TTGACACTAG TATTTTTTAAA 120
 TAGAAAGATA TCAATGAAAA ATAGATTCTT GATTATGGTT ACATGGAATA TTGACGAACC 180
 TGGTGGTGTT ATTAAGCTAA TTAAACACTT GGCTATTTAT AGTTTAGTCA CTGAATTAAT 240
 25 TGGTATGATT TGTTTGTGTT TATCTTTTAT ACCAAAATTT GGTATAGGCA AAGGTTTATT 300
 TTTAAGCTTA TTCACATCAG TATCAGCTTT TAATAATGCT GGGATTTGCC CTTTTTAAGA 360
 30 ATAACCTAAT AGATTATTCT AGTGATCCAA TTGTCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 2473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2473:

CTTCAAATAC TAAATCAGCG TTGCTAAACA TACCGTATAC ATTTGATGGC GTTGATAACG 60
 CGTCCTGCGC TTCTGTTAAT AACTTTTCAG TTTCAGCATC TAATATATGA GGACGTTTTT 120
 45 CATTAAATCAA CTTCAAATCA AATGCGA 147

(2) INFORMATION FOR SEQ ID NO: 2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2474:

5 CTTTAGGTGC TTGTGGTAAT TCTAATTCAC AAGATCAAGG TAACAAAACCT GAACAAAAAA 60
CA 62

(2) INFORMATION FOR SEQ ID NO: 2475:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2475:

CCTTTAAAT CATCTAGAAT ATCTCTTGAG AAAAATTCGA AATCTACAGT 50

20 (2) INFORMATION FOR SEQ ID NO: 2476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2476:

ATAGTGGTTA GTCAATGTAA TTAAATGAGA ATAGAATGGT GATTTCATCT TAGCTTGATA 60
ATTAGCAGAA TCTTTAAAGA AAATTTTGTC TTCAAGCCT AAGTTTACAA CGT 113

35 (2) INFORMATION FOR SEQ ID NO: 2477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2477:

CGTAACTAAC TCAATTTACT GAAAAAATCG CTGCGATGC AATAGCATTT G 51

(2) INFORMATION FOR SEQ ID NO: 2478:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2478:

5 TAGTTGCCGC TACGTTTATA CTCGTATTAA TGAAAAAAC TAGCAAGAA TCTAAAAAG 60

(2) INFORMATION FOR SEQ ID NO: 2479:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2479:

15 TCGGACATGA TGGTAAACC GTATTGGGTA TTCGCACTGA CACCTTAAGG GA 52

(2) INFORMATION FOR SEQ ID NO: 2480:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2480:

25 TTCCTAATTA AGGATTAAAA AGGGTTTCCT AATTAGATTA AAATTCCGGG ACCTGGATGG 60

30 AAAAAAGTTT TTAACTTTTC CATCTGGTCC CGTTTTTTGA TTTTCGATAT AAAAAAGCG 120

CAATTATCTC TAT 133

(2) INFORMATION FOR SEQ ID NO: 2481:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2481:

45 AAATGTTTTG GAAGAACGTA AGAATAATCA ATCTGAAACA AATGCACGAT ATGAAGAAGA 60

ACAAGAAAAT TTAATGGAGC TTTTAGAAAA TATATCAAAT GAGATTCTG AAGCTCAAGA 120

50 TACTTATAAG TCTCTGAAAA GTAAACAAAA AGAACTCAAT GCTGTCATTC GTGAACCTGA 180

AGAACAATA TATGTTTCAG ACGAAGCACA TGATGAAAAA TTGGAAGAAA TTAAAAACGA 240

TACTATAGAA GAGAATGAGG CTAAAAAATC CAGACAGGTT CTCGTTAGTT GGAGTTTTGA 360
GCCATTGAAA GTATTcnggg GGCCAATTAA AACCGCCAAA 400

(2) INFORMATION FOR SEQ ID NO: 2482:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2482:

AAGGTGCATA GTCAACAACA TTTACAGCAT CATTGATTC TGAAC TAACC GAAACATTAT 60
ACTTACCG 68

(2) INFORMATION FOR SEQ ID NO: 2483:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2483:

ATGAGCCnAC ACAGTGGTGA GGTAAATCAAC GGTACAGTGG TTAGTGTGAT 50

(2) INFORMATION FOR SEQ ID NO: 2484:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2484:

CGGAACTCGT CGAATAACTT TTTAGATTCT TCGTTAGCTT TTACATTAGC GAATGCTTCT 60
nTGATTGCTT TGTATTCTTC GCTTTCTCTT AAAGCTTGTT CTAATTGATT TGCATAATCA 120
TATAAATTTA CTGCCATGGT TATAGCACTC CTTGGTnGTG ATGTTTATTA AAACGTTCTGA 180
TATTACTTTA CCACATCTCG CTTTTTTAGA CAA 213

(2) INFORMATION FOR SEQ ID NO: 2485:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2485:

GACCAAAATT ATCTTTAGCA CTTATAGGTA TCTTTTAAAT ACTTTGTGAG TTTTCTATG 60
GCATTCCTTT TTTAGGTGCA ACGTTTATTT TAAGTTTGG ATGGCAGCCT TTA CTCTTTA 120
ATGCATTACT TTATCTAATT CTTACTATTA TATTATTAGT GAATAGACAA AATGCGATTA 180
GACCTATAGC GATTATTTCCA ATATTTGGTA TAGTAGTAG TTTTITAGCT ATTATCCCCT 240
TCTTAGGAAT TTTGATTCAT TGGATTTTAT TTTTCCTAAT GATTCCanTT GTCCTAGTTG 300
GATTATCAGC GCCAACCTAT ATACCCAATA AAAATGCTCG TGNChTTTTA CACACAATAC 360
AAAGATGGAC CTAGAG 376

20

(2) INFORMATION FOR SEQ ID NO: 2486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2486:

30

TTGACCTTGA CGGAAACTTT TTTCCAAGTT CTAAAGTGG GCCAAATCT T 51

(2) INFORMATION FOR SEQ ID NO: 2487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2487:

GAATTTTGGC ATACACATAC ACTTTAAAAG ATATTATTGA AATTACAGGT GTA ACTAAAA 60
GAACTTTACA TTATTACGAT GAAATAGGAT TATTAGTTCC AGn 103

45

(2) INFORMATION FOR SEQ ID NO: 2488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2488:

5 AATTACATTA GCACCAATCC ACACATCATT TTTAATTGTT GTACGGCTAG GTTGGTCATT 60
AAAGTCTATA AACGTTTnCT TTAAGTTAAA TGGATTATTA TTTAGA 106

(2) INFORMATION FOR SEQ ID NO: 2489:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2489:

20 TGAATTTGCT TGAGTCGTGC TGCTGATAAC AATAAAATTG CACATGGATA AAGAATGACG 60
C 61

(2) INFORMATION FOR SEQ ID NO: 2490:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2490:

35 GCTCGTATGA TACAAATTCA TAATCTGAAA CTTCTGTCGT TTGTCGAACA TGTGGTAACC 60
AATTCTTCAA GATGCTGTAT ATTTCTGCGT AATTTTCGTC ATTCCTGAAT AACCTCAACT 120
TTAAATGTC ACCTTGTTG ATATAACGCA TTAAAAATA TTGATCTATA TCTCCCTTAT 180
CTTTAAGATG TTTTACAAAT GGATACAAAT TGTCGATGAT AAATGTATCT TGCGATGGCT 240
40 TATCGATATG AATATGTAAT GCAAACCACT CTTTGTCTATA TTCAATATCT GTATTTTAT 300
ATTTTGGAAT TTCGATTTCG GGTCCCTCGAT AAGATGATTT TTTATAAATT GGTGTAAACA 360
TTTCATACAC ATGATCATT CTTTGATTGAG GGAAAAATGA 400

45 (2) INFORMATION FOR SEQ ID NO: 2491:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GACTGTTTTA TCGCAACTAT TTACACCTAT ATTATCGTTA GTAGGACATC TCGTCGG

57

(2) INFORMATION FOR SEQ ID NO: 2492:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2492:

15

CATTGAACCTT GCTTTTGACG TACACCAGTA ATCAATGCCA TAATACGATC CGG

53

(2) INFORMATION FOR SEQ ID NO: 2493:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2493:

AATACAACTA ACATACACTT ACCCATGTCC GAAGTCCTTG TTGAGGAATG

50

(2) INFORMATION FOR SEQ ID NO: 2494:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2494:

40

GCTGTTTAGC TTGCTCAAAT GATGCATAAA TATCTGATGC AACTATCATA TCAGCTAGTT

60

CATCA

65

(2) INFORMATION FOR SEQ ID NO: 2495:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2495:

55

ATTAAGCTTT CTAAATCATT GATGTTAGGA GCTAATGTGC TCGATAAGCA GAGTAAAGAA 120
 GAATTGCTTA AACAAAGCTAA ACATATAACA GGTTTAGAAA ATCCTAATAG TCCTACACAG 180
 5 TTATnGGCTT GGTAAAGGA TGAACAAGGA TTAGATATAC CTAATTTACA AAAGAAAACG 240
 GTTCAGGAGT ACTTAAAAGA AGCAACAGGA AAAGCTAnAA AAATGCTAGA AATTAGATnG 300
 CAAATGTCTA AAACCAAGTGT GA 322
 10

(2) INFORMATION FOR SEQ ID NO: 2496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2496:

ATCAGTGTTA ATTCGCACGG AATTTCTTC CATTAACTA ATCCGATCAT ATAATGGAT 59

(2) INFORMATION FOR SEQ ID NO: 2497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2497:

CTAATTAAGC CAAAAGGGGA AGGGTCCACC AACCCTTGGT TTCCCCCAT TGCCCGGAAA 60
 35 CCACCAGnAA GTTTAAAGCT TCCCTTTAAG CCGTCCGATG GGTAGTCCGA ACTTTACCGT 120
 TCCCGC 126

(2) INFORMATION FOR SEQ ID NO: 2498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2498:

CACTTTGCGC CAGTTTTTCAG TTGAGTGGCA TAGAGTCTGC TCATCAGTTC CTTGCTCC 58

(2) INFORMATION FOR SEQ ID NO: 2499:

(A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2499:

10 TCATGATGCA GACGCAACAG CATTGGTTA TGAATATGGA CAAATACCAC AGATGCCGGT 60
 AGCATTTCAG TCAAGTAAAC CTTTAATAGA 90

(2) INFORMATION FOR SEQ ID NO: 2500:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2500:

25 TGCTCAAAGT CGTGTAGACA GCCAACTAAT GCATTTTCAA GATCAGTGAC ATCTCCGACA 60
 CCAAAGAAAT CACCGAATAT TTTTGCATGT TCGATTTTAC CTCGTTTAAC ATCAAACCTA 120
 ATTTGTACAA ATCCTTTTTC AAATTTTTC TCGCGTTCAA AGTTATATTT AGGGTTTCTA 180
 30 CCATAATTCC ATTCCCAAGT TCTATATTTG TCGTTACTTA ACTTTTCAAT ATTTTCCCAA 240
 TCTTCATCCG TTAATTGATA TTCTTCACT TCAGTTTCGC CAAAGATAGT TT 292

(2) INFORMATION FOR SEQ ID NO: 2501:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2501:

45 GGTGTGTGTA GAGGTCGAGA GTTGGGGGGG GAGTAACGTG GAAGTTGCCC GGACAGCA 58

(2) INFORMATION FOR SEQ ID NO: 2502:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

ATACGGGAGG TATCAGCACG TACGTGCAGT CGGTAATGGA TCnAAATACG

50

(2) INFORMATION FOR SEQ ID NO: 2503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2503:

ATCCCCACTC TTTTAAAT GATTAAACCA TATTTTATTT TTAATAATAA TATCCATCAA 60

AGTGTATCAA TAAATTTATC ACATGTCAGA AAGTATGCTT CATCTGAATA CACCAATACT 120

CTCATGAAAC TTATTAAAAA TTAATCTCTC AACGTAAAAA ACCATTCAAA TTCATGAATG 180

GTTTGGAAGA ATGATTCATT GTTACGCTAT TTAATCACTA CATCTTAATT ATTGTTGCTC 240

TAAACGATTA CGCTTACCAT TTAAGAAAGC ATAAACGAGA CCTACAAAAA TACCGCCACC 300

GACAAAGTTA CCTAAGAAAG CAAAACGAT ATTTTTTAAA ACGTGTAAAC ATGAAACTGC 360

ATCAAGGGTA AAGAATACCA TACCTGCATA TAGACCTGCA 400

(2) INFORMATION FOR SEQ ID NO: 2504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2504:

ATTATCTATG AATAAAATTT ATAATAACA TATATTGAGA AATTCTCTAA TACCTATTAT 60

TACATTTTTA GGTGCTGATA TTGTAAGTAT TTTAGGTGGA GCCGTGATTA CGGAGACTAT 120

CTTTTCATAT AACGGTATCG GTAAATTATT TTTAGAATCG GTAATAGGCC AAGACTATCC 180

ATTAATGATG GCATTAACTG TATTTTCTC ATTTTATAGT TTAATGGGTA ATTTGATTC 240

TGATATTACT TATGGATTTA TAGATCCAAG AATTAGAAGT AACTAGGGGG GATTAGAATG 300

CAAAATAAGT CAAAATCGCC TTTnAAAATT GCATTTTCTA AATTnATTCA TAnTA 355

(2) INFORMATION FOR SEQ ID NO: 2505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2505:

5 CCGTTAGTTC CATACCATAT TTTTCTCTAT AAAATAATTT AACATCTAAT TGCCTTTCTA 60
 ATTTTTC AAT AGGGGTAGAT ACAGTTGACT GTGAATAGTT AAGTAACTCT GATGCTTTAG 120
 TAAGGTTCTT TGTTTCACTA GTTACTAAAA ATGATTTTAA AATGTTTAAG TTCAAAGTAG 180
 10 TACCTCCTTT AGGGTTCCTT TTTATCGAAT CCTGAATTCT AAGAATTCTG ATTTAATAAT 240
 AATATATnAn ATAT 254

(2) INFORMATION FOR SEQ ID NO: 2506:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2506:

AACTCCACCG TGTAAGTTCG CTTTCATCGCC TTGAGGATGC GATTGGCGCC GTGCTGCGCG 60
 25 GCACGTGCAG ATAGTGCAG CACTTGGGCA GATCGCGCAC CGCCTCCAGC AGGTCGTCGG 120
 TCATATCCTT GGGATAGTTC GTTACGAnTT GGATCCGGTC GATGCCGTCG ACATCCGAGA 180
 TGCGGCACAG CAGGTCGGAC AGTCGCGTTG nCCGCTGGCA GTGTCGTAGT GGTAATGTTT 240
 30 CACGGTTTTG ACCTAGCAGC GTTCACCT 268

(2) INFORMATION FOR SEQ ID NO: 2507:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2507:

AAAAGTGGCT AATATCATCA GCAGAATGTA TAACATAATC GAATTGCAAC CAGCGATTAT 60
 45 ACCTTT 66

(2) INFORMATION FOR SEQ ID NO: 2508:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2508:

ACCTCCGCTT CAAATGTCAT TGATAGACAT TTAAAGCGGA GGCATGTACA TGT

53

(2) INFORMATION FOR SEQ ID NO: 2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2509:

ACCCTATGAN AGATGAAGTn ATTAACCAAA AACCACGTGT TGTAATATTA

50

(2) INFORMATION FOR SEQ ID NO: 2510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2510:

TTAACCTATT ATATTAATTT TAGTATCAAT TCTTTCTCCA GTTCTGCGT CATTTTT

57

(2) INFORMATION FOR SEQ ID NO: 2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2511:

ACGTGTTTCAT AACCCATAAA GGCGAATATG GTAACACCGA ACATCATGAC A

51

(2) INFORMATION FOR SEQ ID NO: 2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAAAGCGGT CCGCGCTTAA AGCGCTTGCT AACTTCGAAC AATGAATCTG CGGAACATCT 60
TGCGAATCCA CGAGATGATC TCATATGACG GGCAGCGAGG T 101

(2) INFORMATION FOR SEQ ID NO: 2513:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2513:

GGGTAATGTA ATAGTATTCA TCTACATCAT CTTGATCATC GTAATGCTGA TTGTACCCTT 60
CTAAATC 67

(2) INFORMATION FOR SEQ ID NO: 2514:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2514:

CCCGTCGTTT TCGTGrTTTT CGCGGCGTGT CTCCTGTTCTG CGCCTCTACT 50

(2) INFORMATION FOR SEQ ID NO: 2515:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2515:

AAGAAAATAT CTCTTGAATA CTGATCGATT GCCATCGAAA AACACTGTTA AATCAAGTTG 60
CCCAGTCCAT TGTGTTCAT CCATTATGAT AATCCTTTGA GTAAAGTGTC GCGTTCAATC 120
CAATCGATAA CTTTCATCAA ACCTTCGTCG GTTTTTAAGT TAGTAAAAGT AAATGGACGT 180
TTACCACGAA ATACTTTAGT ATCTTCAGCC ATTTGTTCTA ATGATGCACC TACATAnGGA 240
GCTAAATCAG TnTTGTTAAT TACAAAGACA ATCTG 275

(2) INFORMATION FOR SEQ ID NO: 2516:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2516:

10 CTGCACCACC AATAACGTAA ATACTGTATA TACTAGTAAT CGCTAATACA CCGATATTA 59

(2) INFORMATION FOR SEQ ID NO: 2517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2517:

20 TCTGCTACTA CGTATACGAT AGAATGGATT TCTTTTGTAA CCTAAACGTG TTAAACGAAT 60

25

TTTAACTGCC ATTTATAAAA TCTCCTTTAA GTCATGTTTT AATTTTTATT TTCTACAG 119

(2) INFORMATION FOR SEQ ID NO: 2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2518:

35 ATTCCTTTT AAGTTTTTAA AAATCCAAAA TCCTTGTGGT AGGGCCATGA AAGGGTTGGG 60

(2) INFORMATION FOR SEQ ID NO: 2519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2519:

ATAGAAGTGA AGCACGTAGA TTGAAACGAT GGTAAATAA CGAGAGACAT TTAGAAAACA 60

50

ATAAAAATGA GGAATAATCA ATGATACATG GAATTGGTGT AGATTTAATC GAAATCGATC 120

GAATACAAGC GTTATATAGT AAGCAACCAA AATTGGTTGA GCGGATTTTA ACTAAAAATG 180

55

GGTTTGCTAC AAAAGAAGCG TCAGTAAAGC ATTAGGCCCC GGCCTnnGGA AACA

294

(2) INFORMATION FOR SEQ ID NO: 2520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2520:

TTTTAGGCCG AAGAnTAGT AATTTCCGGT CCTTTAAGGG GCGGGTGGTT AACCATGGCA 60
 ATTAATCCCA GGGATGACCT TACCTAATAA CCACCTAATA ATTACCCGGA CCAAAGGTGG 120
 AAATAATCCC TCCGGTCCTT CCCGG 145

(2) INFORMATION FOR SEQ ID NO: 2521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2521:

TTTtagTCAC CAAAATTCTC GCATTTAACT GATACGAATG TGCAATAACT AAAAATCGAT 60
 CTAATAATTG CGTTGAAAAA TTTGGCTCGA CAGCACTCAT TACAATTACn AGTGTATCTA 120
 TATTACTTAC AGGTGGTCTT TTCAACTCAT TTTCCCGCTC AAACACTTG 169

(2) INFORMATION FOR SEQ ID NO: 2522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2522:

ATCCAGCCTT TCAACAAATA AATCTGAAAT TCGATGTTCT AAAATTTCTG CTTCTTGATG 60
 TACTTCTTCC CAATTATATT TCAATATT 88

(2) INFORMATION FOR SEQ ID NO: 2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2523:

CAGTAACATC AATCTGTCCT GTAAGCTTGT GGTACTCCGA TACAACCATA AGTCAACGCA 60
CCACCAAAAA CGCCTTGGAG CCGTTCTACT TATTAGTCCA AGTTTAGACA TTGAAATACC 120
AACAACCTTG CAnTCCATAG TATCTGAAAA TG TAGACATT GCCTGCAATA AATTTAACnC 180
ATCATTTTTA TTATGTGGCA TTA CTGCTAA TTTAACGTAT TCTGGGTT 228

15 (2) INFORMATION FOR SEQ ID NO: 2524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2524:

25 CTCATCCATA GCGCTGGTAT TAGTATAGGT GTCAAACCAT TAGCGTATAT CATATCTTCT 60
GGATGTnCTC ACATATTCAT AGATGCACAT TTTACTTCTC TCGTACCTTA GTACTGGGA 119

(2) INFORMATION FOR SEQ ID NO: 2525:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2525:

40 TACCAATATT AAATTTGAAC ATTATAGTTT GACCATCATA ATCTATCTTC TCTATTTTCAT 60
TATAACTAAT ACTTCTATAA TAAATTTGGC CATTTCATATC TACATTCATA ATTAATCTTT 120
CATTTGTTGC TATAAATGCC CCTTCAAATT CATTCTCACC TTGAACTTGA TACTCAATTA 180
45 TTCCTAGCAC TGACGGACCC TTTTTTTCAG TTGGAAATAA ATCATTGGA TTCACATTAT 240
CTAAAATCAT AATATCCCTC CCACTTAAAA CTATAAATA TTCTTCATAG GTATATGAAA 300
TACAAGTGAT TAACTATTnA TnATnAAGCT TAACTTGAT TCCCTTTTCA AGATAAT 357

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(2) INFORMATION FOR SEQ ID NO: 2526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs

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- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2526:

CACGCGTCCG GCCACCTGGA CATGGCCGAC CTAGAAGCCA AGCTGCAnGA GGCCCAGAAG 60
 10 CATCGGCTGC GCCTGGGTGG CCACTGATGG GGCCTTTTCC ATGGATGGCG ACATCGCACC 120
 CCTGCAGGAG ATCTGCTGCC TCGCCTCTAG ATATGGTGCC CTGGTCTTCA TGGATGAATG 180
 CCATGCCACT GGCTTCCTGG GGCCCACAGn ACGGGGCACA GATGAGCTGC TGGGTGTGAT 240
 15 GGACCAGGTC ACCATCATCA A 261

(2) INFORMATION FOR SEQ ID NO: 2527:

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2527:

CTnTAGAGGA TATGAGTTCC TCATCATAAG AATTTCTGGA TCCTTAATAG ATCTCTTGCT 60
 30 ATATATAATG TAATAGAAAC ATCTTTTAAG GATCCAGAAA TTCTTAGA 108

(2) INFORMATION FOR SEQ ID NO: 2528:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2528:

TTTTAAATA CTTGGTAGAA GTTGGAAATGG ATTAATCATT AATTATCTCT CAAGATGTAA 60
 45 TGA CTGTTCA GCACACTTTT CCGATATGAA AAGAGATTG AAnACAATA 109

(2) INFORMATION FOR SEQ ID NO: 2529:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GATTAAATTT GTTATACCTG GCTTGTGTC ACGATCAAAT TTAATAATAC CATCTGAATC 60
 AGTTACTGCG CTTTTAATTT TTTTAGCTGC AACATTCCGC TCGTCTAATA ATGAAATnGA 120
 5 GTTTTTAGCA TTATCATCAC TCTTACTCAT 150

(2) INFORMATION FOR SEQ ID NO: 2530:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2530:

TTCTTTTGG CCAGTGGCAG GAAGTACGGT CTTATTGGT GTTATGTAA GAAGGTATTC 60
 20 CCATTATTT ATCGTTAAAT ATGnATATAG TATAGTAATT TTAATTTGTT GCATCATAAT 120
 ACTAGGT 127

(2) INFORMATION FOR SEQ ID NO: 2531:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2531:

CACATAATGA TTCGAATTAT TGTTTAATT AAACCTTTTT CACATATGTA TAAATTTTAn 60
 35 AGAGCGCATG CGTGAATATT TTCATTTGAT TCAAAGGCAA AAGATAGCCT TATACTCTTT 120
 TC 122

40 (2) INFORMATION FOR SEQ ID NO: 2532:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2532:

50 AAATAATAGA GCAATTGGCA CATGTAAGAA TGCAAATTGA CTATGGCATC CAGTATTTTG 60
 GTCACAAATG GGTGTATAT GAGCATGTTG AAAAATAAGT CTTATGnTAA ACACTTAGTA 120

55

(2) INFORMATION FOR SEQ ID NO: 2533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2533:

GAGAGCGGCC GCGTGTAAAG AGAGCGGCGT TCGTTCGCGT GACGCGAGTG TGGTTCGCGA 60
 GAAGnGGACC AGAGTTCCCG ATCGAGGCTG TTCGGGTAAA T 101

(2) INFORMATION FOR SEQ ID NO: 2534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2534:

TTGCTCATTA AAGATTATCC CAATCAATAT CATCTATATT TGTGTACCA CTATTATCTT 60
 TTTCTCTTTC TCTTACTTTG TnCATTTGTAC CAGTAGATTC AAGATATATT GT 112

(2) INFORMATION FOR SEQ ID NO: 2535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2535:

ATAACGAATC CAAAAATATA GAGAATGACA GTGAAACTTA AATAGGACTC T 51

(2) INFORMATION FOR SEQ ID NO: 2536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2536:

(2) INFORMATION FOR SEQ ID NO: 2537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2537:

GGATGTACCA CCAGCATAAT AAACAAC TTC AAATGGATTG ATAAAGAAGA nACCAGCAGA 60
 GATAGGTAAT TCATTACCAT GTTCTTCTTG TAGACGTTTA CTTTCTTCAA TCTTTTGCTC 120
 ATTTGCATCA AGTTGTTGTT GTAAGTTATC TCGCTTGT 158

(2) INFORMATION FOR SEQ ID NO: 2538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2538:

TATATTCATT AAATCCACAA AGCGGTCCCG TATAACATG GGTTCATT 50

(2) INFORMATION FOR SEQ ID NO: 2539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2539:

AAAGTATACA TATCACTCAA CTAATCAATA ATCATACTTA CTTCAACAA ATTCTTTAAC 60
 ATGCAGTGTT ATCCCTTGAT AATATGGATA TTTnGTTAAT CTA 103

(2) INFORMATION FOR SEQ ID NO: 2540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CAATCAATTT GTCTATCTGT TGAGTGGCAA CCTCTAATAA GCCTTTTATA TTGTCA

56

(2) INFORMATION FOR SEQ ID NO: 2541:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2541:

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TGGAAATAAC GAAAGTATTA TTAATTTAAA GCATCTTTCT CCCAATACTT TAATGAGTGA 60
 TATTGTTTAT ATACCGTATA AAACACCTAT TTTGAGGAA GCAGACGCA AGGGAAACCA 120
 TATTTA 126

20

(2) INFORMATION FOR SEQ ID NO: 2542:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2542:

ATCAGTTTCT TCAAAAATAA CTGAAGTATC TGATGCTGAA AATTGGAATA GTTGATGGGT 60
 CGGGnTATTG ATTTTATCT GATGTAAAAA TCCATAAGTG CCATAAGATG TATATAGTTT 120
 CTTCATATGA AAGGTCCCC TTATGnTTT ATTTATTATA CGATGATAAA CTAGTCATTA 180
 CCACTATTAA TAATTGATTA A 201

35

(2) INFORMATION FOR SEQ ID NO: 2543:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2543:

GAACTTTATT ACAGGAATAG ATAAGCACAG TCGTGTTACA CAGACGCTAA ATGCGCGTTC 60
 GTATG 65

50

(2) INFORMATION FOR SEQ ID NO: 2544:

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(A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2544:

10 AGCTATTAAT GCGCTATAA TTGATACAAT AGTTATGATT AATAAAAAAA TAACCGATAA 60
 CATTGCAATT TTATnATGAA TAAATTTAGG AAATGCAATT TT 102

(2) INFORMATION FOR SEQ ID NO: 2545:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2545:

25 AATCTACATC CAGCATGATC nACATCaAG CnGGATTcAC CCTTACTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2546:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2546:

AACCATTCAA CACACGACAC TAAAGTGCAG TACAATCCTA CAAAACGATT GTTTTTATCG 60
 GGTGGTCTAA CCATTGAATA AATAATGAAT AATGGTAaA 100

40

(2) INFORMATION FOR SEQ ID NO: 2547:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2547:

ATTGAAAATC TTTTATCATT TCATACGTGT GCATAATTAA AAAGGTGAAA CCTCTTATTT 60
 TGAGATTTCA CCTTTTTTAT TGTTAATTTA AATTTAATTT TAATGATTAT TTTGTTTCAC 120

55

(2) INFORMATION FOR SEQ ID NO: 2548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2548:

AAAGTGAAAA TTGGAGGTGT AATTTTGA CT AGA ACTTATA ATATTATTGG TATCCTTTCT 60
 TGTCTTATAT CTTTATTAT TATGGCGTTA CCAATnATTT GGTACACAGC TTCAGCATT 120
 TGGTTCTTCC CAGGTGCAAT CA 142

(2) INFORMATION FOR SEQ ID NO: 2549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2549:

CCCAACCCTA CnAACGACAT TACACAATCA GTAACAGATC GGTATTAAGA CTGGATATCG 60
 TGGCATCTGT TGAGTTAATA TCAACAGTCG TCCAGAACTC G 101

(2) INFORMATION FOR SEQ ID NO: 2550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2550:

TGTAACCATG ATTTAGATGA CTAAACGTGC TTGCCAACAT GCTTCATCCA ATGCCGAATC 60
 CTTTAGCTAC AT 72

(2) INFORMATION FOR SEQ ID NO: 2551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2551:

CAGTAAGAGG ACAAGGCTAT AAGGTGGAGA ATCATGTTTA AAACACTCTA TGCTAGAATT 60
 5 GCGATTTATT CCATTACGGT TATTTTATTT AGTGCATTAA TAAGTTTTGT ATTAACAAAT 120
 GTTACTATC ATTATAATTT AAAAGCATCT AATGACGCGA AAATCATGAA GACGCTTAAA 180
 GAAGCAAGAC AATATGAACA ATCAGCTAAA CCAACGCACA TTCAACAATA TTTCCAnACA 240
 10 TTTAGGGTCA AATGGAATTA CCAAATAATG ACCATGGATC CATAAAGGTC nTnAGACCTT 300
 TTT 303

(2) INFORMATION FOR SEQ ID NO: 2552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2552:

25 TTTACTTTAG CCTTTATTGC ATTTGTAATT TATAGAACTG CGAACAGGTG ACTACTGTnA 60
 ATTTATGTGA TTAAAGTTTC AATGATATTT GATTTATTAG ACCATTGCAA AAGCGCAAGG 120
 TTCTCATGTG CTGCTACAGT TTGCGGTCTT 150

(2) INFORMATION FOR SEQ ID NO: 2553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2553:

40 GCACTCGTCA ATAAAGATGA AGCAGCATTT AATCAATATA CGGCAGAATA CAAAAATT 58

(2) INFORMATION FOR SEQ ID NO: 2554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2554:

AAAATCGTTG AATAATCAAT CATAGCAGTA AGCTATGTnA TATATTTTTTA AAAATTGA 118

(2) INFORMATION FOR SEQ ID NO: 2555:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2555:

15 ACAACTTCAA AGAAATCATG TCACAAAAAA AGTATTTGAT TTTAATCATA nGTGGCGACA 60
 ATCCGCATAC CAAAGCACAA CCTTTAGTCA ACCAATTCAG AT 102

(2) INFORMATION FOR SEQ ID NO: 2556:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2556:

AGATGCATTA GCAGCATTAG ACGTTAAACC AGTTGGTATT GCTGATGATG GTAAGAAAAA 60
 30 ACGTATCATT AAACCAGTTA GAGAAAAAAT TGGGGATTAT ACTTCTGTAG GTACACGTAA 120
 ACAGCCAAAC TTAGAAGAAA TTAGTAAATT AAAACCGGAT TTAATTATCG CTGATAGCAG 180
 TAGACATAnA GGTATTAATA AAGAATTAAn CAAAATTGCA CCAACATTAT CATTAAAGAG 240
 35 TT 242

(2) INFORMATION FOR SEQ ID NO: 2557:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2557:

TGCACTCATA ATCATCGGAA TATGTATAGA ATCAACTATC ACTTTGCCGT GTTTATCTGT 60
 50 GTTAAATGTG TAACCATAAC AGTGTGTCCC ATTTGGATTA TGAATCTCAG AATAATCATC 120
 AAAAATATCC TGAATTTnCA AATTAATTTT ATTATAGCGG nAGCAATGTC TATAAAATTT 180

55

TATTTCAA

248

(2) INFORMATION FOR SEQ ID NO: 2558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2558:

TTTGGGTCGT GATTGAAAAA ATCTAAGGCT AATAAACCAT GTTGTTCTGC GCTTAATAAT	60
TGTTTGAGTA TACGGTTAAT AATTAACCTCT GTATCATGAG GGTGACGCG AAAGTCAGAG	120
CGCATATAAG TCATATAATT CTCGAAGATT TCTCTATCAG TATTGCTTAA TCTTAATGAT	180
TTAACATTAT TTTCTTTTGT TAATTGCGCA GTACTTTTCA TTGTTACTTA AGCGCTCCTT	240
TAAAAATGTT TAATTCCAA TTAAATGGA AATGATTTTA TAGTATTAAT AAGGTCAATC	300
ATATCATATT AAACGCATAA ATATAACGAT TAATATTGGA GAGGAAAATG AGGACACTTA	360
ATAAAGATGA ACATAATTAT ATCAAGCAA TAGCTAATAT	400

(2) INFORMATION FOR SEQ ID NO: 2559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2559:

AAGGGAAATT TAAAAGTATC ATTTGATTAT ATAGATTGGA TTAAATTAGG TTTTGGCCCA	60
TCAGGAAAGG AAAACTACTA TATGTACAAA AAATTTGGTA TTTTACCAGA TATGGAATAT	120
GAAATGGAAG AAATTGAGC AGTAGAGAAG TATGTTAAAG AGCAAGAGTA GCAGACATGT	180
TATAAAGAC TGTGCAAAAT CACCCTCGTT TTACATTTGA TTCAAAGAAG AAGGTAAAAG	240
ATAAGANTAT TTGCAACTTA AAAAGTCAAT TAGCTTATCG GTATCCATAC ATCATGGATA	300
AATGAGTnCA ACTAATTAAC AAATCAGCAT ATA	333

(2) INFORMATION FOR SEQ ID NO: 2560:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2560:

GTAAGACATT CACATTTATC ATTTACCAC AATGGGTTTA CCAACCATGG TTAAACGAAT 60

5 CCAAAACTTT GATGCTCGTA TGTCTCA 87

(2) INFORMATION FOR SEQ ID NO: 2561:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2561:

TTGCATTTTG ACGTAAATGA TTAACAAAT CGTGATTATC TCTTAATTTT CTAACCGCCT 60

20 TTTCAATTTT TAACGGCGTA ACTTCCTTTA GAACAATGCC AAATTTATAT TTnTCAT 117

(2) INFORMATION FOR SEQ ID NO: 2562:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2562:

30 AAGTCAAACA AAATAAGCAA ACAGACTGGT CAGAAGATAA GTTGAATAAT ATAGCTTTGA 60

(2) INFORMATION FOR SEQ ID NO: 2563:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2563:

45 AAGTGTTATT ATTGTGATCA TAAAGTGAAG TATTACCTTT TTTATTCGTA ACCCGATTCC 60

ATGCGCCTTC AACATAAACT 80

(2) INFORMATION FOR SEQ ID NO: 2564:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 64 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2564:

AGACATGGGC TTATCAGATA AAGTAAAAGC ATTACCTAAA GGGGGAGGCG GTAAGTCATT 60

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ACCG 64

(2) INFORMATION FOR SEQ ID NO: 2565:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2565:

GTTTGTTTAT AGTACCCTGG ATTTTCITTA TTTCCATCAT GTGAAACTGT GTCAGTGAAC 60

GCTGAT 66

25

(2) INFORMATION FOR SEQ ID NO: 2566:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2566:

TTAATTATTT GTGACGTATT ACACGCATTA CTTTAGAAAG TGATTCCCAA AGCGAATTAT 60

CTTTACGATA AACTA 75

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(2) INFORMATION FOR SEQ ID NO: 2567:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2567:

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ATATTATTAT ATTGCTTTTT TTCAGTTTGC CGTTGTTACT TTCATAACTT 50

(2) INFORMATION FOR SEQ ID NO: 2568:

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(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2568:

10 TTTTAGGATT TGTAGTAGGT GAGCGACGTA TTTnGGATGC AATCCAGAGA ACAATAAATA 60
 TTGAGAGAGA GCAATTCATA ACGCAATTGA AATACATGTG TTACGAATTG CTTTTATGTT 120
 AGTTTTTATC ACACAAGTTT TTTGATGCAA CCCCGTGATA GCGAAACTCA TATGTAGATA 180
 15 ATACAGCTTT TTCAGCATCA TCTACATGAA TTCCAAAACA TCA 223

(2) INFORMATION FOR SEQ ID NO: 2569:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2569:

AATAATGCCA TACAGTGAAG ACCATGCGCA TCAATCGATG TCTAGTGTGT ACTACGTC 58

(2) INFORMATION FOR SEQ ID NO: 2570:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2570:

40 CGTTTCATTA GTTTTAAATG ATCCCCAATA CTTTTGTAC CTTACCAAC TATCGTTCCA 60
 AACTATCTA CAGCTTTTTC TGTGGTATTT TTAACAGCG TCTATTTAAT GTCATTATCCA 120
 ATTAGTTTTA TCTCTTAATC CAAATTTATT AGTATGAAAA GTCCAATTTT TAAGAATTGT 180
 45 CTAAACAGAT TCCGCAACAA AACCAGCTAn AAACCGTCCA TACTATTGGA ATnAAAACGC 240
 CAATGTTATA 250

(2) INFORMATION FOR SEQ ID NO: 2571:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2571:

AGCTCCTTTC TTTCTAGTTA ATATCATThA ATCTTGTTTT TCAGTGTCAA AATTACCTGT 60
 5 AAAACAACA TTTTATCTT TTAAATAGG GATTACACTT TCCACTTCTA TTTTATTAAAT 120
 CTCAGATATT TTCATATGAA TTTTTTGAAA TCCTGAATCG AAAAGTTTAG TTGG 174

(2) INFORMATION FOR SEQ ID NO: 2572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2572:

CATGCCGTAG GTATTTCTAA TCTATGGACA AATGGCGGAT TTATGCCAAA TGGTATTGTT 60
 20 GGTTCCTTCT TTGCATTATC AATTGTAATT GGTTCATACC AAGGTGTGGA ACTGATAGGT 120
 ATTACGGCAG GTGAAACTAA AGATCCTCAG AAAAATATCG TTAAAGCAGT GAATGGTGT 180
 25 ATCTGGAGAA TTTTAATTTT CTATTTAGGC GCTATTTTTG TTATTGTTTC AGTGTATCCT 240
 TGAATCAAT TAGGAGACAT TGGAAGTCCG TTTGTTGCAA CATTTGCTAA AATCGGTATT 300
 ACATTTGCAG CTGGATTAAT TAACTTTGTT GTAACTAAGT CAGCAATGTC AGGATGnAAC 360
 30 TCAGGGnATT TGCAGTGCGA GTCGTAATGA 390

(2) INFORMATION FOR SEQ ID NO: 2573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2573:

TAGAGTACAG AACATACGCA AGGAACTCGG AGTTTACTCA CGGGACTTnT 50

(2) INFORMATION FOR SEQ ID NO: 2574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2574:

TACAATTACA AACGCATCGT GAGATGTTTT AAGCATCAAT GAGAATCTAA CTCTCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 2575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2575:

GACACAACGT ATGACGCGATG AAGAGTTGCG TGTGACAAT CAAGATGATC ATAGCCAAGT 60

TAGTCTAAAT GGTACACAA AGGGGTCTGA GAAAGATCAA GAAGCATTCA CTAATAATAA 120

GGATGAGGAA GCAGTTGCTG CTAAAAATCC TGAATCAGAA GAATATAAAG TGAATGAAAA 180

AATAAAAAAA GAACATAAAA ACTTTATTTT TGGTGAAGGT GTTTCAnGCG GTAAAAATATT 240

AGCGGCATTA TTATTCGGTA TGTATTATTC GATTTTAAAC CAAACATTAT TAAATGTTGn 300

TTTACCAAAA ATTAATACGG AATTTAATAT TTCTGCGTCA AnAGGGCAAG GTTGATGACG 360

GGATTCATGT TAGTAAACGG TATTTTAATA CCAATTACGG 400

(2) INFORMATION FOR SEQ ID NO: 2576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2576:

TTTAAATCGT ACCTTAAATT TGAAAGTAAT AAGACACACC AATTACCTTC TAACTCTATC 60

GATAGTTTCA AACAAGAAAT CGnTAGTACA TTCAGTTATT TAGAACGCGT TGATTACCAG 120

CT 122

(2) INFORMATION FOR SEQ ID NO: 2577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CACATTGAGG TGCAGTCATA CCTTGTTTAA ATGTCCAAGC ACGTACTTCT T

51

(2) INFORMATION FOR SEQ ID NO: 2578:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2578:

15 AATTATGACT ACAGGTCTGA CTCCTTCTTG TTCAGATCCC TGTACTGGTG ATAAATCTGC 60
 TAAATAAACA TCTCCTCGTC TAATCATTCA TTCGTTGAAT TAGAAGATAA ATATGTTTCG 120
 TTGCAATCGC ATGCTTCACA CTCTATCGGA AAAGCTTCGT TCGCTAGGGA GAGATTTAAA 180
 20 TCAGCCATTT GTGAATATCC TTCTTTTAAA GATTGTTCTA AGCTATGACT TCTATTTTGA 240
 CTAAAAGATA ACATATGAGA ACCTCCAATT GATTCCAAAA GTTATTAAAT GACCTTTAAT 300
 TACTCTAATG ATAACAAATT TTATATGCAC TGACCATATT ATTTTAACAA TTCATTTGTT 360
 25 ACAAAACGGT GGATCACCCA TCATGGATAG AGTCGCGGGn 400

(2) INFORMATION FOR SEQ ID NO: 2579:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2579:

ATAAAAACCT AATTGACTCA TAATCTTCTA ACGGTATATC ATCCACAATC ACAGTATGAT 60
 40 TAGGATTATC GTTAGATACA TCTnTCACTG CCTATCTAA CCCCTCATCA CC 112

(2) INFORMATION FOR SEQ ID NO: 2580:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2580:

CATGAnThTA ACGGATTCAT TCCATATATC AATTGCGTTT GTTATTTTAA TAATGCTATT 60

55

ACTACAACCTT CGATTTAAGC TATATTTATA AAAAAATGCG CCTACTCATA ACATTCTTTG 180
 GCTATTTAAC TTTAATAAGC TAGGGCCAAG TTTGTCATAA GATAAGCGCA C 231

(2) INFORMATION FOR SEQ ID NO: 2581:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2581:

ACTTCGTAAA ATTTATCTTG AGTGGTTGTT TCTATATTAA GATTCATTTC ATTACACTCC 60

(2) INFORMATION FOR SEQ ID NO: 2582:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2582:

GTCAAATGCT GAGTTCTAAT AATGATGTTG GCCACCATGC ATACAAAAAT GCTAAAAGAG 60

AATTACGCAA GATTTTAGAT AGCTATCTCG AAAATGGTAA ATTAAATAT TACGATATTA 120

TCGTTACAAG CAATTTAGCT ACTAAACATC CGTTTTTCGA GTATGCACGT TCATTTGATT 180

TTATCATTGT TTCAGATATC GGTTTAATAA ACGTTGATGT AAAAAGCTGG GGTGAAAAAA 240

CATTTTATCA CTTTGATGTA CCTGATGAGC ATGATACAGA nAnA 284

(2) INFORMATION FOR SEQ ID NO: 2583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2583:

GAGTCAGTCG AAGTTTGTCTG TTCCACCCGT AGAAGTGTA AACCGCATTG TGAATG 56

(2) INFORMATION FOR SEQ ID NO: 2584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2584:

TCGACTAATG TAATGTAGGC ATTGGACGTC AAATGTAATG TGGGGCAATC CGACGAGATG 60

10

ATGGTGTC 67

(2) INFORMATION FOR SEQ ID NO: 2585:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2585:

CGTAACCGCC CCTTGTCGCG GCCCTCCAAG CCTTTTAAGG GGACCCCCCG GA 52

(2) INFORMATION FOR SEQ ID NO: 2586:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2586:

35 ATTAGCAACA ATGTCAGATA ATCGATACCA ACTAATTAGG CGAGAAGCGG TTTCTCATGG 60

TCTTAGTGGC CTAGAAATTG ATGTATTGTA TTTGCATTCA AATAAGTCTA GACATATTAG 120

CTCGTTATCA GGTGGAGAAA CTTTCCAATC GTCGCTTGCA nTAGCTTTAG GGTTAAGCGA 180

40

AATTGTACAG CAGCAATCAG GAGGTATTTC ACTAnAATCA ATATTTATTG ATGAAGGA 238

(2) INFORMATION FOR SEQ ID NO: 2587:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2587:

ACTGGAAAAA ACCGChAACA CGACATTGTC AAAACGACGG CCAGTGCCAA 50

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2588:

GnGCAATTAT ACCACTATAT TTATTTCTTA TACTCCATT TATTATAGT TGTATTAATA 60
 CATTGACTCA AAAACTAATT AATCAAATAT GTTTTTTAGA TT 102

(2) INFORMATION FOR SEQ ID NO: 2589:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2589:

GCATAATATC GGATATGCGn GTGTGTCACT CnCATAGTCG nTGGATTGCG 50

(2) INFORMATION FOR SEQ ID NO: 2590:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2590:

TTAnAAATTG CCTnTCCAAT TnTAAGAATC CTTTTTCCAA GGTAACAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2591:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2591:

CTTCATCCCT TACTTTTAAT TGTCACGTCA AATAATATTT GTCTTTAACT AGTAATAACT 60
 CCAAATATAT TAGTTTGTG GTGCTAGCTA TAAACACAAA TGAnTCATAA CACTATATTT 120

TGATTTTnAA TTATTTATAT

200

(2) INFORMATION FOR SEQ ID NO: 2592:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2592:

TGCATTAATC ATCTTGGATA CTCCTTCTAC CAAAGTAATG ATTGCACTAC CATGACGACG 60
 ACCAGCAATA GTAT 74

(2) INFORMATION FOR SEQ ID NO: 2593:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2593:

CACCTGCTCA CCTCTATTTT CAAACAATTA TGATTGAATT GAATCATTCT AATTTTTGTA 60
 AAGTTACTTG TTTAATTTAT TATATTTATT AACTCTATGA TAACAAAAAT ACTGTTTGTTG 120
 TATAACAATA AATTGAGATA CTCAATAATT TGATAATGTG AAATTGATAC TTTTCAAAT 180
 AGTTGAATAT GACAATTAAT GATTAGTTTT GcATGGTGC TATAAnCAAT ATTTAGCAGT 240
 TATC 244

(2) INFORMATION FOR SEQ ID NO: 2594:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2594:

ATATGGTATG GAACTAACGG AAGAAGGCTT AGCATACGTT AAATATGCTA AAGTGATTTT 60
 AGATAGTAAT AGCGAATACG AGAGAGAnAT AAAAGGACTT TACAATAAGA AGGTAAATAT 120
 AAGTATTAAC ATGCAAGAnA GTCAGTATTT GTATCGCTAC TATAATAAGA TTAGTGAATG 180

(2) INFORMATION FOR SEQ ID NO: 2595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2595:

AAAAAGTATT AAAAATTGCA ATTCTTAAAC TGTTATTCAT ATTAATATTT CTAGCAAATA 60
 ACATTGTAAA ATAAAGAAAA ATAATTADAG TATTGCACTT TATTGAAATT TATATTACGA 120
 TAGTAATGCA GAAATTTATA TATGCAAAAT ATTATA 156

(2) INFORMATION FOR SEQ ID NO: 2596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2596:

TGATCCGCAA ATCGCTGAAC ACGTTCTTCT ATTGGAATCC CTCCATTCAC TTTTAGCTAG 60
 AC 62

(2) INFORMATION FOR SEQ ID NO: 2597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2597:

TTACCTTTAG nTTTAAAC CTGACCCTCC AACCAGCCTA ATTGGTTAAA TGGGGATCCA 60
 TTTATATAAT CCCAGGCCTA ACCTTCCAAG GACCAACCTA AGGGATTAAT CCCCCCAATG 120
 GCCAAAGTGG GATGGGTAAT 140

(2) INFORMATION FOR SEQ ID NO: 2598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2598:

ATTAATTGGG GAGTTAAATT AAAAAAAGG GGTTCCTTCC AACCGGanCC ATTCCCATT 60
TGGATTAAAA ATTCCCGCCT TTGAAAAAAT TGTGTGCCGA ACCGCCCTTA AG 112

(2) INFORMATION FOR SEQ ID NO: 2599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2599:

ATACCGCCCC CAGTTCAATA AGAAGCCCTG GATCAGACCT GACCCTGGTA TGGGGGGAAT 60
CCC 63

(2) INFORMATION FOR SEQ ID NO: 2600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2600:

ATACTATGGA ATGCCTTAAT GGTGGATAAT TTCACCAAAT TAATTTTAAA AAC 53

(2) INFORMATION FOR SEQ ID NO: 2601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2601:

AACTAAAGGT TCTAAAGATA CAGTAAAAAT TGAAAATAAC TATAAAATGC GTGGCGAGAA 60
AAAAGATGGT AGT 73

(2) INFORMATION FOR SEQ ID NO: 2602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2602:

CGGTTGCCAG CCAAACTTG GCAnCCAAGG CAATTATAGC AAGGCACCCA CCTAAATTG 60
CGGACCACCC GGAATGCGGC CACCAAAGTT GGTGGGAGGC CATTTTAA 108

(2) INFORMATION FOR SEQ ID NO: 2603:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2603:

AAGCTTATAA CTATTTGTGT TTGTGATCGA GATAGGTTTG CCTGTAAAAA TGGCCATCA 59

(2) INFORMATION FOR SEQ ID NO: 2604:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2604:

ACGTCCAAAG GGCCGTTTCG CCCAGAnGTG CTGGCAAGGT TCCACAACGn 50

(2) INFORMATION FOR SEQ ID NO: 2605:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2605:

GTCCAATGTC ACATTAAATTG ATTGGTATAA GCGATCACAA GGnCATAGTG AATATTTTGC 60
ACCAGACGGT GTACATTTAG AGTACAAAGG AGTCCTAGCT TTAAAAG 107

(2) INFORMATION FOR SEQ ID NO: 2606:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2606:

GTTTAAAGCA ATTTGGAAGG ACATTGGTTA AAGGATGGGA GTGGCAAAAT CTGG

54

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(2) INFORMATION FOR SEQ ID NO: 2607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2607:

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GTTTTAGCTG AAGTTAATGA TGAAGATATC GGAGCTATGG TAATTAAACT AGTTAAACTT 60

ATTTTCATGC TTGATTATGT TTTATTTTCAT TCAATTCAAA AAAGCTATAC AACACATATG 120

25

AATGAGCTTA AAAATTGTTT CGATTACATA GCTGAATTAG ATAATCATTA TGCATTAGCA 180

ATGTATCGTA GAACGCTAGA ATGTTATACT GAACCACAAA TTGATGATTC AAATGATGGC 240

ATAGTATTCT CTGAGTTAAC ACATCCACTC ATAGCAGATG GCAGTAGCCA ATGATTTCnC 300

30

ACTATCACAn AATATACTGT TAACTGGGGT CGAATGCTTC GGGnTAAATC AACATTTTAT 360

GGAAAT 366

(2) INFORMATION FOR SEQ ID NO: 2608:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2608:

45

TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 60

TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGTA TAAATGCTTC 120

AATAATATTn GAAAAAGGAA GA 142

50

(2) INFORMATION FOR SEQ ID NO: 2609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2609:

GGGTCGTCAA TTGAⁿGGCAG GTAGAGCATT AAGTCAGAAT TG TAGTAAAT

50

(2) INFORMATION FOR SEQ ID NO: 2610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2610:

ATTGGGTGAT GAATTTTGAC GGTATTGTCA AGTCCAGTGG CTAⁿCTCCG G

51

(2) INFORMATION FOR SEQ ID NO: 2611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2611:

ACAAACTTCG GACTGCCAAT TACATTTACC TTGGGGGGTC AGAAACAATG GGTGCATAAA

60

GGCCCGTGTT TCGAAACGGG AAAAAGCCCA GCA

93

(2) INFORMATION FOR SEQ ID NO: 2612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2612:

ATGATGTTTT TCGGCTAATT TTTATACTGA ATTTAGTTTA ATTAⁿCTTAT GATATTTT

58

(2) INFORMATION FOR SEQ ID NO: 2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2613:

TTCTCACCAT TAACTATGCA TACTCACTTT ACACATAAAT TTGCTTAACA TGCAGAACGG 60
 5 AAATAAATCA TTACCACATA TAGATCCCAT CATATATTTA nA 102

(2) INFORMATION FOR SEQ ID NO: 2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2614:

TGAACTACAA GACGCTTATA TCATTGACGC ACATTCTCTG CAGTGAAAGA AACACTTGCG 60
 20 TA 62

(2) INFORMATION FOR SEQ ID NO: 2615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2615:

TGGAGCATTT CACATACATT GGCAACCTCA TGGAGCTTAT CATTCTACCT TGGGGnACAG 60
 35 ATATAACAAC ACTAACGCAA CATGGATGGT GTCGTTGATA ACTTTCAATC TATAGAATTA 120

(2) INFORMATION FOR SEQ ID NO: 2616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2616:

CTGTAGTAAA TTGCCAGAAT CCGTATCAAT ACCAGTCTGT GACTGCGTTG GCC 53

(2) INFORMATION FOR SEQ ID NO: 2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2617:

ACATATGATA TGAGTATATT AACGTTTAAA TTATGGATAC TCTAAAGACA GGCGATTTTG 60
5 ANAAATCAGC AAAAAGTTAT ATGATGTAAG TGGGACAGAC ATACTAGATG TAACACATTA 120
ACCAAGTG 128

(2) INFORMATION FOR SEQ ID NO: 2618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2618:

20 CCTAACCGTG TGTGTATGTA TACCTACAAA AAAATTTACA TTGTGACACT GCGTACGTG 59

(2) INFORMATION FOR SEQ ID NO: 2619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2619:

30 GCCCATGGTC AATCAGACAC ACGGATTGAA CGTTAACAAT TTATGACTTT AACA 54

(2) INFORMATION FOR SEQ ID NO: 2620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2620:

45 ATCATTTGCA CATTGAGTAG CCGTAAAATG GTCAGACGAT CAATGCGAAC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2621:

CTAAGTGTCTG CCCGAATAAC CGTCAATCCA CGGAGCACAT AGGATCTCCC ATG

53

(2) INFORMATION FOR SEQ ID NO: 2622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2622:

TGGGACCGAT AATCATTCGC ATGAACACCT TCCACCGTCT CTTACTCACT ACCTACGGC

59

(2) INFORMATION FOR SEQ ID NO: 2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2623:

ATTAAATTGT TATTTTCGTCA TTAGGTGACA ACTTGTATGT AGATATTTTA ACATATTTTA

60

TGCT

64

(2) INFORMATION FOR SEQ ID NO: 2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2624:

CCGTCCCAGA ATATCATATG ACAAATGTGA AGAGACTTGA ATGATCATAC ACGTG

55

(2) INFORMATION FOR SEQ ID NO: 2625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2625:

GTGGTCACCA GGTACGGGGG ATACAGGGGG TTAATCCCAC CTTGGATAAG TGGAAAACGG 60
ATTTC 66

(2) INFORMATION FOR SEQ ID NO: 2626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2626:

CCACCAATGG GTGGGGGATG GAATAACCT TAATGCGGTG GTACCGGGT AATGGTAGCC 60
CC 62

(2) INFORMATION FOR SEQ ID NO: 2627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2627:

CATGTTTTTT CATTCCTTGA TGACGACACT AGAGGTTCCC GTGTTCATTA TTAA 54

(2) INFORMATION FOR SEQ ID NO: 2628:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2628:

TTGGCCAATG GGCATACAC CCTCTCAATT CGATACATAA CTCAGGCTC AGTCAT 56

(2) INFORMATION FOR SEQ ID NO: 2629:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2629:

TGTCGCTAGG TAACCGTGCA TCGTTCACAG GTACnTATGA TTTCACChGA

50

5

(2) INFORMATION FOR SEQ ID NO: 2630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2630:

15

GAAGGnCCCA AACCAGGCGT TAAAGGCCGA TTGGGTTTAA ACCAAAGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2631:

CGCGAGTGTA TCCGTCGATA TGTCGAGAGG AAAGATTGAA GTGTGGAAGA GTGTTGAGTA

60

30

ACCCT

65

(2) INFORMATION FOR SEQ ID NO: 2632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2632:

TGAAAGAACT TTAGCTAGAC GTTCGTAAAG GTCTTTTGAC ATAAAGCTAG AGA

53

45

(2) INFORMATION FOR SEQ ID NO: 2633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

55

AAAAGCCAAA AGGAATTAAT TAACCCCGGG GTTTAATTTT TAATGGGAAT TTG

53

(2) INFORMATION FOR SEQ ID NO: 2634:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2634:

GGTGTTCACA TTCTGAAGGT TTAGAGAGTT AAGATTATAT ATATATAAGT TTTGGGGTGA
 TAGATATG

60

68

(2) INFORMATION FOR SEQ ID NO: 2635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2635:

CCAATTTTAC TTGGTGCTGC CATTTTCGGTC TCTCGTGAC TTGTGATTGA GGTGCCATTG
 TTCCCGTAGA TGGTTCACAT

60

80

(2) INFORMATION FOR SEQ ID NO: 2636:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2636:

CTTACACCCA ACTTATTGAC TTATAATCTA TTAAAGTGCC ATTTTACAAT CTGAATCCCT
 TAATATAGCA ATAATTACAA CTTCCGACAA ATGACTTGTT TTATGTGCGT GATTCATCAA
 TGAACATCGT AATGCGACAT AATA

60

120

144

(2) INFORMATION FOR SEQ ID NO: 2637:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2637:

5 TAATTCGGCA ACTAATATCA AGATCATGAT CAAATACTAC TGCCATTTTC TTATACCTCT 60
 TAATGTGAAA TCACTGnCAA CACATAACAT CTTAAACTT TGAC 104

(2) INFORMATION FOR SEQ ID NO: 2638:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2638:

20 CATTTCATCCG TTTTTTTGGT TCATGTACAT ACCATTGTTT TGTACACAGC GAAGTCAGTT 60
 AACCTTATAT CCTGTATAA CAGTTGAAAT CGGCAATATT AAACAGTACT TTCCCAATTG 120
 CTTTCTTCCT CAATTGTGCG ACGGACTGTA n 151

25 (2) INFORMATION FOR SEQ ID NO: 2639:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2639:

35 AAGATCAACT GAAATTCATG TGTTGCCCTT TATTAAGATC ACATGGAAAT A 51

(2) INFORMATION FOR SEQ ID NO: 2640:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2640:

TTAGCTAGTT GGTAGGACGG CTACCAGGCA CGTCATAGCG CCTGGAGGGG TC 52

50 (2) INFORMATION FOR SEQ ID NO: 2641:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2641:

CAGGCTTAAA CCTGAGTTAG TGCCATTCAT AATTGCAATC CCAAGCGACG GAA

53

10

(2) INFORMATION FOR SEQ ID NO: 2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2642:

20

ATGTTTGTCA TCTGGAGCnA TAGAACAGGG TTCATCATGA GTCATCAACT TACCTTCGCC

60

GACAGTGAAT TCAGCAGTAA GCGCCGTCAG ACCAGAAAAG AGATTTTCTT GTCCCGCATG

120

GAGCAGATTC TGCCATGGCA AAACATGGTG GAAGTCATCG AGCCGTTTTA CCCCAGGCT

180

25

GGTAATGGCC GCGGACCTTA TCCGCTGGAA ACCATGnCTA CGCATTCACT GCATGCAGCA

240

TTGGTACAAC CTGAGCGATG GCGCGATGGA AGATGCTCTG TACGAAATCG CCTCCATGCG

300

TCTGTTTGCC CGGTTATCCC TGGATAAGCG CCTTGCCGGn CCGCA

345

30

(2) INFORMATION FOR SEQ ID NO: 2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2643:

40

CTTATACGGA TGTATAGGTC GGTCCAAACA TTTGATTTTA GTGGAGAGCA GCCTTTCACA

60

AATTATGTTC AATGT

75

45

(2) INFORMATION FOR SEQ ID NO: 2644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

TACCGGTAA TTAACCAGGG CCCCAGTAA AAAATCCCCG GTATCCCCA TTCCAAC

57

(2) INFORMATION FOR SEQ ID NO: 2645:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2645:

15

AAAGCAATTC GCCGATAAG AGTAGAGACG AATTGCTTTT AAGGTTAAAA CAAAGTGAGT

60

TCAATT

66

(2) INFORMATION FOR SEQ ID NO: 2646:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2646:

30

CAGTATAACT TGTGACCTAT TTAGAGGGGC ACGTTGGTA CAATGAGTCT GAAACCGTAT

60

CAA

63

(2) INFORMATION FOR SEQ ID NO: 2647:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2647:

TAGAACATGG ACCGGTATTT TACATCCTGT ACGCCTAATC TGTTGTAAGT ATCTTTAGTG

60

45

AACCGTTGCT CTGGAATAAC CGCGATTCTG GGCAAACAGT GTGTAAACCG ACTnTATGGG

120

GATGTGTGAG TAATCATTGT GnACTGTTGA TTCTGTTCTG GAATCCCATT TCACAACAGG

180

ATCTTGGAAG TGCTGTCATT TTAGATGC

208

50

(2) INFORMATION FOR SEQ ID NO: 2648:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2648:

10

TTTTAACCTA AAGAATACTA AACTAAAAAG AGAATGATTC TGTACCGCTT TCCTTTTTCA 60
CTCAATAACT TTATATTTAG TTATCCTTAT AATTGTAAAT TATGTTAGTT GGTAAThTT 120
TACATATATG TATTTGATAT GCTTGTAAT 150

(2) INFORMATION FOR SEQ ID NO: 2649:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2649:

25

AGTTTAACTG ACATCGAGTG GTACACAATA GCAATGGTTG TGTGTAAAGT CCTGGTGACA 60
ACATATGAGA GTAACATTTG TAGTGATTAT CTTGTACTGA GAGAATTGAC ATCTATGhAG 120
TTTATCACGT GCAAATAT 138

(2) INFORMATION FOR SEQ ID NO: 2650:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2650:

40

TCACAATTGC AAATTCTGG CACGCACTCA TCTGCGATTT CACAAGCTAC AT 52

(2) INFORMATION FOR SEQ ID NO: 2651:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2651:

GAGTCAAATT AAAATGCCTA TTGGCCATTG TGATGTATAA TCACTTAGTT CACATATACT 60

55

(2) INFORMATION FOR SEQ ID NO: 2652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2652:

GGGCGGTAAT TGTCAACATC ACAAATTGCT ACGTTGAAAC ATCGAGGATT CAAGCTGGAC 60
AGCAGAG 67

(2) INFORMATION FOR SEQ ID NO: 2653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2653:

ACACATCTTA TATGTCTTAC TGATTTAAGG AAAGAATCAG TGGATCAAAC TG 52

(2) INFORMATION FOR SEQ ID NO: 2654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2654:

CAAGCTGTAA ACCAAGAATT CCAGCATTAA ATATCTCTCn TGGTATCGGT TGAGATAAAT 60
ATTCCGTGTG CTCATTAAAT GTAGTAATCT TTATTGTAGT TCCTCAACCT ATGACACGAA 120
TATTGCACAA TATTAGTATA GACAAATATT TCCTTTATAA TCTCATTCAA TTTTCTCCTT 180
TAATTATGTA TCATACATTG TATATTCTCA TATAGACGTT TTGnCATATT CATAGCTTCA 240
ATATTAGTGC ATTTATGTAT T 261

(2) INFORMATION FOR SEQ ID NO: 2655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2655:

AATCCTATTA GCACTTATAA TGATCATGAA AAGATGTCAT CGAGAATCAC CTAGTACACG 60

5

(2) INFORMATION FOR SEQ ID NO: 2656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2656:

CGCCGAAAAC AATAAATTCT CGGAACATAG AATTTATCAC ATACCACGCT TGGATTATCA 60

CAATGGACTG AGTCG 75

20

(2) INFORMATION FOR SEQ ID NO: 2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2657:

TATTAAATAT GCGGTTGCAT ATATCTACGG CATGATTTAA CCGTGAACCA TGAATCATTT 60

TAATCGGGCA CCGGTAAAAT GCTCATTGAT CCGCATAAC CACTATATAT CTAATAGCAA 120

35

GCGTCCAGGA TTCTGTGTTT TATAAATTAA AACTAACTGA AACGTGTGTA TCAGTTCAC 180

CCGnTCGATT ACCACACTTC AA 202

40

(2) INFORMATION FOR SEQ ID NO: 2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2658:

CGTACATGTG CATCATGTAT CTACGTCAAT AAGATGATGG GGTCACATGA TTGGACCATT 60

50

(2) INFORMATION FOR SEQ ID NO: 2659:

55

- (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2659:

10 CTAATCATGT CATGTCTACA ATTATTTGGA GTATTGCTGA CGAAATGCGT TGTACAACTT 60
 TTTCAATTCTA GCACCTTGCG GGGGCCCAACA AAGAATTGG TCCATTCTCA nCATCAGTGG 120
 GGGGCGCGAA TAATTTGAA ATTATTCTGC CACTCCCACT TCATCGATTA AGTTGTAAGT 180
 15 CTACATTACA TTTGTCTTAA ACCATTG 207

(2) INFORMATION FOR SEQ ID NO: 2660:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2660:

TTAATTATGT ATAATACTTA ACAAGATCAC CTGATAGATG TCTAAATATT ATCT 54

30 (2) INFORMATION FOR SEQ ID NO: 2661:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2661:

40 ATTAACAAAAA AATGGGGTAA TTTCCGCCAA ATCCCGTTTC CCCCTTGCCA AGGCCAAATT 60
 TAACCACCCT TGCCAAATna TTAAGCCAAA TTTTCCGATA TTTGTTTCCG TAATGTTTCT 120
 45 TTAATTAATA 130

(2) INFORMATION FOR SEQ ID NO: 2662:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAAGTAAAC CAGTCTATTC AAAAAGGTGA AAAATGGTGA CGCAGCGTAA ATAantGGTC 60
TCTGGTAGGG TAAATCGCGT TGTGGGTTTG TCACATCAGG AACT 104

(2) INFORMATION FOR SEQ ID NO: 2663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2663:

AAAAAGAATA AAAGGACTCG AAAAActCAA AACTTATTnt AGATAGTCAT CGTGACAAGA 60
AACAAACATT TAACTAGACT AAGAAAAATG CTTcGATTAA AAGGCAGACT CATCA 115

(2) INFORMATION FOR SEQ ID NO: 2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2664:

GCATGCGCCA CGGTGTCTCA GCAGAGTGAC TGCCACCTTG TGTGCGCAGA GTCTGCGCCT 60
AGTACAGTCA GGGTGAAACA CnCTATACGC ATTAGGTACA GTACTTCCTG TCTCCGACTT 120
GAGTAGAACG TGACATATCT ATCAGCATTC ACTCGAAAAA GGGA 164

(2) INFORMATION FOR SEQ ID NO: 2665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2665:

AATTACGCAA TntCCCTGTC TTantGAAAG GAATTGACCT GTTAATTCGT 50

(2) INFORMATION FOR SEQ ID NO: 2666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2666:

5 ACAATTCAAT AGAATTTACC CGTAACAGCG TTGCACTGCA CTCAAGACGG CTGACGTATA 60
GCAC 64

(2) INFORMATION FOR SEQ ID NO: 2667:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2667:

GTAGAACCAG CGACGGCGCG GCGGCTGAGC AACATCTGAC TACCTATCGG CCGCGC 56

20 (2) INFORMATION FOR SEQ ID NO: 2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2668:

30 GGATCGATTG ACTACATGAC GTGGnGACGC AATTATACGG ATAGTCCACT 50

(2) INFORMATION FOR SEQ ID NO: 2669:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2669:

45 GCAAGATCGA ATTACAATCA CGACGATCAA CGCACGTAAT CATCTCTGAT CACAGTAA 58

(2) INFORMATION FOR SEQ ID NO: 2670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2670:

ATACCAGCCA GACTTCGATC AACAGTGTTC AACTGCATTG CCCAGTAAGT TGGATAGCTC 60
 GCACATAGTG CTACAAGTTA ACATATACan CGAGTTTGTA TCTCAAGCTT GAAGCTTGAC 120
 TACC 124

(2) INFORMATION FOR SEQ ID NO: 2671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2671:

CGCTTACTGC ATAAAAGCCC CTAACACCGG GGCACACGC TCGTTGCGCG GCTT 54

(2) INFORMATION FOR SEQ ID NO: 2672:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2672:

TCAGCGATTT AACACTAATT CTTCTAGCTA TTCTCTGTAT TTGGACGACG A 51

(2) INFORMATION FOR SEQ ID NO: 2673:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2673:

GATAAGTTGT ACCATATTTTC GATGCAATTC AATGGACAAT GAGGTCACCT GGCTTGT 57

(2) INFORMATION FOR SEQ ID NO: 2674:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2674:

5 TCCTTTGGCC AATTTTTC CA AGTTTAAACC CAAACGGCCC GGGTTGGGTC CCCAATTCCA 60
ATCCAAAATA ATTTTA 76

(2) INFORMATION FOR SEQ ID NO: 2675:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2675:

20 TCCGGGAACC TTACCCAGTG GCCCTACCCT ATGGGTTAAC CCAACCAAGTG GGGCCA 56

(2) INFORMATION FOR SEQ ID NO: 2676:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2676:

TGCGGGGTCT CGTGCCGCCG TCTGCGGTGG TTGTTTGTC GGTGGTGTGT CGGAGTCTTT 60
GCCAGCT 67

35 (2) INFORMATION FOR SEQ ID NO: 2677:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2677:

GGACAGAGGC CTTGACCCCC CCACAATCCT GATTCACCGT AAGTTGCTCT CCCCC 55

(2) INFORMATION FOR SEQ ID NO: 2678:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2678:

AAATTGGGGC TTCCATCCCC ATTCCAAATT ATTAAAACCG TTTAGGGGCC TTATTGGCAC 60
 CATGG 65

(2) INFORMATION FOR SEQ ID NO: 2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2679:

ATTTTGGGAT TAAACCCTTA ATTAAAATTG GCCGGGAAAA GGAAAAGGCC GGTGGGAAA 60
 AGGCCAAGGA AAAGACCTTG GGAACATTA AAAACCTTGG GCCAAGGCCT TCCAAAAACC 120
 GGTGGTTTTT TATTTTGGGA ACCAAATTGG GGGGCCGGGA TTGGGCCAAA ACCTTG 176

(2) INFORMATION FOR SEQ ID NO: 2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2680:

GCCCCAAGA ATTCAAATAA CCnTTCGGAC CCGGTAATGG CCACnTAATT 50

(2) INFORMATION FOR SEQ ID NO: 2681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2681:

TGTGCATTTA TTGCATAACC TATATATGTG TGACCGATAT TTAGTGCGCA CTTCAATGGT 60
 GCG 63

(2) INFORMATION FOR SEQ ID NO: 2682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2682:

TTATCCAAGC TTCCGGATAG TTTCAAGAGA AACCAATGAA ATCCGTTATG GGACCAATGG 60

10

GT 62

(2) INFORMATION FOR SEQ ID NO: 2683:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2683:

AACAGCATTC AAGTGAGTTA CTGGGGTTTA TGCACCATCA TTGGATATCT GCACAAGGAA 60

25

TTTCAACGTG 70

(2) INFORMATION FOR SEQ ID NO: 2684:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2684:

CTTAAAAATTC CCCAGTTTCC TTCCTTTTAA ACCCCATGGA ATTATCCCGG CCAAAAATGG 60

40

ACCATTAT 68

(2) INFORMATION FOR SEQ ID NO: 2685:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2685:

TTTTAACAAA ACACCTAGAT ATGTTGCTG ATCAGAGATG CCTGGTGACC GGTGATCC 58

(2) INFORMATION FOR SEQ ID NO: 2686:

55

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2686:

10 ATCCATCCTT ATAGGCATTC ATCCTTTAAC ACCAACGATT TACATTATGG ATATAACGAC 60
 TTGAGGGGGA ACGTGGGGTC CATCCTA 87

(2) INFORMATION FOR SEQ ID NO: 2687:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2687:

25 ATGGCTGGGC GCTTTACGTG GCCACATTAG GATTATGGCA CTGAAGCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2688:

AACGGTCGTA GGCAAGGGAC TCCCCCnGG nGCTAnATGA ACTGGTCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2689:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2689:

50 GCTAGCATCC ATGGCTCCTA TGCCGAAGCT GAGTAGACTT AGGTGACGGG TGC GTGACAA 60

(2) INFORMATION FOR SEQ ID NO: 2690:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2690:

ACTTAAAAA GGAAGATTAG AAAATTCATA AAAAAATTTT GCTGGGGATT CTTGATCCCA 60
TGGGCCCATn TCTGGATTTA GGTATTGGG TTGGCCAGCC AGGTTAGCGG GGCCCCCATT 120
CTTCCAGGCT CGGTTTCTCC CAGGAC 146

(2) INFORMATION FOR SEQ ID NO: 2691:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2691:

ATTGGTGTCT AGATCATTTA ATACTAAACA TACAACACGA CTAATTCAT TCA 53

25

(2) INFORMATION FOR SEQ ID NO: 2692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2692:

TATTGAATTC AAACATATGTA CTATTTCTTA AATAATACAA TAAAAACGAC TACCATACTG 60
GCCAGAAATA TATTTTATTT GTTACACATT AATTTCAATC CTCCATAATT TGC 113

40

(2) INFORMATION FOR SEQ ID NO: 2693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2693:

GACTTATGTC CGTGTTCGCG TGAAGGCACG TCACGTAAAC TACCCGGTAC AGCT 54

(2) INFORMATION FOR SEQ ID NO: 2694:

55

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2694:

10 CTTCAGCATG AAGAAGTCGC GTGATATACA TCATATCGAT ATATACCGAT TATATCATCA 60
 GAACATTCTC CTGGTATCAT TAGATAGATG ATAATTTGAC ACAGTCCACA ATTTGTnACA 120
 ACGCCGAGAC TCAATGGCAT CCTGTACnTG ATCTATGCCG GAAAACACTA GTCTATATGC 180
 15 CCGCAGACGT CCACTATATG CATC 204

(2) INFORMATION FOR SEQ ID NO: 2695:

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2695:

ATAACTCTAA TTTGAATTAT CTCTCACTAT TAAAACGCGA GCTGTGTAAT AACGAACGCT 60
 30 GACATAATCT TGTATTGTCG CATCATTCGC TGGTATTATC ATANTGCCGT TA 112

(2) INFORMATION FOR SEQ ID NO: 2696:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2696:

TGGCAAAATT AGATGTCTGA ATAGTTTTAT TTACAAGTAC AAACCTTGTA CCATTTTAAC 60
 GTAAACACAA TTTACTTATT GAAAAGAAAA TAAATGTATT CATGAAnACA CACTTTCCAT 120
 45 AGCACTCATC TATAGTACTC AAATTCAG 148

(2) INFORMATION FOR SEQ ID NO: 2697:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2697:

CCTATAATGC TAAACTTCAT ATATCTCTTT GGCAACTATC TCCCTTCTAT TACCAAAGTT 60
 5 ACGATAGCAA TACAATAAAG CAAGCATGTC ATGCTTACTT C 101

(2) INFORMATION FOR SEQ ID NO: 2698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2698:

TTGATAACAT TTGAAAAGCT GCTCCGATAT CAGCAACCAT TTCATCGACC ACAATATACG 60
 20 ACATAGTCAC AAAACTGATT AGAAGACACC AATTGCTGAT TATCAAATCA CAAATTTAAG 120
 ATGAGATTCA A 131

(2) INFORMATION FOR SEQ ID NO: 2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2699:

GATAGCGGTT GTTAATCAAA CGATGGTACA TGCTTACATG ATGCGCCATG TTTGATAACA 60
 35 GCTCTCTATG ATTACGATGG AAGAATGGTT TATTTCATCT CAATTATTCC TATTAAATGn 120
 AACATGCCCT AGCAAACGGA TACAACACAA TCACAACATC ACTTTGAAAT TGTTAAACCT 180
 40 GAGAACCACA TACGCGnAAC AC 202

(2) INFORMATION FOR SEQ ID NO: 2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2700:

TTCGAATTTA ACAAACGTAT CACGCCATAA AGGTTGTATA TGTTGTTTGT AAATTC 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2701:

TATTGCGGGC TTATTAGTAC ACGATCTATA TGATGGTCAA ACTTATGTCT TTCATATTCA 60
AGTGTGACAT TGTGCGGTGA TTATATTTAC GCGTCGTTAT CTACGAACGC CACATTAAGA 120
TTCGAAACTG ACAATCAACT CATAACGCCA TGGTCCTAGA AAn 163

(2) INFORMATION FOR SEQ ID NO: 2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2702:

TAnACAATCG TAATCGAGTC AATGATGTGA ATTGCCCCAG TGAGCGCTAA GAATGCGACA 60
TTCCACACGA TAAGGCAGTG CGCATGCGCA CTGACCTAAT AACACTGAGG ATGAGTACTA 120

(2) INFORMATION FOR SEQ ID NO: 2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2703:

CTGCTTGATT AGGATCGTAT TTATATGAAG ACTGTGTTCC ATAATGATGT GCGTTTTGGC 60
TGAAGTCCCT TAAATGTACn TGTGTATAAA TGCTATAATT TAG 103

(2) INFORMATION FOR SEQ ID NO: 2704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCTATAACGC CTCTCATCGT TTGGTCACAT ATTACCATTAT TTCATTTTAT GTTCTCGATA 60
 ATTGTATGCG ATGTTTCTCA CTGTCATCAC ATTGATACAA CTCATTGTCA CTTTATACGA 120
 5 TTCACACACC TCGATACGAG TGATGATATA TGACAAAGCT 160

(2) INFORMATION FOR SEQ ID NO: 2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2705:

TTATTGTTTA AGATGGTTAA ATGTCATCAT ATAACAATTAT ATTTTGTAGCA ATTCGATATG 60
 20 CCTATAACCT ATAAATTTC ACGTCAACAGA AAGTGACAGG CATACGGATG TGTGAA 116

(2) INFORMATION FOR SEQ ID NO: 2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2706:

TTACACCTGC AGTGTATGGA CTATGGCTAG ATACAATAAT TTTAGTCATC AACTACATC 60
 35 ATACAAACTT ACGACTTACA CATATCTGCT TCTAATCTT CTAAGTATT AAAGCTCGAC 120
 ATCGGAAGCT ATTCTAAATT ATTATCATAT ATCTAACTAA CTGACCTAAT ATATACTACC 180
 ATAAATAACC CGCCTCAAGG TTCGCATCCG CATATAATGC TTAGAAGTC 229

(2) INFORMATION FOR SEQ ID NO: 2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2707:

TCCATATCAA TCCTGAAAGT ACACATATAT CGTACACCAT ATGGTACAAT TTCCTATAT 60
 50 ACACATCAGC CATCTTTCAA GACACATGTT AGGCGCTGGT CGGTGTATCT CAGAAATGCA 120

(2) INFORMATION FOR SEQ ID NO: 2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2708:

GGAACTTTTC TGATTAAGTG TTCACACGCC AACCATACA TGTATTCATG CACACAATTG 60
 TTGCTAAaCT CACTAACAAc ATACGACCAT TTTACTTTCA ATACATATGA TCCGTATAAC 120
 TCGAATTChC TGCTTATAAA TGACCATTTT GACGTTCAcA ATGTTAAACG ATTGGAAATT 180
 TTAAAGTTAG CATGTCCACA TCCGAGCAGT AACTATGCCG TACCATTTGT ATA 233

(2) INFORMATION FOR SEQ ID NO: 2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2709:

TTGTACCTAC CAACGAGGAT ACAATGGATG TCACACGAAA ATTGGGATAT AGATGTCCCA 60
 GT 62

(2) INFORMATION FOR SEQ ID NO: 2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2710:

CTTTAAAAAG GATAAATGAT TGAGAAAAAA ACCCATTCGA AAATCATGCT GCTCATGCTG 60
 TAGACTTATC GTTTGGACAC TCGCGTAAGA GCGAGCAGTG AAAT 104

(2) INFORMATION FOR SEQ ID NO: 2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2711:

GTCCAGAATA TTAATCTGAC ACAACCATTT TAGCnGGTGG ATTAAATATA TACGACCTCA 60
 5 CCGCAAGAAT CTCTATTTAA CTTAACCTAT CATGAATAAA CTGGCGCTTG TGATATCATA 120
 TGAAGATTAG CGAAAGATAG C 141

(2) INFORMATION FOR SEQ ID NO: 2712:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2712:

20 TGGTATTGAA TAGCAAAATT TTGACACTAT TTGCATACTC AATGATACAT CATATCGTTA 60
 TATGGATTTT TATGGTCATT AATGGTAAGA ATTTGATACG GAATATTGGC AGGTTTGGAA 120
 ATCAAATAAT ATGAGAAAATT GTATTAACnA TTAGTCAAGT TAACGCTCAT AAATAGACTC 180
 25 ATCnCGCGCT ATAACGCTTA CC 202

(2) INFORMATION FOR SEQ ID NO: 2713:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2713:

TTGAACTGTC TAAGACTTGG ACGCTAAATG AATGCGTTGA TACAAACGGT GAATCC 56

(2) INFORMATION FOR SEQ ID NO: 2714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2714:

50 CATGACCGAC ATCAGGTGCA AACTCCCTCA TTAATCTGGG AAAACTGTAT CCCGGTAGCT 60

(2) INFORMATION FOR SEQ ID NO: 2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2715:

CCTATAACTA CTCAATATTG CAATTACACA TCCTCACTTT TGTCAATTGT TTGACAATCh 60
 AATACACGTT ATGCACAACCT CCATTTTAAAC GGAATGGAGA GCACATATGG ACAGTAAATT 120
 AAAT 124

(2) INFORMATION FOR SEQ ID NO: 2716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2716:

GGAATATGTA CTATTATCAT TTGATGTTAT TACTCATATT TTTTGTAATG AATGCTATCA 60
 CCTACAAAAA ATTTACTTGA AACAGTAATA ATAATTAATT ACCACAAACC ATGATAAATT 120
 TAATAACTAA TCTAAAATAT CGCATGTTCA NAGCCACAAG ATATAACGCG TTCGCTAGAT 180
 GGAAGTAGAT AGTATAAGGC GCCGTGGAGC CTGGCCT 217

(2) INFORMATION FOR SEQ ID NO: 2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2717:

ATGACATACG CGCATATACA TGCTATCCCG AACTAATATT GATGCGTATT ATGTAATTGG 60
 AGCGAACACT CA 72

(2) INFORMATION FOR SEQ ID NO: 2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2718:

CATATCATCA CTATATCCAT TGCCTAATAG TGATGATATT GATTGGCATA ATGGTATATG 60
10 GCAGATACGA TAACATAACn AACACCTCGG ATAATTGCTA TTAGCTGCGA AGTTATCGTG 120
CCTGATTTAA CGATGTAGA 139

(2) INFORMATION FOR SEQ ID NO: 2719:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2719:

25 CTCTATCATA TCTAGCCATA TGCATGAGAT TATCGTTTAT CTCGACACGC TCTTAAAAGG 60
CGACACCGGC ATATGATGT 79

(2) INFORMATION FOR SEQ ID NO: 2720:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2720:

40 CAATCACAAT TGAAATTACA CAAATACAGC CCATTGCATG ACACAGACCA ATC 53

(2) INFORMATION FOR SEQ ID NO: 2721:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2721:

CGCCCGAGGC TACCATTTTA CCATAAAGAC CGGTCTAAAT CCTTCCGGTT TCCATGGGCC 60
ATTG 66
55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2722:

TACCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA 60
 GAAGACAGTC ATAAGTGCGG CGACGATATC ATGCCCGCG CCCACCGGAA GGAGCTGACT 120
 GGGTTGAAGG CTCTCAAGGG CATCGGTCGA CGCTCTCCCT TATGCGACT 169

(2) INFORMATION FOR SEQ ID NO: 2723:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2723:

CCGGGCCAAG CTGGTGATCA CCGATGTGGA GCGCCAACAT CGCATCGAGG AAAT 54

(2) INFORMATION FOR SEQ ID NO: 2724:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2724:

ATCGGTGATC ACCAGCTTGG CCCGGGACAA CTGCAGAGCG TGCAGCAGGA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 2725:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2725:

AAAACCATTG TCCACCTTTA GAAAGCTTTT GTTTTGGGAA TACCTAAACC GTGGTTAATG 60

(2) INFORMATION FOR SEQ ID NO: 2726:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2726:

TTTAGGCCCT GTAACnGnTT GCCGnTTGn CCGTGTGTAT ATCGGGGGAA

(2) INFORMATION FOR SEQ ID NO: 2727:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2727:

GGATCATTAA ACGTGTATCA CCATCCAGTT TGCAAGACGG ATAAACTGCT GCAACG

(2) INFORMATION FOR SEQ ID NO: 2728:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2728:

ACCCATGGAG AATTAAATTT AAAAACCGTA TTCCGGGTGG ATGCTGGGTG GGTAAGTTGG

CCATACTGGG

(2) INFORMATION FOR SEQ ID NO: 2729:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2729:

ACCACCTTCC CCAATAAGCT GGCCTAAAGC CCCATAATGG GCCATGGTGC GGCC

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2730:

TGTTTGGGGA CCTTAAATGG TTCCAAATTC CAACCACCCA CCAAAGAAT TCCAGTTTCC 60
AATTAAGCCA GCCA 74

(2) INFORMATION FOR SEQ ID NO: 2731:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2731:

AAGTTGGGGA TTAAGGCCAG TTATGGAAAG GATGGATGGT CCATTGGGC TTATTAGAAG 60
AGCATT 66

(2) INFORMATION FOR SEQ ID NO: 2732:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2732:

TTTGnAAAAG CCnGTAAGAG TATTGATTT TGTTGGAGGC CAAACCAGAA 50

(2) INFORMATION FOR SEQ ID NO: 2733:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2733:

AGTACCAGCG GACAATTCGG ACCCAACTTG GCAATTTGnG GTTTTGGACC AGGAAATAAA 60

(2) INFORMATION FOR SEQ ID NO: 2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2734:

CCAGGCTGGC AGTTTTTCTA AAATGGTGGT AGGAAAATTA nCCAAACCAT TTAGGATGGC 60
ATGGTCTTCC ACGGATGGCG GCCGTTAACC CCAAAAAGG CCATTCCATT T 111

(2) INFORMATION FOR SEQ ID NO: 2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2735:

CGTATGGGAT GGCCATTCTG ATGACACACA ACGGTTAGGT TAGCAACGTT GTCAAA 56

(2) INFORMATION FOR SEQ ID NO: 2736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2736:

CAATCCGGGT GTGCGGGCGT GTGTACAAGA CCCGGGACGA TTACCGACAT 50

(2) INFORMATION FOR SEQ ID NO: 2737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2737:

TAACATTTAT TGTGGAGAAA GTrAGGTATC GTGGTACTGA GGATTGTGTT 50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2738:

TAAATTTAAA CCCGTCCCGG TTTCCCAAAT TTGGAATTTT TTGGAACCCC TGT

53

(2) INFORMATION FOR SEQ ID NO: 2739:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2739:

ATACCCACCT TGGATTCTTA ATACCCCAAA AAGGCCGGGG CAACTTGGCT TAAAAAACTG

60

GCTTGTTTAA ATTGGATTTC CGGCT

85

(2) INFORMATION FOR SEQ ID NO: 2740:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2740:

GGAAAGTTTA GTAGTTTAGA GTCGAAAAAT TAGTTTTCTA GTGTAACGAA TCCGGACCCA

60

AATTTTTTTC

70

(2) INFORMATION FOR SEQ ID NO: 2741:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2741:

CGCGCCAATT TACCTGGCGC AGCAGACGCT CAACGAGGAG CACGGCAGCT GCG

53

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2742:

TGAAGAAATC GCACACACTA TCGAACGCAG ATCGCACATC GAATGCATCA GAATCAGCTC 60

(2) INFORMATION FOR SEQ ID NO: 2743:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2743:

TATCACCTCT TTTGCATATT ATTAGAATAT ATAATGATCT TTATAGAAAG GAAAGAAGAA 60

GAGTTATCAT nGCGATATCG CCCAGCGCGT CGTACACTAT GCCATGAATT ACACAATCAT 120

GCCTC 125

(2) INFORMATION FOR SEQ ID NO: 2744:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2744:

GAATTTCCCC CGAAACCGGG AAAAATTTTT CCAACCGGT GGCCTTCCCC CGTTCCCGT 59

(2) INFORMATION FOR SEQ ID NO: 2745:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2745:

TTTTCCTTAA GTTAGTTTTT TTATTGGGCC AAAACCGGCC CCAGGAATTG A 51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2746:

TAATTGGTC ATAATGTTGT TTCAGATGAA ATGCTAACAA TAACTGATT ACAGT

55

(2) INFORMATION FOR SEQ ID NO: 2747:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2747:

ATGGTGAAT GGGATTAGG TGGATGGCCC CCCCAACCAG CCGGTCCTTT TTAAGGAAC
 TTGT.

60

64

(2) INFORMATION FOR SEQ ID NO: 2748:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2748:

AACAAGAGTT ACATTGGTTG TGGAAATCAT CGGTTTAAAT TAGTCCAAAA GGATGGATTC
 AATCGGTAGG GGGGTAAG

60

78

(2) INFORMATION FOR SEQ ID NO: 2749:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2749:

GCAAGTGGCG GAGTCACACT TATAGACAAG AAGTACGACA TCTTGATGT GGTG

54

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2750:

10

TATTTAGATT CAAAGCATCA AATTGGTTTC GTACCTTTT GCACATCGGT TGGGATAA

58

- (2) INFORMATION FOR SEQ ID NO: 2751:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2751:

25

GGAAAACCCC CCAAATTTTC CCCCCCGTT GGGAAAAGAG TTCCCAAAGT TGAATTAGT

60

TCCCAAACCC GGGAGTTCC

79

- (2) INFORMATION FOR SEQ ID NO: 2752:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2752:

40

AGAACCGAGA GATAGTGCCG AGAGAGCGAG AGGTTTTAAT AGAGATGTTT GGCCGTACTA

60

GTTAGCCG

68

- (2) INFORMATION FOR SEQ ID NO: 2753:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2753:

ATAATCTATG GGGGGACCGT CTGGTAAGGA ACCTGGTTGC CCTGCCAATG AAGCCACCCT

60

55

(2) INFORMATION FOR SEQ ID NO: 2754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2754:

ACAAAGGTTT TACGCCCAA TTGTTCACTG GCTAACTGGG CGATGGTTAG TATTGGCAGC 60
GCAAAAGTGG CAGGGG 76

(2) INFORMATION FOR SEQ ID NO: 2755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2755:

ACCTCAGGGA CAATTAAAAG TTTTCTTCG GAATGAATGA CAACAACAAA T 51

(2) INFORMATION FOR SEQ ID NO: 2756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2756:

ACGTATTCCC TCGTTCTTAG GTCTTCTAAA CATAGGTGAC TTTTGGTTCG 50

(2) INFORMATION FOR SEQ ID NO: 2757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2757:

AAATGCTTCG TATTAACGCC TATTTTAGCT CCGTTATAGA CACAACTTAC ACA 53

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2758:

10

ACACGGCAGC GAATACTCGT TTGGTGAGCC TGTACACATC TAACACGAGA A

51

- (2) INFORMATION FOR SEQ ID NO: 2759:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2759:

25

GGGAAAACCA ATTAAGGATT TAAAGGTTAA TTAAAGGGG CCGCCACCGG GTTGGGGATG

60

CCCTTTGGGC ACCTTAAGAA AGCCCCGATG GAAAGGGACC GGTACCTTA ACCGG

115

- (2) INFORMATION FOR SEQ ID NO: 2760:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2760:

40

TTTGCCAGG CCAATTAATT CCTGGTGGCC AATTAAATTT AAGGGGACCT TTGGGGGAAT

60

AAGGTTTAAA ATTGGAAAAT GGTCCAATTT GGACCTTTTG GCCAATTGGA TTCCCGGCTT

120

AAAAAGATTT GGACCGGTAA ATCCCTTTT AAATTACCTC GGGCCanGGC CCAACCAAGC

180

CAAACCAATT TAAATCCGCC TGGAAACCAA CCCATanTTC CTTTACC

227

- (2) INFORMATION FOR SEQ ID NO: 2761:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ACACTATTGT GCCAGCGCAC CTTGAGGTA TCTTGCATCA CTCAGCTGTT TTTTACTGT

59

(2) INFORMATION FOR SEQ ID NO: 2762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

TTATCCTGTT CTAAGCCCG ACGGCTCGGC CACACGATTA ACCTTTAAGC CCATCTTGTC
CAACCTGT

60

68

(2) INFORMATION FOR SEQ ID NO: 2763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2763:

TGGAAAGTAC CATATAAGTA ATGGTAGTCG TTTCAGAAAG ATATAAATCG TTGGGAAAAG
AAGAAATGAC AATTAAATGT AAATATTTGT TCATGTACAA ATAAATATAA TTTATA

60

116

(2) INFORMATION FOR SEQ ID NO: 2764:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2764:

TTGTTACAGT GGTGTAGCGG ATCGCACGGC CTTCAACTAA GTGGTTCAAT GCTTGATACC
AGTTATGAGT GTTGGTGC

60

78

(2) INFORMATION FOR SEQ ID NO: 2765:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2765:

ATATATTCGT ATGCACCTTT TGTAAGGCTT TGTAATACGA AAATTATCAC TACAATGATT 60
 5 GCTGTAAACGA GTAACGACAT ATATGGCACA CCGTTTTTAT TnGTTTTACC AA 112

(2) INFORMATION FOR SEQ ID NO: 2766:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2766:

TATTGAAGAT TTTTTCGAAG ATAAAGGTGA CACATATTCA TGTCATGTTT AATATCGTTA 60
 20 CCTTACGTAA CCATATAAGA CTGTAAGTGG TGTCATATCA TTCGTAGAAC nTTTGGAAT 120
 GAT 123

(2) INFORMATION FOR SEQ ID NO: 2767:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2767:

GTCCGCGCCA CGGAATGGCC CACGGGACGA TAAGTGAGGG CACCGACGGC CGAACCCAAG 60

(2) INFORMATION FOR SEQ ID NO: 2768:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2768:

GTACGCGGAG CACGAATTCC GCGGATCTGG GAGCATCTCT AGGTAAnTTT 50

(2) INFORMATION FOR SEQ ID NO: 2769:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2769:

CTTAGGTAGC TCAGTGTGTT ATTGAGAGGC CTGTTGGCAG GCCCCGGACG ATC

53

(2) INFORMATION FOR SEQ ID NO: 2770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2770:

AAATTGATAG CGTGCACAAA CCAGGTCCAT CCACGAACAT GCCAATCCAG CCCAGGAAGT

60

AATTGCCCCG

69

(2) INFORMATION FOR SEQ ID NO: 2771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2771:

ACGATCATCT GGATGGATAT ACAGAACAGT GTGATTGTAC GTGGTGGGGA AA

52

(2) INFORMATION FOR SEQ ID NO: 2772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2772:

TTAACAGTAT GATATTATCA CACGTGAATA GGATATGCCA AACTGGCAT CGTTGGGGAT

60

AGCGTAATAC

70

(2) INFORMATION FOR SEQ ID NO: 2773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2773:

5 AACATTGTAT TCGTGATTAA GACTTCGATC GGTTCAGTAT TCGGCAGATC CACATGTGAC 60
CATGCTT 67

(2) INFORMATION FOR SEQ ID NO: 2774:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2774:

CACCCTTG TG ATATCACATT TGTATGTGTT AAGAGGGAGC CCCTTTCCCG ATCAACTGGC 60
20 GATAAAAACA GTTGAAAGT GGGCGGGGGT TATTATTCTT GATGACGGCG GGGTTTTTTC 120

(2) INFORMATION FOR SEQ ID NO: 2775:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2775:

AACCGTTGCA GGTAAGCTG GGCAACCAT TCTTCTCTAT TAATGGTTCA 50

35 (2) INFORMATION FOR SEQ ID NO: 2776:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2776:

CATGTACGGT GTCCACACAA GAAGTATTTA GGTGGTTGTT CCCGGATTTA ACCTGGC 57

(2) INFORMATION FOR SEQ ID NO: 2777:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2777:

AACGACCCCG GGTTCACCG GGTCCATTA AGCCAAGGGC CAGGGGACCC C

51

(2) INFORMATION FOR SEQ ID NO: 2778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2778:

TTGTTCCGGC CTAAAAAATT TAAATTGAAC CCAAGGGTTG CCTTGGGTTG GGTAAATCCAT

60

TTTTTGAATA AACCTTTGhC CCTAATGAAT TTTTCCGCCA TTAAAGGGT GTCCGCCAAT

120

CCGG

124

(2) INFORMATION FOR SEQ ID NO: 2779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2779:

GTAAATTTGG GAATTACCGG AAAATTAAGG AAAGGCCAGT AAGGGGTTTC CAGGCCAA

58

(2) INFORMATION FOR SEQ ID NO: 2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2780:

GCACTCCAGC CTGAGCACCA GGGTGAGACC CTGTCTCAAG AACAAAAACA nCAACAnCAA

60

AAAACCTGTT CAAAACTCAC TTCCTGCAGT AATCTTTCCT TGAACAACT CACCCTCTAA

120

TTCCACCTG CAATTGTGTG TAGAAATCCA TTCTCGTGTG TAATTTTGGG CTTATATGCA

180

CACATTGAAA ATCCAAGAGC CAGAAAGAGC TCTAAGGAAT TATCCAGTCC AGCTCTGTGC

240

AGCCTGGGCT AGGACCCAGA TCTTTCCCAT TTCCCTGTTT CAAAAATTTT nGGCACAGGG 360
TGGCCACCCT G 371

5

(2) INFORMATION FOR SEQ ID NO: 2781:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2781:

GGGGTTGCCA AAGGGGTGTT AAATTTAAGT CCGATGAAAA TTAAGhAAAA AAATCCCATT 60
TTCCCTTCCG GGTCCGTTGT TGGGGCCTTA ATTCCCGCC AATCCAAGTT TGGTGAATGA 120
AATTAATTAC CGT 133

20

(2) INFORMATION FOR SEQ ID NO: 2782:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2782:

GTTCAGTTG ACGCTGGATC ATCTGGTACA CACGTATCCT GCATACTATA GATGTCAT 58

35

(2) INFORMATION FOR SEQ ID NO: 2783:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2783:

GCTAATTATA GGCCGTCAGG CATTACGnGA TCGAATCTGG CAACTCACAA 50

(2) INFORMATION FOR SEQ ID NO: 2784:

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2784:

GCCnCnCTCT GTGACACTGT GTATATACAC CCGCGGGAAT ATCTCCAACG

50

(2) INFORMATION FOR SEQ ID NO: 2785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2785:

CTTTGTCTGA CATATTGGGG CAGTGATTTT TGGGACGGTT CTACATGTCG AGTACTTTAG

60

TCAGAGTTGT GAGTAGCGGA CGGGTtTACT TGATATACCC TTAATGTGTA T

111

(2) INFORMATION FOR SEQ ID NO: 2786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2786:

CATGATGATA CTTCATGTA CGTTGTACGT GAACGTACAG TTACGTTGTC

50

(2) INFORMATION FOR SEQ ID NO: 2787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2787:

TCAGCAAGTA GTAAGGATAT CAACTATGA TCTATTTGAT GTTATGCCAT AA

52

(2) INFORMATION FOR SEQ ID NO: 2788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GCATCATGGA ATATTAAAC AGCTGATATG TTTGAGTAAT GATTGATTGA CGAGATATGC 60
GGCA 64

5 (2) INFORMATION FOR SEQ ID NO: 2789:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
10 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2789:

TGAGAGAACT CACAGTCGCC AGCGGCAAAG AACCCGnnAA GATGTGnGCA 50

(2) INFORMATION FOR SEQ ID NO: 2790:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2790:

CAGTGTATGG AATCTTGTTT GAGTGTGAGA GTCAAAGACT TGGTGATTGA ATGGAAAAAT 60

30 TGAA 64

(2) INFORMATION FOR SEQ ID NO: 2791:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2791:

ACAAnGGGTG AAGTTCTCCC ACATGCTGTA TACCGTGGGA TTATTTTAA 50

45 (2) INFORMATION FOR SEQ ID NO: 2792:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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.ATTCTATTTC AACACGGAT ACATAATCTT TTATATCTTC CTTCTAGTCA TATGATACTG 60
GAATAAGTGA TATTTCTTAT AAT 83

(2) INFORMATION FOR SEQ ID NO: 2793:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2793:

CATATGTCAT CGTACGTAAT CATCGATGAA ATATCAACAT CTCGACTTAA TAGGTCAACA 60
AGAT 64

(2) INFORMATION FOR SEQ ID NO: 2794:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2794:

CCCTACTCCG CGCAATAACC GCATTACCAG ATGCGCTTCC ACTGAGGAAC GACGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2795:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2795:

AGATAAAGTG TCATCTATAT CCATCTATCA ATATAGATAT GTTTACGGCC GATTTCAATC 60
CGCAA 65

(2) INFORMATION FOR SEQ ID NO: 2796:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2796:

TATACGCCTC ATTACACCCA ATTGGACCCT TTACGTATGG AGTACATTAT AGAATCGA

58

5

(2) INFORMATION FOR SEQ ID NO: 2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2797:

15

ngCTAAGAAT TTATAAGAGG TTTCGGCAGA TATATATACG CAAGTATCTG

50

(2) INFORMATION FOR SEQ ID NO: 2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2798:

AAGCAGTCTT TCACAAAAAG TGAATAATCA CTAGTTCATT AATTGTCATT TGAACCTTCA

60

30

TATAATGCAT ATTACTTAAT GTACAAGCAA AGATGTATTT ACCTATCAAA GAATTTnC

118

(2) INFORMATION FOR SEQ ID NO: 2799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2799:

CCATAGAACC TGTGAATACC TATACATATC ATACTGTGGA ATTCGTTACG AGG

53

45

(2) INFORMATION FOR SEQ ID NO: 2800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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CCAATTCAGA CTGTTATTCT CTCTTCGTGA TAACCCGTGA TGTTCGTCTG C

51

(2) INFORMATION FOR SEQ ID NO: 2801:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2801:

GGGGGnGCAT ACCGCACCGA AGCATCAGAC GATGTGAGCG ACCTACCTCC

50

(2) INFORMATION FOR SEQ ID NO: 2802:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2802:

CCGTAGCGCA CATATGACGA GACCAAGGAT AACGTGCAAn GncATATTGT

50

(2) INFORMATION FOR SEQ ID NO: 2803:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2803:

CACGTCATGA ACGTGCAATC AACACAATCA TTTACGAGAT GGACCAAGAC

50

(2) INFORMATION FOR SEQ ID NO: 2804:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2804:

TATGGTGTTC ATTTAGCGC TnGTTGTGCT TTGTCTTCAG CATCTATAAC CTAGTGCGAT

60

CTATTG

126

(2) INFORMATION FOR SEQ ID NO: 2805:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2805:

AAAAGCGCAT ATGGTGTMTT TCTCATATCA CTCCAGGACT CAGCAGCTGG AAGGAGTTAA 60
 15 GAAGTAATAA GGTGCCACCC TAAATCCA 88

(2) INFORMATION FOR SEQ ID NO: 2806:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2806:

TGGATCCGGT ACCAAATAGG GACTACCGGG AATGTCCCGG GGGGCCTAAT GCCGAATGGG 60
 30 GCAACG 66

(2) INFORMATION FOR SEQ ID NO: 2807:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2807:

CCCGCTAACG TGGGGAAAGT TTTGAAGTTA AGAAGGAATG GATTCCTAAC GGGGCGGGGT 60
 45 CCAAAC 66

(2) INFORMATION FOR SEQ ID NO: 2808:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2808:

ACAAAGCAGT ACTGAACTGG TTTCGTTGGA GCCCGTGTG CTGTTTATTC ACGGCA 56

5 (2) INFORMATION FOR SEQ ID NO: 2809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2809:

AGGGGGCGTA CAACATAGAT TTGCGAGATA CTCAGCATT CACTTCCATT TAACTTATTA 60

TCC 63

20 (2) INFORMATION FOR SEQ ID NO: 2810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2810:

30 TTAGGCGCCT GTTCCAACCG CACCCATATA AGGCGGTCGG CTGCACGCAC GACGTATG 58

(2) INFORMATION FOR SEQ ID NO: 2811:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2811:

AAACCCCAAA GGAATTAATT TTCCGGTTTT CCAACCCCTT AAAAAGGGAA AGGCCAAT 58

45 (2) INFORMATION FOR SEQ ID NO: 2812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- 50 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

CATCATTAAAG GCAAAAACCTT TCACAAAGTC ATGAGGCGCA AAAGGTATTA TTATAACACA 60
TCCCGCGTTG GG 72

5 (2) INFORMATION FOR SEQ ID NO: 2813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2813:

CCATTTAAAG CGGTACGGGG CTTGGTTCAG GAACGTCGTT AGACAAATTC GTT 53

(2) INFORMATION FOR SEQ ID NO: 2814:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2814:

TAGTACCCAA TTTCCAGTCG AACCAGGATG GGACCAGAAG CCAAACCAAC GTT 53

30

(2) INFORMATION FOR SEQ ID NO: 2815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2815:

GAAAAAAGG CCTTGTTTAC CAAAGGGGCC AATTTTTTCG GTTCAAGGTC CAAACCTACC 60

TT 62

45 (2) INFORMATION FOR SEQ ID NO: 2816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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TCTGAATGAC GCCGAAATCC CATCTGAATT CATGGGATTT TCCACTTTCA

50

(2) INFORMATION FOR SEQ ID NO: 2817:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2817:

CGTTACTAAA GCTACATAGT GCGTCATTTA AGATTATAGC AAGTAGCATA T

51

15

(2) INFORMATION FOR SEQ ID NO: 2818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2818:

CATTCAACCAT AATATTCATT GTTCCATTAG CATATCAGGC ATGTCACGTG CACA

54

(2) INFORMATION FOR SEQ ID NO: 2819:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2819:

GTGTATCAAA TGAGCATGTT nCAATGGTTC AnCATGGCGT TTATGGCACT

50

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(2) INFORMATION FOR SEQ ID NO: 2820:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2820:

ACAATTGCGG CTGCTCATTG TGAGCAGAC TTTATCATGG TTGGGTTGAG

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2821:

CAGTAGTACG TAAAAATGAA TCACTTGAAG ATGCGTACGT AGATTTTAAA CGTCAGTTCT 60
AAAAAGTGGG CAATCCAAGA GACGTAACGG AATTTCGAA AA 102

(2) INFORMATION FOR SEQ ID NO: 2822:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2822:

GAGTACTTAA TCCGGCACCG TTTACTTCTG GGGGCATCGA CTAAGTGGGG CGGCC 55

(2) INFORMATION FOR SEQ ID NO: 2823:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2823:

ATTGGTTTCT CATAAACACT TTTCTATGAA TTTGTATGTA TTTGTTTATT AAAATCTCTA 60
ATTCTTATGG A 71

(2) INFORMATION FOR SEQ ID NO: 2824:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2824:

CCATTGAGTG TGAGTATATC ATCGATCAAT ATGCAACATT TATCAGGTGC ATGTTGCTTA 60

TGGATAATTG AACA

134

(2) INFORMATION FOR SEQ ID NO: 2825:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2825:

CCAGAATGAT GAGCTACAGG ATCAGCCCAG ATATGCAGGT AAACGGGCCA ACCATTG

57

(2) INFORMATION FOR SEQ ID NO: 2826:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2826:

CAATAATGCT GAACAGCAAC GCATCTCATT CTAAATCGC TCAGAATCAC ATCCCATGCA

60

CACATAATAA GTGGCACTTA GCTTAAAT

89

(2) INFORMATION FOR SEQ ID NO: 2827:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2827:

CGGATTAGTG GTGTAAACTG GGTGACCCAT ACCACACCTC GCGTGTGTG AAAAAAGGAC

60

TTAA

64

(2) INFORMATION FOR SEQ ID NO: 2828:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TATACAGAAA ACAGCGTGCC GTTATCCATT ATCACATGAC ATATGTAGTC C

51

(2) INFORMATION FOR SEQ ID NO: 2829:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2829:

GAGATACGGT CTTCGTATAT GATATGTGCA TATTTAGATA GTCATTTATG AGAGAACGTG

60

15

GACGTGAG

68

(2) INFORMATION FOR SEQ ID NO: 2830:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2830:

TGATGATTGT TTATGATACG ATATGTAAAT GATAATCATC CAGGAGGTCT AGCATGGT

58

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(2) INFORMATION FOR SEQ ID NO: 2831:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2831:

CCTAACAAAC ATAATTAAAC CCATAAATGC ATCCAATGCG GTTAAACCAT GAAA

54

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(2) INFORMATION FOR SEQ ID NO: 2832:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2832:

55

(2) INFORMATION FOR SEQ ID NO: 2833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2833:

GTCTGCTACC CTTTCAGAGC AACATGCTGA GTGTATAATG CCGTGATATAG GGGACAATGC 60
CATTCACTA 69

(2) INFORMATION FOR SEQ ID NO: 2834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2834:

AACACCAGCT GGTAAGTATC ACGTTACATT TTGTGTCTTC ATGATTAATA AAAAC 55

(2) INFORMATION FOR SEQ ID NO: 2835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2835:

AGAGCTTGGA TGTGTTTGGT AATTGATGCT CTAGCTCCAT GGGGCCCCATG 50

(2) INFORMATION FOR SEQ ID NO: 2836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2836:

TTTCGTCACT ATTGCTCATG CATAGACATT TGCAATACCG GCAAATGACG ATGGnATATG 60

TTAATGGTCA ATACAGGG

138

(2) INFORMATION FOR SEQ ID NO: 2837:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2837:

15

GTTGGCAACT TCAGTCGCTA CTTTAACGCA TCTCACAGTC CTCCTCCCAA AGAGAACGTA

60

T

61

(2) INFORMATION FOR SEQ ID NO: 2838:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2838:

30

ACGTGAATCC CGTGAGGCCA ACAGTGATTT GGATAATTAC ATGGATGTTT GACTAATGGT

60

CATTACACCC CAGATCAG

78

(2) INFORMATION FOR SEQ ID NO: 2839:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2839:

45

ACTTAAAATC TCCTCTTGCC TAACTTCCAC ATTCTTATCG ATATGAATAC ACCATACGTT

60

TTATAGATAA GTTGATGTTG ATGCATATGT

90

(2) INFORMATION FOR SEQ ID NO: 2840:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2840:

TATATTAGT CTGTTATACA AGGTGTATCA CAGCGGTAAT ATGCCTCTAC ATGGCCATAT 60

G 61

(2) INFORMATION FOR SEQ ID NO: 2841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2841:

GGGCCCCGGC GGCAGGGAGG AAGGGGGCAA GGGCGGCGCC AAGACCACGA CCGGCACC 58

(2) INFORMATION FOR SEQ ID NO: 2842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2842:

TGTACAGGTG CAGTTAGACC GCCTGACGGA ACGAGACGTG CAATTGCCAG CAACGCACAA 60

(2) INFORMATION FOR SEQ ID NO: 2843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2843:

AAACATGTGA AGTGATCGAG GTATGGACGG AGTAATGATC GCACAAGACA TAGCATCCCC 60

GT 62

(2) INFORMATION FOR SEQ ID NO: 2844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2844:

ACGATTTAGT TTGAATTTCT ATTAGGGTTT GGTGATTCTA CTACTTCTGA TA

52

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(2) INFORMATION FOR SEQ ID NO: 2845:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2845:

GATTATCACA ATTATGCAAA GTTGTCTAAT CGTTAGACCA ATTTCTGTTC AAACACCACA

60

15

ATC

63

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(2) INFORMATION FOR SEQ ID NO: 2846:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2846:

CGTTATATAA GAnCGACATG GAAGCATGAT GAAATATTGA ATACATCATA

50

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(2) INFORMATION FOR SEQ ID NO: 2847:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2847:

CCACAGGTGC ATCCGCCTGG TATGGAGCCG GCCAGTCTTC ACTGCTTTCA C

51

40

(2) INFORMATION FOR SEQ ID NO: 2848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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AAACTGTCC CAAGCTGTTT TTATTAGAG CAACCAATCC AATTAAACC CCCACCATT 60
ATTTTAAATA ATACCATTCC AGCGAAAGCC CTTTCCANGG TTTTGGATA TAA 113

(2) INFORMATION FOR SEQ ID NO: 2849:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2849:

CATCTGGAAC TTTTAAATTC CAGAAGGGTT CCAGAAGGTT TCGAAATCCC TCCTAATGGG 60
CTCCATTAAAC GGATTTTAAA TTTTAAATA ATTTTAGGCC AAAAAATTAA TTTCCAGGAA 120
AAGTAAGTTT CCAACCGGG TAAGAAATTA CCAAA 155

(2) INFORMATION FOR SEQ ID NO: 2850:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2850:

CACAACTAA CATAGAAGGG CCATCATCAG GTGCTATTAA ATATCTACGC TAGATTGTAA 60
ATCA 64

(2) INFORMATION FOR SEQ ID NO: 2851:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2851:

AATTATTCAT CAATAGCTCT TTACGATTCA CAAATCTAGG TACTTTTCAG ATCT 54

(2) INFORMATION FOR SEQ ID NO: 2852:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2852:

AAGCCCCCTTT AAAGTGGGCC TTAAAGGAAC GGTGGCGAAA ATCCCCAAAT TCCGGGCA

58

(2) INFORMATION FOR SEQ ID NO: 2853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2853:

AAAGGTTTCC ATTCGGTCCC ATTAAGATTT TTTTGGAAAT TCCATGGAAG GATGGTTGGT

60

CCTTTAGGCC TGGTAGGTTA TCCTTTTTGn AGGTGGTATC CAG

103

(2) INFORMATION FOR SEQ ID NO: 2854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2854:

GGCCACGGTC ATTCCTCCAA GCCAACCAGT GGACAAGATG GGTGGAAGGC GCAGG

55

(2) INFORMATION FOR SEQ ID NO: 2855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2855:

TATTGGCAT TCAAATAACG TAAACGGATT TTGAAGTAAT TTACATAAAG AGG

53

(2) INFORMATION FOR SEQ ID NO: 2856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2856:

ACAATTTGAC AATGACTGGG ATGCTGACAC TTGATATGAA GACAATTGAA GAT

53

5

(2) INFORMATION FOR SEQ ID NO: 2857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2857:

15

AACTGCGTTA CATGCTTTGC TTTTAACTGA ACCCAGAACA ACGGTTTCGG

50

(2) INFORMATION FOR SEQ ID NO: 2858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2858:

CTTTTnTAnC TTCATCTCTA TTATTATTGT CCGAATTACT ACGTGGACAA

50

30

(2) INFORMATION FOR SEQ ID NO: 2859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2859:

40

TCCAGGTCGA ATTTATTGCC AATTAGCCTC CCGGGTTAAA AGGGTGGGTG TCGGGTAAAA

60

TCGTAC

66

45

(2) INFORMATION FOR SEQ ID NO: 2860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55

GGTATCCAGT CCCCCGGAGG GGTGACAAAC TTCCACGCCC AGTGGGGGGA CTACCGTTTT 60
GGACCAAAGC CC 72

5 (2) INFORMATION FOR SEQ ID NO: 2861:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2861:

AGTGTCGAAC AATTAAAGAT ATTGAGTGAC AGGATTGCTT AAGGGCCGGT CGGAACAG 58

(2) INFORMATION FOR SEQ ID NO: 2862:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2862:

TTAGCGGTAA ATCCGAAGAA CTAAGAAGAC GTCAAGAAGG GGATATACGC 50

30

(2) INFORMATION FOR SEQ ID NO: 2863:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2863:

GCAAAANTGA GAGCTCAANC TGCANNAAGC AAATCAACGA AAGATTAGGT 50

(2) INFORMATION FOR SEQ ID NO: 2864:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2864:

55

AACTATTCTG GATTGTGCA GTGGCTATGG GGATGAGTGC GTTCCCCTCT TTCATGACGC 120
AGGCGAACGC CAGCAACGCA ACCACTGATC AATGCTGAGC CAGCTGTAGC CGCCCAGACG 180
5 GAACAAAATC CGCAGTGGGG GCAAGTGATG CCGGGCGTGC AnGGCGCTGA TnCAgTTcG 240
TGGCAG 246

(2) INFORMATION FOR SEQ ID NO: 2865:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2865:

20 ACAGATGATA CCTCTTGATC ACTTGCCAGA GATCGTCTAA GTCGTCCTTG 50

(2) INFORMATION FOR SEQ ID NO: 2866:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2866:

30 AATACCACGC TGACCTTAAT AAGCCATCAT GGGGGAAATC ATGACCGCAA T 51

(2) INFORMATION FOR SEQ ID NO: 2867:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2867:

45 CAACTTGGTA AGTGGTCGTT TTGGGCCCCA CCCTACCCGT TTGGACCTGG 50

(2) INFORMATION FOR SEQ ID NO: 2868:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2868:

5 CCCAACCCCG TTCCGGGCCT TAATTTTTTn CCTTTTAAAG GAAAAAAGG AAAAACCGGT 60
 TAATTCCGGC CCAAAAAnCC CGGAAGTTGG AAACCTTTTT TTAATAAAAA TAATGGACCG 120
 TCCCAACCTT TGTGCCCCAA AGGTGGCCTA AAGGTTTAAA AAAAACCGTT AAAATCCATG 180
 10 GCCAGGATCC AGCCTAAAAT TGAAACCATT ATAATTGATA AAC 223

(2) INFORMATION FOR SEQ ID NO: 2869:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2869:

20 TGGACCTTTG GTAATATGAA TTGAATGGTG CTTTGTGGAA ATCGGGAATT CGCCTCGTGC 60
 CTTGTA 66

(2) INFORMATION FOR SEQ ID NO: 2870:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2870:

35 AAnAGCCAnG ATCATGGTAT ATCCATTAG AGACGAGAAG ATCGATGCCC 50

(2) INFORMATION FOR SEQ ID NO: 2871:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2871:

50 TTATTTGGAC TTACAAGGAG AATAGTCAnT TCTAGGAAAG TGGTGCGAAA GTCACCTTACC 60
 AATATACGGG GATTATTCAT CCATCGTCTGG TCGGTCATAT GATACGGAAT TAACACGCCA 120
 CTCCTG 125

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2872:

CAACACCTGA CGTGATAGA ACTCATCTCT TCAATAACGT CGCTGTCAGG TTACGAAGTC 60
 GA 62

(2) INFORMATION FOR SEQ ID NO: 2873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2873:

TATACATTCC ATTTAACACC TTAACACATG CAACTTACTT CCTCCTCAAG CATC 54

(2) INFORMATION FOR SEQ ID NO: 2874:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2874:

GCTGAAAGGA GACTTCTGCA GGTGTGATCA CAACTGCAC ATCTACACAA GCCATT 56

(2) INFORMATION FOR SEQ ID NO: 2875:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2875:

AGCGCGACCG CGAGAAGGGA GGGGGAGCCA GAGCAGCAGC AGGCCCCAGG GCGAAACCCC 60
 CAAGAGGAGC GAGnAAGAAG GAGGGAAAGC CCAGCAGGGG CGCCCAGGCC AG 112

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2876:

GnGCGTTnnA nCGGTCGCGT AGAGATGTCG GGTCTGTAGT AGATCTGGGG

50

(2) INFORMATION FOR SEQ ID NO: 2877:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2877:

ACCTTGACTT TGCAGACGAT GATGCTTTTG GCTGGGATCT TCACCATCTG GCAACTGAAT
 ATGGTTGG

60

68

(2) INFORMATION FOR SEQ ID NO: 2878:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2878:

CTCCACCTGA TGCATGCCCC CATATCAGGA AAATGATAAC CTCGGACACC TTC

53

(2) INFORMATION FOR SEQ ID NO: 2879:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2879:

GGGAACTTTG ATCTGCCCTT GAAATCCTGA AAAATGTTTG CAAACGGGAA TGATCTTGTC
 CCTTGCTTTG AATGA

60

75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2880:

AGAGAGGCCG AGATGGCAGA TGAGATTGCC AAGGCTCAGG TCGCTCGGCC TGGTGGCGAC 60
ACGATCTTCG GGAAGATCAT CCGCAAGAAA TACCAGCCAA AATCATTITT GAGGATGACC 120
GGTGCCCTGC TTTCATGAC ATTCCCCTC AAGCACCAAC ACATTTTCTG GTGATACCCA 180
AGAAACATAT ATCCCAGATT TCTGTGGCAG AAGATGATGA TGAAAGTCTT CTTGGACACT 240
TAATGATTGT TGGCAAGAAA TGTGCTGCGG ATCTGGGCCT GAATAAGGTT ATCGAnGGTG 300
GTGAnTGAAG TTCAGnGGTG GACATCCGTC TATCACGTTC A 341

(2) INFORMATION FOR SEQ ID NO: 2881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2881:

GCGGTTACTG TGTAATGGCA TTAAATATGA AACGAGCCGA TGGAGCGTTG 50

(2) INFORMATION FOR SEQ ID NO: 2882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2882:

CTCATCATTT GTAGTTGGAA AGGTTTATGT ACATTTGGAA AACACCGACA CATGACGTAT 60
CTCCATTGCA ATTTACACAA G 81

(2) INFORMATION FOR SEQ ID NO: 2883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2883:

5 TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TTTTTTTTTT TTTTTT 77

(2) INFORMATION FOR SEQ ID NO: 2884:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2884:

20 ACGGTGTGCT TGATGCACTT GGAAGTGTGA GTTTGGGTGT GACTTTGCTT TGGCTTGCTT 60
GCTGAATGTT TTGACTATGC ATTGCGTATA TGACTTGnAG CGCG 104

(2) INFORMATION FOR SEQ ID NO: 2885:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2885:

35 AGCAACGTGT CTGTCAACGT GGTGTCATTG GAAAAGGCGT CATGTATTGn CCGGTGGGAT 60
TTACGTGTAG TCACACATGT GCCCAATTAT TGTTTTGAGG CCAACTTGAG TAGGTTGATG 120
GTTATGT 127

40 (2) INFORMATION FOR SEQ ID NO: 2886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2886:

50 TGAGCGAGTG CTGTGTGAGC GCGAGGTTGT GAGAGTTAGA ACCTTGTGAG C 51

(2) INFORMATION FOR SEQ ID NO: 2887:

55

- (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2887:

10 TTGAAACCGC GAACCTGAGT TCTGGTTAAC TACAGTCTGG TATACACATT GAGGGAAACT 60
TCG 63

(2) INFORMATION FOR SEQ ID NO: 2888:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2888:

25 AGTAnCATAc nCAACTATCT CAGCATAcAA TATTGGrCAC CTCGCAGCTT 50

(2) INFORMATION FOR SEQ ID NO: 2889:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2889:

AAAnATAATC CCGTTTTTAT CCCCTACCT AATTAGTGGG AAAAGTACCA ATTGCCAATT 60
GGTAAATAG GTTGCCATAA CGGCCTCCCA AAAGTAAATT CCCTTTTTTG GTTTA 115

40

(2) INFORMATION FOR SEQ ID NO: 2890:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2890:

AATCGGTCCG TTATACTCTT CATAATATTG TGGCGCAACC ATTTCAACTT TATCTTTTCT 60
TATAAATAGC ATCATCGCAA TAnTAAAGAA TAATATCGGA ATGATTAAAG TAACGATAAG 120

55

(2) INFORMATION FOR SEQ ID NO: 2891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2891:

```

AACACAACAA GTTGTTAAAG ATGCATTTTT ATCACAACAT AAATCTATTG GACGTAAAGC      60
TCAAGAAGCA TACTTATCAT ATCGTTTAGA ACAAGAGTAT AGTAAAGATG ATATCTTCCA      120
AGTATATCTA AACAAAATTT ACTATTCTGA TGGCGTAACA GGTATTAAAG CTGCTGCTAA      180
GTATTACTTT AATAAAGATT TAAAGATTT AAACCTTAGCG GAAGAAGCTT ATTTAGCCGG      240
TTTACCTCAG GTTCCAAACA ACTATAATAT TTATGATCAT CCAAAGCTG CTGAAGATCG      300
TAAAAACACT GTTTTATACT TAATGCATTA TCATAAACGC ATTACAGATA AACAGTGGGA      360
AGATGCTAAG AAAATCGATT TAAAGCGAA CTTAGTAAAT      400

```

(2) INFORMATION FOR SEQ ID NO: 2892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2892:

```

CCTAATTAAA CCTCCATCCA TCCTTTTGAA GGGGGATCTT TAATAAAACC GGAAAGTTTG      60
GGGGAAAAAT CCTCCATCCT TTGAAGGGGG GGGCTTTCCA ATGGCCTTTA AGAATGGCCT      120
TTTCCAAGCC AACTTTTAAT TCCCCCGGT      149

```

(2) INFORMATION FOR SEQ ID NO: 2893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2893:

```

GCCCGAAGTA TTCTTGTAAG TATTATGATA CTCGGTnCTT TTTATGATT ATGTTAATTT      60

```

TTATGTTAGT

130

(2) INFORMATION FOR SEQ ID NO: 2894:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2894:

GATGAGACCT GAATTGATTG CAACCCAAAT CGGCATATGC AAATTGCATT AAAGTTGGTT 60
CAACG 65

(2) INFORMATION FOR SEQ ID NO: 2895:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2895:

CGCACAACAC ATTTAGCGAC TCAGATGTCG CGCGAATGGA CCGATATGGC GTGTCTACAC 60
ATTGTCATAT TGTACGAATA GATGAGAAAT TnCAAAGACC GA 102

(2) INFORMATION FOR SEQ ID NO: 2896:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2896:

ATTAAGTGAT GGGCTAATGT TTACGCCCCA ACCAAAGGTT TCCAAAGAGC CCTGTGTTGG 60
CCTGTGTTG 69

(2) INFORMATION FOR SEQ ID NO: 2897:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2897:

ATTGAATTAA TGTCCCAACC AAACGAATGG TTGCCCTTTT TCCATCCAAA GGGGGCTAAT 60
TGGGAAGGGT ATTGGTTCCC 80

(2) INFORMATION FOR SEQ ID NO: 2898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2898:

CAAATCCTGG AGATGAGCGT AACCAAAAAT AACGTTGAGA AAATGACCAC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2899:

ATCGTGAACC TCTCATCCAA TCACTCATGT GAGTGAATTG GATGACCTGA A 51

(2) INFORMATION FOR SEQ ID NO: 2900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2900:

AGCTTTCAGG GCTATATCAG ACCCAGCAT TCATCCACGT GAATGAAACA CG 52

(2) INFORMATION FOR SEQ ID NO: 2901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTACTGACA GAGGGACAAG GTGGAAAGGn TGCCAATGTA AGAATACGGT

50

(2) INFORMATION FOR SEQ ID NO: 2902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2902:

TGTCTGGAAT TCAGGTGAAT TGATGCGGAG ATTTAGGTGA TTAAGGAGTG TTGATTATGA
AGATGACCAC TT

60

72

(2) INFORMATION FOR SEQ ID NO: 2903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2903:

CATGCCAAAG CAGTAGGCAA GCCGCTTAGC AAGCCAAAAA CGTCAGCCCA

50

(2) INFORMATION FOR SEQ ID NO: 2904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2904:

TTGATGTTAC CTGATCGCAA TCTTGACCAC CTGGCAGGGT CTCATTGTTG GGTATCGA

58

(2) INFORMATION FOR SEQ ID NO: 2905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2905:

GCGGTCTAT

69

(2) INFORMATION FOR SEQ ID NO: 2906:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2906:

15 ATTCCATTAG GTTCAATTAA AAATTAACGG GGTTATGGTT CCGGTAATTC GGG

53

(2) INFORMATION FOR SEQ ID NO: 2907:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2907:

25 AAAGCTAAGA AAGGAGGATT AGCTGGTAGT GGAGGAATGT TAAGTGAGGC TGGTGAT

57

(2) INFORMATION FOR SEQ ID NO: 2908:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2908:

40 GGGAATGGCG CATGAACGTG CACATCAAAT GACACTGCAG GAAATCAATT AGCACGGATA
TGGCATAAAG ACAATGGTAA AAGTGG

60

86

(2) INFORMATION FOR SEQ ID NO: 2909:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2909:

55

(2) INFORMATION FOR SEQ ID NO: 2910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2910:

GAATTTGTTT CGAGGTATCG AGGACTACGC TTATAAGGTG CTTACAGATA CATTTCATCAT 60
TAATGGCGTG TGCTGCTGTA TGGGTTATAC TGTTACACAGG TTTAAGAGA 109

(2) INFORMATION FOR SEQ ID NO: 2911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2911:

TTGTCCCAT AGGGAGAAAT AATTCGCCT GGGCAAACC AAATCCACGA GCTTCTAAGG 60

(2) INFORMATION FOR SEQ ID NO: 2912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2912:

TAGATGTATC CAGCTGACAT TAGCTATTGG TAAGGTAACG GCTTACCAGG CAACG 55

(2) INFORMATION FOR SEQ ID NO: 2913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2913:

GCCATGAGGC CCACCCATCC ATGTTTATGG ATGGTGGATT GGGGAATTAC TTGTTTCAA 60

TCA

123

(2) INFORMATION FOR SEQ ID NO: 2914:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2914:

ATCCGTAATT CTGGCCTACC AAGGGTTTAG GCCAATGGGC CATTCTTTTA TTAAACCC

58

(2) INFORMATION FOR SEQ ID NO: 2915:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2915:

TGGTGCGACA GTGGTAGGCT TTTTACGGTn TGcngGCGAG AGTTCTGTAG

50

(2) INFORMATION FOR SEQ ID NO: 2916:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2916:

CTGTTACGCT ATGCCCCCA GTTGTATGTT GAGTGAATC GTGTTTTTCG ACCTGCCTTT
GCTTTTTT

60

68

(2) INFORMATION FOR SEQ ID NO: 2917:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2917:

GGAAA

65

(2) INFORMATION FOR SEQ ID NO: 2918:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2918:

AAATTCCAAT CCTGGAATG GGATTCCATG GTnTTCGGAA AAATCCGCCA CCCCCAAAAA
ATAAATGGGT CCCTTCCCTT GGAAATATTA CCTTTACCAG G

(2) INFORMATION FOR SEQ ID NO: 2919:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2919:

TAATAAATCC ATGACCACCG TCACGACGAT CTGACTGATA AACTAATGAC ATATGACTGG
TGTACACACC GTATG

(2) INFORMATION FOR SEQ ID NO: 2920:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2920:

CTTGGATTGA CCATCATTAG TTTTGGTCAC TCTAAGTTGT ACTGTCCGTT GTACAA

(2) INFORMATION FOR SEQ ID NO: 2921:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCTCATTGCT TGTATATTAA TCCCTGAAAT TGACCGTGTA TATCCCGTCG ATCTATCTTG 60
TCCTG 65

5 (2) INFORMATION FOR SEQ ID NO: 2922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2922:

GCAATATTCT AATCTGTATG TTACAGCACA TGGATATAGC ACATCCGGGC 50

(2) INFORMATION FOR SEQ ID NO: 2923:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2923:

30 TGTGATTTAA CAGGATTACA CAGGTGTACC AGCCGATAGT TGATTAAGCT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 2924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2924:

ATCCTGGGAA GTGCTGAAAA ACCACTnCAC TAAAGGCATA GGanCCACAC 50

(2) INFORMATION FOR SEQ ID NO: 2925:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2925:

(2) INFORMATION FOR SEQ ID NO: 2926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2926:

TTGGTCACAT TTATTCTCGT GTTGTGCCGT TCTTCTTCAG TACTAAAGAC AAGGTGATTC 60
 GG 62

(2) INFORMATION FOR SEQ ID NO: 2927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2927:

CAAAAGGCTA TCCCACCTGA TTGCAAAAG GAACTGGACT GCAAGGGAAG TCTCAG 56

(2) INFORMATION FOR SEQ ID NO: 2928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2928:

TGATCTTGCT ATTTAGTTGC GGCTTGGATT CATTTGGCAT GGTTAAGATT AAATTAGATG 60
 CTTCAATTCAT TCAAGATTTC TTCATGTTAG CATTCTTTAC GACAATCGGT CTTGGTGAT 120
 CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT ATACTTTATG TTTTGTGCTA 180
 TCATTTTCAGT CATTCAAAAC ATAGTTGGTG TATCACTAGC AAAAGTATTA AATATTAAAC 240
 CTTTGTTAGG ATTAACAGCA GGTTCATGT CTATGGAAG CGGTCATGGT AATGCTGCTG 300
 CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC ACTGACAGCG GCTCTTGACG 360
 CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TATCGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 2929:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2929:

10 CTGAACCGAT GCGCACTTT GCTACGCCAC CTACAGCAGA TCCCA_nGGGG G_nGAAGCTT 60
 ATACTGAAGC TCTACGTTCA ACATTTTTC ATTGGGGATT CCATGCTTGG GCTGTTTATG 120
 GTGTTGTTGC GTTACGTTTG GCATATTGCG AATTCCGTAA AGGTGAACCA GGTTTATTAT 180
 15 CTAGAACTTT ACGTCCTCTT TTAGGTGATA AAGTAGAAGG TCCTATTGGG ATTTTATTG 240
 ACGTTTTATC TGTATTTGCG ACAATCGTTG GGGTAGCCGT TTCGTTAGGT ATGGGTGCTC 300
 TACAAATTAA TGGTGGTTTA CATTACTTGT TCAATGTTCC AAACAATACG TTTGTACAAG 360
 20 CGATTATCAT CATTGTTGTT ACTATCTTAT TTATAGCAAG 400

(2) INFORMATION FOR SEQ ID NO: 2930:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2930:

ATGTAGATCT ATATGATGAC TTTTACAAG ATCCATCATC TGTACCAGAA GATTTAAAGT 60
 35 CTTATTACAGC ACAATTAAGA ATGATGACTC AATTGTACCA GCTTTAAAAA GTACAAGTAG 120
 TC_nAATAGC GACGGCACAA TTAAGCGTGT CATGCGTTTA ATTGATAATA TTCGCCAATA 180
 40 CGGGCATCTT AAAGCCGATA TTTATCCTGT AAATCCTCCA AAAAGGAAAC ATGTACCTAA 240
 ATTAGAGATT GAAGACTTTG ATTTAGATCA ACAGACTTTG GAAGGTATAT CAGCAGGAAT 300
 TGTTCAGAT CACTTTGCCG ACATTTATGA TAATGCCTAT GA_nGCAATTT TAAGAATGGA 360
 45 AAAACGTTAC AAAG_nCCAT TGCATTTGAG TATAC_nTAT 400

(2) INFORMATION FOR SEQ ID NO: 2931:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GGTTATACAA TCTAGAATCG CATGATAATT TAATGCTACA AATCGATAGT ACAATATATC 60
TACCGTGAAT AACTGTGCAA ATAGTGACGT TGTAGCCGCC ATACGCATTT CATTTTTCATC 120
5 AGTTCTGCCA TAAATCAATG CATAGTCTGC AATTTGAGCC ACTGGATTAT TAGCTGTACT 180
AGATATAGTT ATGATGGGAA TACTGTAATG TGTGGCCACC TGTGCAATTG ACTGCAATTC 240
ACTATGGACT ACCTTGGATT CGTCACAAAA ATCATGCAAT CTCTATCATC ATGCGTCGCA 300
10 AATGTTGACA CAAGTGAAAT GCGTTTCCAT GTAATAACCT GACATTTGAA GCCATACGAG 360
ATAACTTTGG AAAAAGATCA CCAATAGnCC AACTCGATGG 400

15 (2) INFORMATION FOR SEQ ID NO: 2932:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2932:

25 CTTTCAGTAG CAGCTACAAT TGTCTTTAAC ATTTAAGTTT AAAGCTGTAT GTGTCAACCG 60
CAAATACCGA TAGCCATTCA CTAATGAAGT TTCAACTAAT TTAGTACGAT CTGACAATAA 120
30 CTTTTTGTA TCTTGGGCTG CTTTCAGCTGA TACAGCAATA TTTCTCATTG TTTTAACAGC 180
TTCTTCAGGA TATAAACCAG CAGCAGTTTC ACCAGATAAC ATTACTGCAT CTGTACCATC 240
ATAGATTGCG TTGGCAACGT CACTAGCTTC TGCACGTGTA GCACGTGGGT TACGTTGCAT 300
35 AGAATCTAAC ATTTGTGTAG CTGTAATAAC TGGTTTACCT AATTGTnAC ATTGTCTGAT 360
TAAATCTTTT TGAACCATTG GGACTTTnTC AG 392

(2) INFORMATION FOR SEQ ID NO: 2933:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2933:

50 TGA CTATGGT ATCGCATGTT GTGTATCAGC GATGACAATT GGTAACAAA TGCAATTCTT 60
CGGTGCACGT GCGAACTTAG CTAAACATT ACTTTACGCT ATCAATGGTG GTAAAGATGA 120
AAAATCTGGT GCACAAGTTG GTCCAACTT CGAAGTATTA ACAGCGAGTA TTAGAATATG 180

55

ATTAAATGTT ATTCACTACA TGCACGATAA ATACAGCTAT GAACGTAATT GAAATGGCAT 300
 TACATGATAC AAAAAATTGTA CGTACAATGG CAACAGGTAT CGCTGGTTTA TCAGTAGCAG 360
 CGGACTCATT ATCTGCATTn AATATGCACA AGTTnAAACC 400

(2) INFORMATION FOR SEQ ID NO: 2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2934:

AAAATATGCC ATGACTGGCA TGACAAGAAT TGGACGTTAG AAGCATCTCA AACTGGTACG 60
 TTCAGAGGTC GTAACnTAA CTTCAATGGT GAAGGATTCT CACGTCAAAC ATTTAAAGTA 120
 AATGCCGTTA GTCAAAAAGA CTACGACAAA TGGGTGAAAG AAGTTAAAGG TAAGAnAACG 180
 TTAGATCAAG ATACATTTGA TAAACAATTA TTACCAAGCA CACCTAATAA AGCTTTAGAA 240
 TTTAATGGTA CACATATGGC GTTTGTTGAT CCAGCAGCCG ATCCAGAATA CATCTTCTAT 300
 GCATATAAAC GTTTCAATTT CGGATTGAAG GTCCCAAAC TCACTAGTGA GGAAATATG 360
 TTTAAGGTGT ATCAGACAAA CCCTTAATAC CTGCTCGTGA 400

(2) INFORMATION FOR SEQ ID NO: 2935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2935:

ATGGAGTATA CAACTACTTC GGCATTGGCG CTTACGACAA CAATCCTAAC TACGCAATGA 60
 CGTTTGCAAG GAATAAAGGT TrGACATCTC CAGCAAAGC AATCATGGGC GGTGCTAGCT 120
 TCGTAAGAAA GGATTACATC AATAAAGGTC AAAACACATT GTACCGAATT AGATGGAATC 180
 CTAAGAATCC AGCTACCCAC CAATACGCTA CTGCTATAGA GGGTGCCAAC ATCAAGCAAG 240
 TACAATCGCT AAGTTATATA AACAAATCGG CTTAAAAGGT ATCTACTTCA CAAGGGGTAA 300
 ATATAAATAA AGAGGTGTGT AAATGTACCA AATAAAAGAT GTGAAACGAG AATTAAAAAT 360
 GATGGTGTG ACTTAGGTGA CATTTGGCTG TCGTTTTTACA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2936:

AAACAATACA AACAAAAGAA AGTCAACCAA GGATGGATTC CTATTTTAAT CCTTGGTTGA	60
CTCTTATTTT ATTTAAATTG TAGAACCTAG AAAATAAAGT TTAATTAAAA GCACCAATCA	120
TTTCTACTTT GAAATCTAAG GTTTCTAAAA TAGCAATGAC TTTCTTTATA TCGGTTGTAA	180
TTGCAGAATC AGCCTGAACG AAAAATCGAT ACATACCTAA TTGTGTTTTT AAAGGACGAG	240
ACTCAATCCA GGGTAAATTA ATATTAAACA AAGCAAATGT ATTAAGCACA CTTGCTAACA	300
ACCCGGGTTA TCATGCATTG GTGTAATTAA AACATCAAT GGTGTCGCAT TTTGATCAAA	360
TGCTGCTGAT TTTTATAAC TAAAAACGTG TCAGGTATGT	400

(2) INFORMATION FOR SEQ ID NO: 2937:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2937:

TTATTATCTT GATACATTGA GTGTATATTC CATTTTCCAT GAGGCGTTAA ATAACGCATA	60
CCAAAGCATC TGTACCACCT TTAATTTTCT TATCTCTATT CCCAAATACC ATTGGCGGCA	120
ATGTCGGTTT ATATACTGGT AAGCTCTCCC CAAATTGTTG GAAAACCTCG TGATCCACAT	180
AATAACTTTG GACGTCCTGT TAATGTTCTA AAAGGTACTA GACGTTCTAT ATTCGTTGTA	240
AATGGTGGAA TATCGTCGAC CTTGTTTATT TGAACCGGGG AATACTGCTG TCGGTATTAC	300
TTCTCGTGGT TGTGGAAGTT ATATTTAAAA ACGGAAATTT TCTCAGCAGC GntTTCGTTA	360
GGAAATATCT TTAAACGGGC ATTCCAGTTT GTTCntCGGG	400

(2) INFORMATION FOR SEQ ID NO: 2938:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2938:

5 TATCTCTTAA AGCCGGTGAT GGTGGTAATG GTATTACCGC ATACAGAAGA GAAAAATATG 60
 TACCATTTGG TGGACCAGCT GGCGGTGACG GTGGTAAAGG TGCTTCAGTC GTATTTGAAG 120
 TGGATGAAGG TTTAAGAACG TTATTAGATT TTAGATATCA ACGTCATTTT AAAGCAAGCA 180
 10 AAGGTGAAAA TGGCCAAAGT AGTAATATGC ATGGTAAAAA TCGGGAAGAT TTAGTATTAA 240
 AAGTTCCACC TGGTACAATT ATTAAAAATG TTGAAACAGA CGAGGTTTAG CAGATCTTGT 300
 TGAAGATGGT CAAAGAGCTG TAGTAGCGAG GCGGCTCGAG GTGGCCnAGG TAATTCACGT 360
 15 TTGCAACAC CTAGGAAACC CTGGCACCTG GACTTCATGG 400

(2) INFORMATION FOR SEQ ID NO: 2939:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2939:

CTAACCTCGA GTTCGTATTA TGCCCAACCAC ATGTCGTCTG GCTTGTCTGTA AATATTAACA 60
 30 GATTTCAAAG TTTGACAAGC TTTTGGAAA CCTTCTTCTA CTGACATAAT AGGATCTTCA 120
 TGTTC AATAC TTAATACATA ATCATATCCA TTAATAATAA GTTGACTTAT GATATCTGCC 180
 CATACATATG GACTATGTCC TAAGCCAACCT GTACGGAATG TCATGCTCTT GTCGCAACGT 240
 35 TACCATATGG TTGCATATCA GTTAGACCAT ACATATTTAC ATTTTCTTGG ATTAATATAC 300
 GTATCTTTAG CATGGAAGTG ATGAATTGCA TTTGCTTGGn CTAATATGCG AATCGCAGCC 360
 AATTGGGTCA ATAnCnTGGC CACC 384

(2) INFORMATION FOR SEQ ID NO: 2940:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2940:

50 TTTTCATATTT TTCTATTAAT GATTCATATT GTAGGGTGAT TGCAATGTCA TCTAAGCCAT 60
 TTACAAGTTT ATTCTTCCAA GTTTCATCAA TTTCAAAATG GAAACGCTTG TCTGGTGATG 120

CACTTTTTTC TAAACGATA GGCAACATCG CATTITTTAGT GCAATTCATA TAAAAATATGT 240
 CACTGAAACT TCCTGCAATA ATAATATGAA AACCATAGTC CTTAAGAGCC CAAGCAGCAT 300
 GTTCACGACT TGAACCATAT CCAAAATTAT CTCCAGTnAT TAAATnGGAG GCCCCTTTAT 360
 ATTGTGGTTT GTTAGGGTTG AATCAGGGTT TnTnGGAACC 400

(2) INFORMATION FOR SEQ ID NO: 2941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2941:

ATCATAATCC ATCGTGCCTC CAAGAAGTAC TTGATTATTT AAAGTTTGTA TTGTGAATCC 60
 TGTGCACATT GTTCTCACTC CTCTGTACCT TCATTTACTT TAATCACTTT CAAATAAAGC 120
 TGTITCACTT AAACATACTA TAAAAAATCA ATTATACAAG CAATTAATTG ATATTCATTC 180
 TCAATAACTG TGGTATGATA TGTAAGGAAA TCATGACTTA TGTGTGAGTG AACGATCATC 240
 TATACATCCG TTCACTTCAT CTCATGACTT TCTATATTTA ATTTTACAA GGgAGTGACA 300
 TCTGTGAATa ACACACAATC TTCACCACGC gTAaTaTtAT TaTTGCGATT ATGTTGTCTG 360
 CATAACATAT GGTGTGTGCA CAATCATTAT TAnTATAGGA CCTCCGTTG 409

(2) INFORMATION FOR SEQ ID NO: 2942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2942:

ATGAAGTGTC AAAAGGTTTA AAAACATCTG AAAGGGGTTT GCACATGTTT TAACTTTTAA 60
 AAATAAAGGT GGATGTCCAA AATGTCGACC AGCAATCAAC TATTATTTAA ACATGGTTTA 120
 TCCACATGAT CATGAAGATG AAAGAGAATC AAGATTTGCT AACGAACGTT ACCATGCGAA 180
 TATTCAAAAT GATGGTACAT TTTCTGTTAT ACCTCAAATG CGTGGGGGTG TTACAGATGC 240
 AGACCAACTG ATTCGTCTAG GAGAAGTGGC TAAGAAATAT CATGTGCCAC TAGTTAAAGT 300
 GACAGGTTCA CAACGTGTTG GTTTGTATGG AGTTAAAAA GAAGATTACC AAATATATGG 360

(2) INFORMATION FOR SEQ ID NO: 2943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2943:

ACCTGGAAAT GTATGTGCCA TCTCTTTAAG CCAATCAGTA TCTTGAATAC CTTTCGTTCC 60
 AACTATGCAA TAATTAATCC CTGCGGCAAA GTAGTCCATG ATTGTGACTT CGTACGAATG 120
 CCACCACCTA CTTCAATATC TTTGGTTGTT AATCTCCTCA ATGACTTAAT ATAATCAAAC 180
 TCTCGGGCAT GCTGTGCCTT AGCACTCATC AAGTCGACGA TATGAATACG ATTCACACAT 240
 TCAAATTGAC TATAGTAAGC AATACTTTCT TCAGCCGAGC GTGGACATTT TTTCTTCACT 300
 ATCATATTTA CCCTCTGTGA ACCTCACACT TGTGACCCA ATCAAATCAA TCGCTGGGCC 360
 ATAATTCAAT CATTTnATAA ATCCCCCTTG TATTGGCCTG 400

(2) INFORMATION FOR SEQ ID NO: 2944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2944:

AACAAAAGGG GTCTATCGTC AATCGTTTCT TGAATAGTGT TGAAAAAATC GGAAATAAAT 60
 TGCCAGATCC TAGCGTCTTA TTCTTTTTAA TGTGTGTGGG CTTAGCCATT ATGACATGGG 120
 TTATCTCATT ATTTAATGTA TCTGTTAAGC ATCCAGGTAC GCATCAAACC ATTTATATTA 180
 AAAATATAAT TAGCCATGAT GGATTTACGA TGATAATGAA TGATACGATT AAAAATTTCT 240
 CAGAGTTCCC AGCATTAGGC TTAGTACTAG CAGTGATGAT TGGTATTGGT GTTGCAGAGA 300
 AAACAGGATA CTTGATAAG TTAATGATTT CTGTTGTGAA TCGCGCACCA CGTTTCTAAA 360
 TTTACCGCTA TAATATTAAT GGGnATTTTA GGGAGTCAGA 400

(2) INFORMATION FOR SEQ ID NO: 2945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2945:

5 ATTTTACAAG TAACGGTGCA TCACCAGATT CTAATTTAAT GTCATGCTCA GCAGCATTTT 60
 GATAACCCAA CTTTTCAAAG TAGTCAAAC AATGGTCTAC AACAAACCGTA CTATACTCTT 120
 GTGCTTTGGC CGCTCTTCTA CTGCTTGAAC CAAGCCACGA CCTAATTTT GTCCACGTAA 180
 10 TTCAGGATGA ACTGATAAAG AGGCAATCGC CAAACCATAA TACGTCTTAT CATCACTATT 240
 AATTTCTACT TCAATTAATA AAACGTGTCC AACGACATCG TTATTTTCAT TTTTCGCTAT 300
 TACTTCTAAT TCAAATTAT AGCAAGGAGA TTTTCTTAA TGTTTACTT TCGGCACGTG 360
 15 CCTGGCCAAC TCGTTTTTCAG GATTATCATC CAACTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 2946:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2946:

GGAAATAATT ACTTGAGCTA GATAAGTTGA CAGCTGTGCA ATTATTTTCA GCAGCTAATT 60
 30 GTAAAATTCG CTCTAATCTT GCTGATGAAT GTTCAGGCCC TTGACCCTCA TATGCATGAG 120
 GTAAGAATAA TGTTAATCCT GAACGTTCTC CCCATTTTGA GCGAGAACTG AATAAGAAGT 180
 TGTCAAAAAT CATTTGTGAC ATATTTGGCA AAATCACCAT ATTGTGCTTC CCAAATATTG 240
 35 AAGCTTTTTT TGTTTTCCAC ATTATAGCCG TATTCAAAC CAACTACTGC TGCTTCTGAA 300
 GCGGAGAATT GTGTATATCA AATGTCGCTT TTTGANCAGG AGCATGATGT AAAGGTGTAT 360
 40 ATGTTnACC nGTTTGCTCA TCATGTnACA CGGCAGCCGT 400

(2) INFORMATION FOR SEQ ID NO: 2947:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2947:

50 AAGTGGCATA AAAAAATCAC ATGACGATAC ATTGTCGTCA TATGACTTTA AATATTATTC 60

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TTCAATTGTG TCACCGATTT TTAATACATC TTCCACTTTT TCAATTCTAT TTTTTGAAAT 180
 5 TTGTGAAATG TGAAGCAACG CATCTTTACC TGGGAATAGG CCTACAAACG CACCGTATTT 240
 TTCAATACGT TTAACAGTGG CTTGGATAAG TTTGACCTAC TTCCGCTTCA CGTGTAATTT 300
 CCTCAATGAT TTCACGAGCA CGATTTATCA TAGCTTGATC AACAGCACCC ATAAAGATAG 360
 10 TACCATCCTG GnCCATATCh AATTTAACAC CnGGnTCCTC 400

(2) INFORMATION FOR SEQ ID NO: 2948:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2948:

TTTTTCAGT TTTGCTGAAG GCTTTACACA AGGCTATTTA ACAATGGATG CCATTGCAGC 60
 25 AATTGCTTTT TCAATGATTG TTGTTAATGC AGTAAACTA ACAGGCATTA CTAAAACAAA 120
 TCAAATATTC AAACAACTT TGA CTGCTGG TTTAATTGCA GCCGTAGCTT TAATTTTCAT 180
 ATATATTTCA TTAGGTTATA TTGGTAATCA TATGCCAGTA AGTGACATGA CGTTAGATCA 240
 30 ATTGAAATCC AAAGATCGAA ACATTGGGAC ATATTTATTA ACGACAATGG CTTCAACAGG 300
 ATTTGGTCAT CCGGAAAATA TTATTGGGCA TCATTGTGGC GCTGGCATGC TAACTACAGC 360
 ATGCGGGCTA TGGTGCACTT CCTGAATATT CCATAGATCG 400

(2) INFORMATION FOR SEQ ID NO: 2949:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2949:

CATGGCTTCA GATTGTTTGA ATTGAATGGA CAATTTTGGn TTCTGTCCAA AATTCTTACA 60
 AAATCTTCTA CCGATAAACT ATCAAGTTCA ACTCTAATCG GAAAAACGAC CTTGCAATTC 120
 50 TGGTATCAAG TCACTCGGCT TAGATACATG GnaAGCTCCA GCACCTATAA ACAGCATATG 180
 TTCAGTATTC ACAGTACCAT ATTTGGTTTG AATAACGCTA CCTTCAAGTA TAGGTAAAAT 240
 ATCTCTTTGA ACACCTTGTC TTGAGACATC TTGACCACTA TTATGATTAT TCGTCGCAAC 300

GTTAGCGCTT TCTTGATCA~~n~~ TTAGTTCATC CGCATAACTA

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(2) INFORMATION FOR SEQ ID NO: 2950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2950:

TTGACTTTTGT AACTAAACTA CTCACTCGAC CGACTCAACT GTTTAAATGT TTCAGATGGT 60
 TTA~~A~~CTCTAA ATACTACGTA TAAATCACCA GCAGGTCCTC CATTACGCC TGGAGAGCCT 120
 TCACCAGCTA ATCTAATTG TTGTTTATTG TCGACACCTT CAGGTACTTT CACTTCTAAT 180
 TTA~~A~~CTGTTT TATTTTCAGT ACCTTTTCCG TGACATGTTG GACAAGCTTC TTCAAATTCT 240
 TGACCACTTC CATTACATT AGGACAAACT TGTTCACTAC GAACTCTACC TAAAATTGTG 300
 TTTTGTCTTA CAGCTACATG ACCAGCGCCA TTACAGTAAC TACAAGTCTT TTTACTTGTT 360
 CCAGGCTTTG CACCATCACC ATGACATGTT TCGCATGT~~n~~A 400

(2) INFORMATION FOR SEQ ID NO: 2951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2951:

CAATGATTTT AAAAGATGCA ATAAACCAA ACTTAGTACA ATCAATTGAA GGGACACCTG 60
 CATTAGTTCA TGGTGGACCA TTTGCGAATA TCGCACACGG TTGTA~~A~~CTCA ATTTTAGCAA 120
 CTGAAACAGC ACGTGATTTA GCTGATATCG TTGTAACGGA AGCTGGATTT GGTTCACT 180
 TAGGCGCTGA AAAATTCATG GACATTAAAG CGCGTGAACA GGATTTGATC CGGCAGCTGT 240
 CGTTGTTGTT GCGACAAATC GTGCGTTAAA AATGCATGGT GGTGTAGCGA AAGATAATTT 300
 AAAAGAAGAA AATGTAGAAG CAGTAAAAAG CAGGAATGGT TAATTTAGAG CGTCATGT~~T~~A 360
 ATAATATTAA CAATCCGTG TAGA~~n~~CCGGT TGTGCCATA 400

(2) INFORMATION FOR SEQ ID NO: 2952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2952:

	TCAAGTAGCA AAAGAAACAG GTGCTTCAGT TATCGGTATT GATATTGGTC CACAAGCCGT	60
10	TGACCTAGGG CGCAGAATCG TTAACGTCTT AGCACCAAAT GAAGATATAA CAATTACGGA	120
	TCAAAAGGTA TCTGAACTTA AAGATATCAA AGATGTGACG CATATCATAT TCAGCCGACA	180
	ATTCTTTTAA AGTACAGCAT TTTAGAAGAA TTATATGATT TAACAAATGA AAATGTCCGT	240
15	AGTTGCAATG CGCTTTGGTG ATGGCATCAA AGCAATATTT AATTATCCGA AGAAACAGCG	300
	GAAGATAAGT GGGCCATGTG TGAATAAACA TATGAGACCA CAGCAAATTT TTGATATAGC	360
	ACTTnATnAA AnAGCCGGCT ATAAAGTnGG TATTACGGAT	400

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(2) INFORMATION FOR SEQ ID NO: 2953:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2953:

	CGCAATTCAC AATAACATTA AATAATTTTT GGTCTCATAT TTTCAAAAAA CATACTGTTA	60
	TTATCCCATG GgntTAAAAA TATCATTAGT ATATAAACGA AACACTTTAC GATAAATGAT	120
35	ATCTGCAAGC CAAGCTGTTA CAAATGGTAC AACAAAGAAC GCTACTACAA TTAGTAAGAC	180
	ACTCAACCAA GCAGAATCAA CCTCCATAAA TTAAATGCA TTAATCGGTC CTACCATTCC	240
	TATAAAACCA AATCCAGCTG ACTCTTTTCGT TCCATGAATA CCTACTAATG CTGATACCAA	300
40	ACCTGATACA ATGGCTGTCG TAnGGGCGGG GngCATAAGA ATTGGATATT TCACCATATT	360
	AGGTATCATC ATTTTAAACG CTCCAAAGAA GACCGGATAA	400

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(2) INFORMATION FOR SEQ ID NO: 2954:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2954:

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AACACTTTAA TGGAGATTTA GCAGGCACTG TTACTGAC AGCAGGTTTA GGTGGTATGG 120
 GTGGTGCGCA ACCGTTAGCA ATTACTATGA ATCATGGGGT AGCAATTTGC GTGGATGTTG 180
 5 ATGAAACACG TGTGATAAG CGAATTGATA CGAAATACTG TGATGTTAAA ACAGCTGATT 240
 TAGATGAAGC ATTAAAATTA GCAGAAGAGG CGAAAGAACG TGGGAGAAGG ATTATCAATC 300
 10 GGGTTAATTT GGAAATGCTG TAGACATCCC ATCCAAGCGG ATTCTAGGAA AAAGGGTTTT 360
 AAAATTGGAC ATTAATTACT GGnCCCAAAC CAAGTGCCCC 400

(2) INFORMATION FOR SEQ ID NO: 2955:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2955:

TTCAGAATAC GAGCAATGTC AGTTGCAGTG TTTAATAAAT TTTGTTGCT ATTTTGTAGG 60
 25 CATCTTCTAA AGTGCTAGGT GAAGAGATTA TAGAATAGGC ACTATCAATA CCGAAATCGT 120
 AAACATGTTG ATAATTTTCG CCTAGACTGC CACAAATCGC GATGACAGGA ATATGATATT 180
 30 GTTTTGCAGC TAACGCAACG CCTACGGGTG TTTTACCAA GATGGTCTGA TAATCCATGC 240
 GTCCTTCTCC AGTAATAACG AGGTCTGCAT CTTTAATTCT TTGATGAAAA TCTGTAATGT 300
 CAAAGACGAC ATCAATACCT TTTGTTAAAG TTGTCTCACA AAACGnTAAT AATGCTGCGG 360
 35 CCATACCGnC AGTGCACCAG AACCTGGTAT TTGGTTnACG 400

(2) INFORMATION FOR SEQ ID NO: 2956:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2956:

AATACGTCCT TTATATAATG TTAATAACCA GTTAAACAAT TTCACACCAG TTGAATACC 60
 50 AATCAGCATT GTTGAAATTG AGAAGAATGA GTTGATTAAC GCACCAATTAC CCATTGTGAA 120
 GAAATGGTGA ACCCAAATA AGAACTAAG GAACGCGATA CCGGCAGTTG CCCATACCAT 180
 ACTTTGATGT CCGAATAAAC GCTTACGAGC GAATGTCGGG GATAATTTCT GAGTAAATAC 240

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CCAAAGCATT GGGCATACCG CCATGTGGCA CTGTGGAAGA ATGCTGTGTC CAATATTCCG 360

nTCATTGGTh CATTAAATGGC TAACGCTAAC GGTTTAAAGG 400

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(2) INFORMATION FOR SEQ ID NO: 2957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2957:

TAGTAATTAA TACGATGTCA GCACCTACTG ATTTTGCTTT GTCTGCTAAT AATCTTAAAT 60

GTTCCGTGGA CCTGAACCAG AGATAATTAC AAATACATCA TTCGACTTAA TCGCAGGTGT 120

20

CGTTGATTCT CCAACAACAT GTGCCTGTTT GCCGAGCTGA TTTAAGCGCA TTGCAAAACT 180

ATTGCCACG AATCCTGGAA CGTCCTTTGC CAGCTACAAA TATATGTTCA GCATGTAGTA 240

TTTTGGGATG CAAAAGTTGG AAAACTCCAT CCGnTTCAAC ATGTGACAAA GTCATCTTTG 300

25

AATTCATCTA GAnTTAATTG ATAGTCACTA AnTTTAGCCA TATTACTTAC CTTCGGTTGC 360

CAGCGCGACC ATTGTTTCGC AGCTTCTTAC TGGG 394

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(2) INFORMATION FOR SEQ ID NO: 2958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2958:

AATTATTCTA CCTATAATTA AAAATGCTGG CAAAGGTGTA ATGATGATGA GTAATGAACC 60

TACAACATTT AATATCAATC CTACATAAGT AATTTTGACG CGACCAAATT TATCAGCAAC 120

ATCACCAGCA CCTACGATAA ACAAACCAGC AAATAAGGCA GATAAGCTAA CAGCGATTAT 180

45

TTATCGTTCC AACGTCACTA CTATATGTTG ATTGTAATGG GACAACAAGA TTAACAAGTG 240

ACTGCGCGAA TAGCCAAAAG GTAATAACCC CTAAAACGAT ACCCAAAGC AATCGGTTGT 300

TCACCTCTTA AATTGTTTTG ATGTGTCCnT GGATTAGGAT AAGCCTCCTA TGTTTAGGAA 360

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AAACAATTTT TAATATGGTA TATTAAGGAN ACATTTCTTT 400

(2) INFORMATION FOR SEQ ID NO: 2959:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2959:

10 CTCTTTTCTC AACATCAAAG AACATATGGT TTTGTTTCAA ATATTCTTTT ACTAGCGCGA 60
 TATGTTTCGTC TGATCTACCA GTTAACTTCA TATATTTAAG AGATTCATCA TCAACTGGGA 120
 AGAATCCGCA AGTTGCTCCA TACTCTGGTG CCATGTTTGC AATTGTAGCA CGGTCTGCTA 180
 15 GTGGTAAATG TTGTACACCT GGACCAAAGA ACTCCACAAA TTTACCAACA ACACCTTTTT 240
 TACGTGGCTC TTGAGTTACT CTTAACGCTA AATCAGTTGC TGTTCGCCT TGTGGTAATG 300
 AATTTACTAG TCGTACACCA TTAACCTCTG GAATTGGGGA AATAGGAGGG TTGTCCAGGC 360
 20 ATTCCAGCTT CAGTTTCAAT ACCACCAACA nccctcctag 400

(2) INFORMATION FOR SEQ ID NO: 2960:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2960:

ACGTCAAATG TAATCACAAT CGGAAAGTAT CGTGACAATG CATATATAAC AGGGAGGGTT 60
 35 TAAATATGAG TTACTAAGGG GATTTTTAGA TTTAGGTGCA CTGTTTATTT TACCGGTTGT 120
 CATATTCTTG CTGCGCTAT TCTTTAGGCA GAAAATTGGA GCGGCATTTA GGTCTGGTTT 180
 AACAATAGGT GTGGCTTTTG TAGGGATTTT CTTAGTCATC GATTTATTAG TTAAAAATTT 240
 40 AGGGCCAGCA GCACAAGCGA TGGTTAAAAA TTTAGGCGTC AntCTGAATG TGGATTGATG 300
 TAGGTTGGCC AGCAACATCA TCTATCGCTT GGGCATCATC TGTnCGCnCC ATTTTATTAT 360
 TCCACTCGGG ATTCATAGTT 380

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(2) INFORMATION FOR SEQ ID NO: 2961:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GGCCATTGGT CGAACTTACG AAGAATCATT GTTAAAAGCA ATTCGATCAC TTGAGTATGG 60
 TGTGCATCAC TTAGGATTAC CAAATGGTGA AAGCnTCGAT CTTGATTATA TTAAAGAACG 120
 5 TATTTACAC CAAGATGATG GACGATTATT TTTCATCGGC GAACAATTAG AAGAGGCACA 180
 ACAGTAGAAG AAATTCATAA TATGACTCAG ATTGATTACT TCTTCTTACA CAAGTTCCAA 240
 AACATTATTG ATATTGAGCA TCAATTAAAA GAGCATCAAG GTGATTTAGA ATATCTTAAA 300
 10 TATGChAAAG ATTATGGnTT TAGTGGTAAA ACAATAGCGC ATCGCCTTAA TATGACGG 358

(2) INFORMATION FOR SEQ ID NO: 2962:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2962:

TTTGGGCATC ATTAGGAAAA TTCTTTGAGC AACTTTAGTG TCTACTGGGT AATACAATTT 60
 25 TATCACCATG TTTTCTAAT AAATCTTTTG CGAATCGATT TTATCTTCTT CTAATAATGA 120
 AATACCAATT TCTTTACCTT GCGCTTTTAA GAAAGTATAA GCCATACCTC CGCCGATGAT 180
 AATTTTATCA GCTATGTTAA CTAAGTTTTT GATGACATTA ATTTTGTGAG ATACTTTTGr 240
 30 GnCACCATAA ATAGCAACAA CTGGTTTATG TGGATCGTTA ACTACGCCGC CAATAAACTT 300
 AATTTCTTTA TCCATTAAGA ATCCAGCTGC AGTTTCTAAA TGTGTAGAAA TACCAACATT 360
 35 ATTh 364

(2) INFORMATION FOR SEQ ID NO: 2963:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2963:

GTTGATTCTT TGAAAGATAA TAAAAAATTC AAAGAAATGG GATCTAGGAT TCCTAAAGGT 60
 GTCTTACTTG TTGGACCTCC AGGTACTGTT AGAAACATTA CTTGCTAGAG CGGTTGCAGG 120
 50 TGAAGCTGGC GCACCATTCT TCTCTATTAG TGGTTCAGAC TTTGTAGAGA TGTTTGTGG 180
 TGTTGGTGGC AGCCGTGTTT GTGACTTATT CGATAATGCT AAGAAAAACG CGCCTTGTAT 240

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TCATGATGAA CGTGGAACAA ACCCTAAACC AATATTAGTT GAAGGATGG TTTnCGGTGG 360
 AAAATGAAGG TG 372

(2) INFORMATION FOR SEQ ID NO: 2964:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2964:

TTAGCAGAAC GCCCACAAAA CCTATCTCTT GCTGTAAAAG AATTTGTGAA nCTGCTGGCT 60
 TAAAACGTGT TGGCATAATT GCAGCTTTAG GAGCTACAGT TATGTTAGGT TTAAGTACAA 120
 TTAAAAAATT ATGCCGTAAA TAGAGCAAGA CATAACAAT AATTTAGGAG TCTGGAACAA 180
 TAATCAATGT TCTAGGCTCC TAAATGTTAT ATTGGCAGTT CTGAAACATT TATAAATCTT 240
 TGATTATGAA CTCACAACAG TGCTCTATGC TTTTATAGAT TTTAATAAAT TAGCCATTTT 300
 AATTGCACTT ACTGCTGCTT CACACCCCTT ATTGCCAGCT TTCGnACCTG CnCCTTCCAC 360
 AGCTGGGCAA TACTGCCAGC CG 382

(2) INFORMATION FOR SEQ ID NO: 2965:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2965:

GGGAATCATA CAATCATTAC CAATAACAT GTTACTTATC ACATGAAAGT CGGTGATGAA 60
 ATCAAAGCAC ATCCTAATGG TTTTATAAT AACGGTGGTG GACTTTATAA AGTTACTAAG 120
 ATTGTAGATT ATCCTGGTAA AGAAGATATT GCGGTCGTAC AAGTTGAAGA AAAATCAACG 180
 CAACCAAAAG GTAGAAAATT CAAAGATTTT ACTAGCAAAT TTAATATAGC ATCAGAAGCT 240
 AAAGAAAATG AACCTATATC AGTCATTGGT TATCCAAATC CTAATGGAAA TAAACTACAA 300
 ATGTATGAAT CAACTGGTAA AGTACTATCA GTGAATGGAA ATATAGTGAC ATCTGATGCG 360
 GTTGTCCAAC CTGGCAGCTC TGGTTCACCT ATATTAAATA 400

(2) INFORMATION FOR SEQ ID NO: 2966:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2966:

10 TGGGGATTCA CAGGCTAATA CATTGACTT TATTAGCTGG TGGCGGTAAC GGCGCTGAAC 60
 TTAAATGCG ATTCAAAGTG CTGCAATTAT AAGTGCAATC CCATTCTCCT TTGTCGTCAT 120
 ACTCATGATG GTAAGTTTCT ACAAGGATGC GAACCAGGAA CGTAAATTCC TAGGTTTAAC 180
 15 ATTGACTCCG AATAAACATC GCTTACAAGA ATATATCAAG AGTCAACAAG AAGTTATGAA 240
 TCTGACATTC TTGAAAAGCG TCAGTCACGT GAAATATAGA GAAAAAGAT AACTAATAAA 300
 GTTTAGTTAA GTATTTTAAT AACAAAGTAGT ATGTCATTCT AGTAGCTAGA ACGGTnATAC 360
 20 TACTTGtnTG TTTTGTGGA AATTGAGTAT TTCAAAGGTT 400

(2) INFORMATION FOR SEQ ID NO: 2967:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2967:

ACGAGGAATT AGTGAAGTAC AATATTATCG GTGGTTTTGA TTTAGGTGTT GTTTCAGACG 60
 35 ACTTTAAAAA TCACATGTTA ATAGCTGTAA CTGAATTAAG AACAAAAGAT GAAATCGATA 120
 CATTGTAGA AAAGGCTGGT GAGTTAAATG ACTAGTAAAT CAAGTCCATT AATTTTTGAA 180
 AGATCTCGTG AAGGCAGATA TGCATATTCA TTACCAAAAA GTGATATTAA AACAAATTCT 240
 40 GTTGAGTCAT TGTTAGATGA TAAATTTATT CGTAAAAACA AAGCGGAGTT TCCTGnAGTT 300
 GCTGGAACTA GACTTnGTAC GTCATTAATC CTGGACCTTT CCAAATAAAA AATCCGGnG 360
 GTAGACACCG GGTTTAACCC ATGGGGT 387

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(2) INFORMATION FOR SEQ ID NO: 2968:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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AACAAAGTGCA AGTGAGTCAA CATCAGAAAG TGC GTCAACA TCACTCAGTG ACTCAACAAG 60
 TACAAGTAAC TCAGGATCAG CAAGTACGTC AACATCGcTC AgTAACTCAG CAAGCGCAAG 120
 5 TGAATCCGAT TTGTCGTCAA CATCTTTAAG TGATTCAACA TCTGCGTCAA TGCAAAGCAG 180
 TGAATCCGAT TCACAAAGCA CATCAGCATC ATTAAGTGAT TCGCTAAGTA CATCAACTTC 240
 10 AAACCGCATG TCGACCATTG CAAGTTTATC TACATCGGTA AGTACATCAG AGTCTGGCTC 300
 AACATCAGAA AGTACAAGTG AATCCGATTG AACATCAACA TCATTAAGCG ATTCACAAAG 360
 CACATCAAGA AGTACAAGTG CATCAGGATC AGCAAGTACA TCAACATCAA CAAGTGACTC 420
 15 TCGTAGTACA TCAGCTTCAA CTAGTACTTC GATGCGTACA AGTACTAGTG ATTCACAAAG 480
 TATGTCGCTT TCGACAAGTA CATCAACAAG TATGAGTGAT TCAACGTCAT TATCTGATAG 540
 TGTTAGTGAT TCAACATCAG ACTCAACAAG TCGGAGTACA TCTGGTTCGA TGAGTGTGTC 600
 20 TATATCGTTA AGTGATTGCA CAAGTACATC AACATCGGCT AGTGAAGTAA TGAGCGCAAg 660
 CATATCTGAT TCACAAAGTA TGTGAGAATC TGTAAATGAT TCAGAAAGTG TAAGTGAATC 720
 TAATTCTGAA AGTGACTCTA AATCGATGAG TGGCTCAACA AGTGTCAGTG ATTCTGGCTC 780
 25 ATTGAGCGTC TCAACGTCAT TAAGAA 806

(2) INFORMATION FOR SEQ ID NO: 2969:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2969:

ACCATCTACT CCGTTAATAG TTACACTGTT ATCATTGGTG TTTGGACTTT CAGCCCTTGC 60
 40 ATCTAAAAAT ATAAGCTGAT TAAAATCTGT TATTACTTCT TCCTTGTAAC CATCTATGAT 120
 TTTTACAAAA GATTGCATTA ATTAGTCAAA CCTCCCATAT AATTATTTGC ATTTGCTCTA 180
 45 TGCCCACTTT GTTTTGACAA TATTTTTTCT AAACCTCTAA TTGCATCATT AGAACCTAAG 240
 GATTATCCTG AGAAGAAACA GTTTGAATCA ACGCATCTGT TAATTnATTn CCTTTATCAC 300
 TTAACATAAC AATTGGTTC AACAATTnTn AACTGTAGAA GTATCATTAT T 351

50 (2) INFORMATION FOR SEQ ID NO: 2970:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2970:

5 AGTGCTTGAT GAATTTTGAC CACAAATTCA AATGTATCAG GCGTTTCTTT TATCCATTTT 60
 AATATATTTT TTTCCGGTTG TATCGCATAG TATGTGCGAT CTAATTCGAC AACCGGAAAA 120
 TGTCCAGCAT ATGTTTTAAG TTTATCGGTT TGGCGTTCTA AATCTTCATA TAATGAATAG 180
 10 TGATCACCCC AACCTGTTAA TCCGATGTTT ATCATATATA TCACCAATGT CATCATACCA 240
 TATAACTTTT ATCATAATCA TTTCAGCGAA CTTTAGTTTG ATGTTTTTGC TTGATTAAAA 300
 TCTTTTCGGC GAnCCTCAGC TTGATGTTTT TCGTTGATTA AATGGTAAAT AGnnACGCA 359

15 (2) INFORMATION FOR SEQ ID NO: 2971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2971:

25 CAGACGGTCA AGAATCTTAT ACTTATCAAA ATTTATACTG TGAAGCGAGT CTATTGGCTA 60
 AAAGACTCAA GGCTTATCAA CAATCTCGTG TTGGGCTATA CATAGATAAT TCGATTCAAT 120
 30 CGATCATTTT AATACATGCA TGTGTTGGTGG CAAATATTGA AATTGCGATG ATTAATACAA 180
 GGTGACACC TAATGAGATG ACGAATCAGA TGAAGTCAAT CGATGTACAA TTGATTTTTT 240
 GTACCTTGCC ACTGGAATTA CAGGGTTTCA AATTGTATCG CTGGGTGATA TTGAATTCGC 300
 35 TGGAGGGATA TTACAnCGAn CAGTTGTTGG GCAACACAAT GGGTATCCAT TTGAACCATC 360
 GGATGnAACT TTGTGCCGAA GGTGCGCTCC ACATnTAATG 400

(2) INFORMATION FOR SEQ ID NO: 2972:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2972:

50 TCAACCGCTT TACAGCCAAC CGGCGACGCT GACATGGATC GCCTGGCCCA TGCCCACGCC 60
 TTGGCGCCAT CATTATTAAT TGCTGCAGTT ACGGTATCTT TAATTGCGTT AAATAAACCT 120

55

AAATCACCGA AATGTTATTC GCTTAACGTT TTGTTGTTGT TATTTTAAAA TAAATTTGAT 240
 GCAATTAGTT TGTtTATCCG CACAACATCT TATAATGTAC TTAAGTGTAT TTtAAAGAGA 300
 5 AAAGAAATAC AGTTAGGCAT TCAAAACTGT ATTTAACACA ATTAAGTTGC CTGAATTCGT 360
 ATTTAAGTCT TATTGAACCT TTTTnAGATA An 392

(2) INFORMATION FOR SEQ ID NO: 2973:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2973:

20 ATTGCAATGA TAGCAATCGG AATCGCACCT GCTAAAATAA ACGTTGTGCC ATCCGTCGCA 60
 TTTGTACCAC GAATCACAAT GTCACCAAGC GTAGGTGCTC CTATAAATGA TCCAACGGCA 120
 ACAACACCTA TCGCAACAAC CAAGGCAATA CGAATGCCAC CGATAATAAC CGAAACAGAT 180
 25 AACGGTAATT CAATCATTCG TAGCACTTGA TTGCGTGTCA TTCCCATACC TTTGCCAGCA 240
 TCCTTAATAT TCGCATCAAC ACTAGCTATA CCAGTATAAG TGTTTTTATA ATTGGAAGTA 300
 ACGCATATAA AAACACTGTT AAAGTACTGT TCTGAnCTAG CCTGACTACA TTAAATAGTn 360
 30 ACATTGCATG ACTGGACTGn TGGATATATT GCATGGATnC 400

(2) INFORMATION FOR SEQ ID NO: 2974:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2974:

GTATTCTTTA GGTAATGCAA CTTTAAATCC TTtAATATCT TTACCAATTT CAGATGTAAA 60
 45 GTCTACATCA TCAACTGGTG CACTTGTAGA GTCATTAACA TCTGCACCAG AAATAGCTTC 120
 TAATACGATT GCATTATCTT TTACATTTG AGTCAATGGA CCAATTTGGT CTAATGAAGA 180
 TGCAAAAGCA ACTAATCCAA ATCGAGATAC ACGACCGTAT GTTGGTTTCA TACCGACAAC 240
 50 GCCACAATAT GGCAGCCGGT TGTCTAATTG AACCACCTGT GTCTGGAACC TAAGCTAAAT 300
 GGTACTAAGC CAGCTGCAAC TGCTGCTGCA GATTCCACCT GAnGGAACCA CCTGGGCACG 360

(2) INFORMATION FOR SEQ ID NO: 2975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2975:

GAGATCGCGG GTTCGATTCC CGTCGAGACC GTACAAATGC CTATCCAAGA GATAGTTTTG 60
 TnTTGCGTTT AATATTATAT TAATAAAAGA TATATGGACG AATGATAATC ATATTGATTT 120
 ATCTGTTTCG CCATTTTCTT TAAAATGTAT GAACCTCAAG TAACTTAGTG GTTGGATATG 180
 AAAGATAAAC GTnGACAATA AAATCTTTAT TAGACGTACA AACATATGCT ACTGTCAACA 240
 TATTTCTTCG TTGTGATATG CCACCAGTCC TCCATAACAT CAATTGTTAA AGTAACGAAT 300
 AACGAATAAT GATATTTnAT TTCTGAGCCA TGACGTGCCA CTAGAAGTTG CCCATTATCC 360
 T 361

(2) INFORMATION FOR SEQ ID NO: 2976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2976:

TGCTGCTTCT GAAGCGGAGT AATTGTGTAT ATCAAATGTC GCTTTTTGAT CAGGAACATG 60
 ATGTAAAGGT GTATATGTTT CACCTGTTTG CTCATCATGT AACACGGCAT GCCTATGACT 120
 GAATGTACCA CGTTCACTAT CTTGACCAGT TAAGCGAATC GGTGTACCAT CTTGTAAAAT 180
 TGTCGCAAAT GCAAGTnGTT CTGCTTGTGC CCAATCAACT AAACCATCTT CTTTATTAAA 240
 CGGCTCATGA CGCTTCTCAA GAACCTTGTG TAACTTTTTn CAAAATGTTA AAGCCATCCG 300
 GATATGTAA CAATGCATCA TTATTTCTTT CAAGTGATCC AAAAGTAAAG GnTTGT 356

(2) INFORMATION FOR SEQ ID NO: 2977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2977:

CTTTAGAGCG ACACCTAGTC ACTGCAGCAA GCTATTTCTT TATTGCTAT GCTATAnATC 60
 5 GTTAATTACT AGACCTATTG CTGGTAGATT GATGGATGAT AAAAATGAAA ATATTATTGT 120
 CTACCCAGCA TTTATCATGC TTTTCCTTTC ATTTGTATGC TTAATTTCAA GCTATCAAAG 180
 CTGGTTAATA TTAATTGCTG GTGCTTGCCT AGGTTTAGGG TATGGAAATT TATCATCTGC 240
 10 AATGCAATCT ATTGCGATAA AAGTCTCACC CCCGATTAAA TATGGTATCG CGACATCTAC 300
 TTTTACGTT GGTCTAGATG CCAGGTGTCG GCTTCGGTCC AGCATTCTCT GGGTTAnTTA 360
 15 CGCAGnGTTT T 371

(2) INFORMATION FOR SEQ ID NO: 2978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2978:

TTGTAATTTT ATGATTACAC CTCAATTGTT CTTGTTGTTA AAACCTCAATA TTTAATTGTC 60
 TGCGCTCAAT AATTTGTTGT TTAAGTTGCT CAATATGATT TGATTGGAAT TCTTCCAATA 120
 30 ATGCTTTTGC TATTTCAAAT GCTACGACAT GTTCGCAGAC GATACTTGCT GCAGGAACAG 180
 CACAACATATC AGAACGTTCA ATTGTTGCTT TAAAGTCTTC TTTAGTATTA ATGTCTACTG 240
 AATTTAATGG nTTATATAAC GTTGGAATTG GnTTCATTAC ACCATTACGA TAATTGGCAT 300
 35 CCATTGACAT ACCGCCTCTA ACCACCTAAG TGATTAGAnC ACGATAATAC CAATTCACTA 360
 TATAT 365

(2) INFORMATION FOR SEQ ID NO: 2979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2979:

TGATTATATA AATCTAACCA GCCAAGTTTC GTCTGCGGTG AGACATTGAC ATTAATTGCT 60
 GCAGATAATG ATTTAACAAAC ATGTGTGGCA TGTGATTGAT TAACGATGAC AATATCATGT 120

TGGCGATGGG TAACATTGTT AACATTGCTT CATTTAAAAC GATATCGAAT TGATTGTCAT 240
 CAAAGGGCAA TTTAACAGCA TTCGCTTGTT GAACTTGAAT ATATGATTCA nGACCTGCTG 300
 5 CGGAAATGTT TTCCGTGCTT TTTCTAAGCC TTCnTATTAT ATCAACGCCT GAnGTGACAC 360
 CAnAGTGTGA GCCAGATAAA TAGAGGTGTG CACAGATACA 400

(2) INFORMATION FOR SEQ ID NO: 2980:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2980:

TTTCTGCTTT TGATAATCTT TCATCAATGC AAAAGCTACA TTGGACAGTC CTATAATGGA 60
 AATAATGTTT ACAATTGCCA TTAAGCCCAT AAATAAGTCT GCCGTATTCC ATACTGTTTC 120
 TGTTTTTACA ACTGCACCGA CAAAGACAAG TACTACAACA AGACATCTAA AGATAAATAA 180
 25 TATTACACGG TTTGTTGATA AAAATTCAAT ATTAGATTGA CCGTAATAGT AATTACCTAC 240
 AACAGATGAA AATGCAAACA GTGnAACGCT TATTGGTTAA GAAAATACCT CCAGCAGAAC 300
 CTAAATGCTC CTTAAGTGCC GATTGGGTAA CTGCAACACC nTGGAGGGCG TTTATCACCA 360
 30 AATTTnCGTC CCGAATATAG TAAA 384

(2) INFORMATION FOR SEQ ID NO: 2981:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2981:

AATTCTAACG ATATCACCAT TTTTACAACC ACGTTCTCTA AGCGCATCAT CAATACCCAT 60
 45 CGAACGCATT TGACGAGCAA ATCGACGTAC TGCTGGATCA CTGTTAAAGT CAGTCATTTT 120
 AAACATTCTT TCAATAGCAT TACCACCTAC CACATAAGCA CCATCATCAT CTCTTGGAAG 180
 TTGTAAATTT ATCTTGTGAC GGTGTATGTT TATATAATAC TCGGTTAATG CCAACTGACT 240
 50 CCTCTTCTTC AACTGTGGAG TCAACATCTT TATATTCTTC TGAATTTATC TGCTTATTGC 300
 ATATGAATAA TTGnnCAATG ATTATCACGC GTTATTGTTG GAAACTGGGA TTAAGTGGCA 360

(2) INFORMATION FOR SEQ ID NO: 2982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2982:

CCTCAACCGC TTTACAGCCA ACCGGCGAGC GCTGnACATG GATCGCCTGG CCCATGCCCA 60
 CGCCTTGGGC nCATCATTAT TAATTGCTGC AGTTACGGTA TCTTTAATTG CGTTAAATAA 120
 ACCTTCCATT GAAAACACTC CTTAAAATTT AAATTTGAAG ATAACAAAAA CGTGCGTACT 180
 TTnTGAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT GTTGTATTAT TAAAATAAAT 240
 TTGATGCAAT TAGTTTGTTC ATCCGCACAA CATCTTATAA TGTACTTAAC TGTATTTTAA 300
 AGAGAAAAGA AATACAGTTA GGCATTCCAA AACTGTGATT TTAACACAAT TAAGTTGGCC 360
 TGAATTCGGT ATTTGAAGTC CTAATGGAA 389

(2) INFORMATION FOR SEQ ID NO: 2983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2983:

ATATTCCTAT GACAATGTTT AGGCAACGAT TCCAAGGATT AAGAAAAGAT CAACCGGTAT 60
 ACTTATGTGA TGCCAATGGG ATTGCTAGCT ATAGAGCCGC TCGTATTTTG AAAAAGAATG 120
 GATATACAGA TATCTATATG TTTAAAGGCG GCTATAAAAA ATGGACTGGA AAAATAAAGT 180
 CTAAAAAATA GTTTTTGTAA ATTTAATATA CGATTTAATA AAATCTGAGT GTTAATTGAT 240
 CATCAATAAC AATACTCAGA TTTTAATTTT TTAACAAAGT CTGTTACTAT ATTTCTCTAG 300
 CTTCACTGAT CATTAAACCT TAGTTTCAGC ATAATTAAGG AAGGTCCGnC CCATTTCAT 360
 CGnGnTCCAT TACCGCCAC 379

(2) INFORMATION FOR SEQ ID NO: 2984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2984:

5 ATGCTGAAAA TATGGTGCCG TTTATATGAA TCAATTTGAA TCCGAACATA ATCCGGATAC 60
 ATATTTTCAT ACATTGGGAC CCGAATTGAC TTCAGCATT AAGCAAATTG ATTATTTTGT 120
 GGCTGGTATT GGCTCTGGCG GTACATTAC AGGTACGCAC GTTATTTAAA GCAACATCAC 180
 10 GTGCAATGTT ATGCCGTTGA GCCAGAAGGG TCCGTGTTAA ATGGAGGGCC AGCTCATGCA 240
 CATGACACTG AAGTATCGGT TCTGAGAAAT GGCCGATATT TTTAGAGAGA CGCTTGTA 300
 TGGGnTATTT ACGATTAAGA TcNAGATGCC TTTCCGAATG TCAAAGTTTG CTATAATGAn 360
 15 GGTGTAGTAA GCAG 374

(2) INFORMATION FOR SEQ ID NO: 2985:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 464 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2985:

GGAGCCACCA TTGGAGCAnG TTACGGTGGA AAAGATACGG nAAGGTTnGT ATGACTGTAn 60
 30 GTCTTGATA GAGTAACAAA CCTAATTTGT TAACTCTAGG CCCCATATGT CGCAGTACCA 120
 TCTGCATGTG TTGTTAcATT GTATGCATTT GTTTTACTTG GCTTCTTGtA TGTCGGGCGA 180
 GCTCCGTATG ACACTTGACC GTTTGCATGT GTTGTACGT TGTATGCATT TGTTTTCCTT 240
 35 GGCTTGTTTT GTGTTGGGCG AGCGCCATAT GATACTTGGC CGTTTCCATG TGTGTTACG 300
 TTATATGCGT TTGTTTTGCT TGGCTTGTTT TGTGTGGAC GAGCTCCGTA TGATACTTGG 360
 CCGTTTGCAT GTGTTGTTAC ATTGTATGCA TTCGTTTCGC TTGGCCTCCT GTATGTCGGA 420
 40 CGAGCTCCGT ATGATACTTG ACCATTGCAT GGGTGGTACG TnnG 464

(2) INFORMATION FOR SEQ ID NO: 2986:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2986:

AACTATTATA TTAACATACA ATGTAGGGAT GTGATGCGCG TGAAGTTTAG GGATAAAGAT 120
 AATCGTCAAG TTAATTTGAC ATTTAAAAAG GATAATGAGA TAGCAGATGG CAATCATGTG 180
 5 CTAGCTATTC CAACGTTTAA AAATCAATTG CTTTTTACCA AACATAATTT ACGGGGGATT 240
 GAATTTCTCG GTGGTAAAAG GGAACGCGGG GAAAAGTAGT GCTGGAAGCA GTTACACGTG 300
 AATTATATGA AGAAACAGGC GCCAAATTGA AAAATGnTTA TTACATAGCA CAATGTrCC 359

10 (2) INFORMATION FOR SEQ ID NO: 2987:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2987:

TAGAATTCTT CTAATGAATG AGCTTCTTTA GAATGATAAC CATAACGAAT TCCGTCAAAA 60
 CGAGAAAGGT TTGACGAAGC TTCTGATGAT GCAATCACGT AATATGATGG AATACCAAAT 120
 25 TTAGTATTTG GCAATGATAC TTCCTCAACG ACAGCACCTA AAGATTTTAA AGTTTCTACA 180
 GCGTTTTGAA CTGCTTCTTT TACGTCATCA GCTACACCTT CACCTAAGTA TTCTTTAGGT 240
 AATGCAACTT TTAATCCTTT AATATCTTTT ACCAATTTCA GATGTAAAGT CTACATCATC 300
 30 AACTGGTGCA CTTGTAGAGT CATTAAATC TGCACCAGAA ATAGCTTCTT AATACGGTTG 360
 CATTATCTTT TACAnTTCGG GTCATGGnCC CATTTTGGTC 400

35 (2) INFORMATION FOR SEQ ID NO: 2988:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2988:

45 ATTCAATCAT AATTATCAAT CCTTTGTGTT AAATTACTAT ATAAATAGTG TACGnATTTT 60
 CGAAATTTGT GATCATAAGT TTATTCAATG CTAAACAATA AGGTTGAGAC ATAATCGTAT 120
 CTCAACCTTG AAATTATTAT ACGTTGACGT CACTAGTCAT TCAGTTTTCT TAATGCTGCT 180
 50 ACAATCTCTT TTTTAGTATC TTGTACTTCA GAAGCTTGCT TAATCACTTT TGCAGGTGTA 240
 CCAGCAACAA CTGCACCAGC TGGTACATCT TGTGTCACAA TCGnGCCACT GGCAACAATA 300

nGATTATAAC CGTGGAG

377

(2) INFORMATION FOR SEQ ID NO: 2989:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2989:

CCAGGnACCT GGACACGCCG GGTCTTATCA TCAATAATAG TAGCATGACA AATCTACTAT	60
TTTTTCGCTA ATAAGTGGAT GTAATGCTAA TAATGTTGCT GTAGGGAAAC AGCCAGGATT	120
AGAAATGAGC TTCGTTCCAT TGTTATCAAA CGATTGCCAT TCTGAAATGC TGTAATAGT	180
CATGATTCAA ATCATCTTGT GCCTGCAGCA GTTCTTTTGT AATATGCTTC ATATATTTCA	240
CGnTTCTTAA TTCTAAATGC GCCAGATAAA TCGATAACAT GAATACCTTT TTCTACTAAG	300
GGAGGGATAC ATGTTTTTACT TACGGGTGCT GGTGTCGCAA AGAAAATTAC ATCAAn	356

(2) INFORMATION FOR SEQ ID NO: 2990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2990:

TCATTTTCCA AGTGAGACTC TGCTCTTGCT TTGGCTAATT TAGCTCTTTC AACATCAATT	60
TCTCTGTCAG TTTCTGCAGT CTGAACAATG ATTGAACTT TATCTTTTCT AACTTCAACA	120
AAGCCATCGC TTACAGCAAT ATATTCAGTT CCATCGTGGA AATTTCACCTT TTACAAAGCC	180
TGTTTTTAAA GCAGCTACAG TTGGGAATAT GTCCACTCAT GACACCTATC TCACCAGCTG	240
TTGTTTGCAT AACACGAGT TCAACATTAT CACGATTGTA AACAGAACCA TTAGGAGTGA	300
CAATATCTAG GTTTAAATGT CCATTATCCA TTCCnCCnGA ATTGGnTGA	349

(2) INFORMATION FOR SEQ ID NO: 2991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2991:

5 ATGCCACGT TCATGCCAAT AGCTGTCGTA GTCGCATTTT CACGTTCTAG TATTGCATTT 60
 TTTAAATGCG ATGTGTGCTC TACATAACGG CAAATTTTAA GTTTATGAAT CAACATATCA 120
 ATTGCTTCGT TTCGAGACAT GTCGTGGATC AGTAATTATC ATAGTTTGTT GATCAAAAAC 180
 10 ATGAGAAGGT TTATTGAGAT GTGAATGTTT CGCGGTGTTA TCTACATTGT CAACCTCTGT 240
 ATCATGTTGT GTAATATCTG TATCATGAAG TTGCGGTTGC GCTGGTGCAT CTACTGCTAT 300
 AACTGGTGTA TTGCGTTTTA ATAATAGTAC AGTAGTnCAT TGTnGACAAG ACTnACCGAC 360
 15 TTA 363

(2) INFORMATION FOR SEQ ID NO: 2992:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2992:

AAGTTTATTT TAAAATTCGT AATAAAAATA ATAACTCAT CGAACGATTT AATGGTCTAG 60
 30 GTTTCATAT CAACTATGAG TACATTAAAT TCAAATTCGA ATCACGTAAC GTAAAAGATC 120
 AAACAATCCC TGAATAAAC ACCAAGCAAA TACCCTACAG TACATCATTG GCATGTATTG 180
 TGGGTTTTTC TACTTTTTGT AAATATTGAn AATTATnAGT AGTTGTTTTT TACTATTAGG 240
 35 GCAGAATGCT TTACAATAAC ATGCAAGTGT CAATTAAGGG GAGCACTTGC ATAAATAGTA 300
 TAGGnGAGTG AGTAGTCCTG GCCATTTCTT GGAATTCCTT AATCGGCAC 349

(2) INFORMATION FOR SEQ ID NO: 2993:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2993:

50 TTTGTGCAAT AAGCGCTTTT TGTTGTTTTG CTTTGTGTC TAATTCATCT TTCGCAACAT 60
 CTTTAATTGT TGTATCTGCA GTAATACCTT GAATATCAGC AACTGCTTGA TCTTTAATTT 120
 GCGTAACATC ATTAGTTGTT TGTGCATTTA AGATATCTTG ATACGCTTTT TCTTTAGCTT 180

TTGCTTGATT TTGAGTTGTC ACAGCTTGAT CAACATCATT TTTAGCATTG ATTTAACCGC 300
 TGTGCTGGTT GCGGCTTGAA TTGAATCTTC CAGGCTTCGC TGACTACACA TACACAGTGA 360
 5 GnGnAATATT TCGGCTGAAC GCGTGCATGT GAAnGCTCT 399

(2) INFORMATION FOR SEQ ID NO: 2994:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2994:

AATGACAGGA ATCGTCGTTG CCTTTACTAA TTGACCAGTT AATTCAAAGT TAGGTCCGGA 60
 20 CATTTTGCCA TCTTTAGCAA TATCAGTATA TATAATGCCG CCAAGAGGTA TATCCGATAA 120
 CCGTCTCACA AACTAAATAA ATTTAACTCT GTGTCCTCTT CCCATCCGTT CACTTTAATA 180
 TCTTCTCCAT AGGCATCAAC AGATAAATAA ATGCGACCTG GAAATGTATG TGCCATCTCT 240
 25 TTAAGCCAAT CAGTATCTTG AATACCTTTC GTTCCAATA TGCAATAATT AATCCCTGCG 300
 GCAAAGTAGT CCATGATTTG TGACTT 326

(2) INFORMATION FOR SEQ ID NO: 2995:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2995:

CTAATGCCGA TGAGCAAAAC ACAAGCATTG GAAATTATTA AAAAAGTTAG GTACGTATAC 60
 AACATTGATT TTGATAAACC GAAGTTAGAA ATGTGGATTG ATGTATTAAG TCAAAATGGA 120
 45 GATTATCAAC CAACTGTAAA AGCGGTAGAT GTTTATATCA ACAGTAACAA CCCGTACCCG 180
 CCTAACTTAC CAGCAATCAT GCGTAAGGAA CCTAAAAAG TATCTATCGA GCCAGTAGAT 240
 AACGAAACCG CTACACACCA TGGGAAAATG CAGAATGACC CGAATTGTCA GACAAGGAAA 300
 50 ATAGCGCTAG ATAGTTCATG AATAGTTGGC AGATTGGGGC GAACGATGAT ACGnCATTCG 360
 ATTGAAGTCA TATCGTCGTA CTTAACACCG GACGTTnGAA 400

(2) INFORMATION FOR SEQ ID NO: 2996:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2996:

10 GAATGTAAGT GTCCCTTAAG CATAGTGCTC CCACCTTAAA TTTTGTACA TACTTTCATG 60
 GAATGTACGA GAAATTACAT CTAATTGTTG TTCACGTGTT AATTTAATGA AGTTAACAGC 120
 GTAACCAGAT ACACGGATGT TAACTGTGGG ATATTCTTCT GGATGTTCCA TTGCATCTAT 180
 15 TAATGTTTCA CGGTAAATA CGTTAATATT TAAGTGGTGA CCACATTGCA TTGCGTAACC 240
 ATCTAACATA CTAGTTAAGT ACGGTTTGAT CTCTGGnTCT TTACCTAATG ATTTGGnACG 300
 ATACTGATGT ATTGAAATAC CATCCTTACA GCATCGTAAG GGGTCCTAGC CACAGAACTT 360
 20 ATGAAGAAAT GCACCTTTTn GGCACnGGCA TGCATGGGGT 400

(2) INFORMATION FOR SEQ ID NO: 2997:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2997:

ATGATATTAA CCTGTTTACA AGATGGTTGA TACTTGCGCA TGAATTGTA ATCTTCAACA 60
 35 CCATATTATT ATGGTACATA CGAACTGAA AATGAATCCA TAGTTACTGA CAAAGAAAAA 120
 ATCTTAGTAT TAGGCTCTGG ACCAATTCGA ATCGGCCAAG GTGTAGAATT TGACTATGCG 180
 ACAGTTCACG CCGTTTGGGC AATTCAAAAA GCAGGGTACG AGGCGATAAT TGTGAATAAC 240
 40 AATCCAGAnA CAGTTTCAAC AGATTCTCAA TTTCTGACAA ATTATACTTT GAACCTTTAA 300
 CTGAnGAGGA TGTGATGAAT ATCATTAAAT TTGGA 335

45

(2) INFORMATION FOR SEQ ID NO: 2998:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2998:

GCAGTAACTA ACTTTTGTAC AAAAGGATCA TTTTATCAA CATAATGTGG TGGTTGGACT 120
 TTACCTAATT TCACTTCAAA GtATTGTTGA ATCTCATTTG CAAAACGATC CATAGCTTTT 180
 5 TCAAATTCAA ATCCTTCTGG GTAGCGTAAt TGATACCGAA AAGACCTGCG TTTTCATTAT 240
 CATATGTAAT AACACCAATG TTAGTTGTCA CGTCACCCAT GgACATCTGT ATGGgAATTT 300
 CATTCCCAnc TTTTTCACCA AAATCnGGAA TTGAAATAAG TGAGCGATTA CGAAATGGCG 360
 10 ACAAACGCCT GTGGCATTGA TnGAGCAAGA TThAAGG 397

(2) INFORMATION FOR SEQ ID NO: 2999:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2999:

AAAGCTGTGT TGGTAAAGAG TTTTGTGAT TTGGTACGCA ATACACGACA CGACTTGGCA 60
 25 TTCGTTTAGA AAAACATTT GAATACATCG ATACACCTCA TAAATTCAAA ATGGGTGTAT 120
 CAGGCTGCCC AAGAAGTTGT GTTGAATCAG GTGTTAAAGA TTTTGGTATT ATCTCAGTTG 180
 AAAATGGGAT TCCAAATCTA TATCGGTGGT AATGGTGGA CAGAAGTTGA AAAAGCTGAA 240
 30 TTTTAAACAA CTGTAGAAAC AGAAGATGAA GTAATCAAAT TATGTGGTGC TTTGATGCAA 300
 TATTGAnCGC GAAACAGGTA TATATGcGG AAAGAACCAG CGCCCAGGTT AAGAAGACCT 360
 GGATTGAAA ATGThAAAAG AAGTCCTTAC CTGGGCCCCG 400

(2) INFORMATION FOR SEQ ID NO: 3000:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3000:

AACGGTAGTA TTACAGAAAG CTCTACTTAT GGTGATAATG ATACACCAGC GCCACCAACT 60
 GACGAATTAG GTGGTAGTTG GACACTATGG AAAAATTTAG CGCGACAAAG TCCTGAATTT 120
 50 GGTAATCCTG ATAAGTTTTG CCAAATATT CCTAAAAAA GTTGGTTTGT TTCAGCAACT 180
 TCTACAACAA ACAATAAAGA GATTATCGAT ACAATAGAAA GTATTTGTAA ACGTGACCCA 240

AGTTTTACAA TCAATCGTCA GCMACAGTTT aAAGACCAaC CTGrAAATGA AaTATCTACA 360
 TGGATTATG CCTTATATyC AGATGTAAaC GGCGATTATA TTAAAAAGCC AATTACAGAA 420
 5 TGTAGTGGTA ATGAAATATG CCAAGnATGG CTGTATCnCT TnGGTGTATC AACTGACAAG 480
 ATTGAAGACT TAGCAAAACA TCGGTC 506

(2) INFORMATION FOR SEQ ID NO: 3001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3001:

20 ATTGATGGCA TCGAAAACT TTAATAAGAC AACAAGTTGA TGAGATATAT GTATATAGGT 60
 TTGGCATGGA TTTGATTGC AGTTAATTAG AATAGCTCAA TGCTATAAAT GTAAGTAGTT 120
 GATATGAAGA AACTAATGAA CTAAATGCAA GTATTGTCTA AAACAATCAT TTTATTGAAA 180
 25 TTTAGTAGAG CTGAAATTAA TATAACGTCG TTAATTGAAT AACGCTTATG TTATAAGAGC 240
 ACTCATACCA nACCATAATC ATCTATAGnT ATAACAATTC ACGTATAAGG GGCTGTGTTT 300
 GGCATAGCCC TTAGGTATAC ACCTAATTCC CATTAAAATA GTAGGGGnTT AAA 353
 30

(2) INFORMATION FOR SEQ ID NO: 3002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3002:

CAACAAAATG TCTATATGGT AAGTGGTAAA ACGAAAAATG ATGAAGACTA TTCATCAACT 60
 ATTTTATATA ACAACGAAAA AGAATTACAA AAAATTACTG ATGCTGCTAA AAAGCAAAAC 120
 45 GGTGTAAAAT TAACGATTAA AGAAGAAGAA AAACAAAGTG TCTTTGTGAG TATACTTTCA 180
 ACATTAAATC CAGTTGTAGT CATAGCGTTA TTATTCTTTC TCTTCCTAAG CCAAGCACAA 240
 GGTGGCGGTA GTGGCGGTG TATGATGAAC TTTGGTAAAT CTAAAGCAAA AATGTACGGT 300
 50 GATnAATAAA CGTCGTGTTC GTTCTCTGA TGTAGCCAGG GGCCAGATGn AGGAAAACCA 360
 AGGnTTAATT GGAAATTGTT GGTTCCTTGG AAAGGTAATG 400
 55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3003:

ATAACATCGG CACAGCAGCT AAAATAACCA TACCCAAAAT GANTGTATCT TTAAACGTGC 60
 ACCGTAAAGn CTTCCGACTA GCCATGTATA AGCTTTGGCA GCAGATAATT GCTTCGTTGT 120
 AATGAGTAAT CCTTGGACAA GCGCAATAAA CAACGTTTGC ATCGAAATAC CGATGATTAT 180
 GAGTGTGTGTC GGGCGTATTT GTCCTTTCGT TTGAAACACT AATAGTATCA TCATTGCAAC 240
 TCGCCACCT AATACTGCAA ATAGTGGAGT AAATGTATTG TTAAAGGCTG AAAATGCAAT 300
 AAAGACAACA GCACTTAAGC TAGCACCACC TGTGATACCG CTAATATCAG GTGAGGCCAA 360
 TGGnnTTTTT TTATACATT TGGCAACATT TAACCACTTC 400

(2) INFORMATION FOR SEQ ID NO: 3004:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3004:

CTAATAACAA ATGCGATGAT GATTAATACT AATTTACCTG CTGCTAATAC AGAATCTCCA 60
 AGGAATGAGA AGAATGGTTG ACGTTCAACT TCATTGTTTT TAAGACTGTA GATAATATCT 120
 TCTTTCTCTT CAACACTTAC TGGATTCAAC AAGCATGACA CAATAATCGC GTTAACGGAT 180
 ATTTAGTGGA ATTGCCGTTA GTACCAGTTC TCCTGGTACC ATTTGTACAT ACGCACCTAC 240
 AATAGCTCCC GATACAGAGC TCCATTGACA TCATTGCGAT TGTTAATACA CGCATTTTCAT 300
 TnCAGACGTT TTAGTTGCTC ACTTGGATAC GGGCTAANGC TTnCGTGAAT TGCC 354

(2) INFORMATION FOR SEQ ID NO: 3005:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGTCAGCTTA TTGAACAAGG GACACGTGAA TCAGTCTTGC ATCATCCAGA ACATGTTTTAT 60
 ACGAGATTTA TTATCAACGA AGAAGAAGAT TAATGATCAT TTAAACATG TGATGAGGGG 120
 5 TGATGTACAT GATTAAATT AAAGATGTTG AAAAGTCATA TCAAAGCGCA CATGTTTTTA 180
 AGCGTCGTCG AACACCTATC GTGAAAGGTG TGTCATTTGA GTGTCCAATC GGTGCGACGA 240
 TTGCGATTAT CGGAGAAAGT GGTACGGnTA AATCGACGTT TGAGTCCTAT GATATTAGGT 300
 10 ATTGAGGAAC CGGATAAAGG TTGTGTACCC TTAAATGATC CACCGATGCh TAAGAGGAAG 360
 TGAGCCGCCA CChATTGG 378

15 (2) INFORMATION FOR SEQ ID NO: 3006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3006:

25 ACnTTAGTTG GCCAAGCCTT TATCCGGAAT TATTGGGCCT TAAAGCCCCC TTAGGCGGTT 60
 TTTTAAGTCT GATGTGAAAg CCCCGGCTCA ACCGTGGAGG GTCATTGGAA ACTGGAAAAC 120
 TTGAGTGCAg AAGAGGAAAG TGAATTCCA TGTGTAGCGG TGAAATGCGC AGAGATATGG 180
 30 AGGAACACCA GTGGCGAAGG CGACTTTCTG GTCTGTAACT GACGCTGATG TGCgAAAGCG 240
 TGGGGATCAA ACAGGATTAG ATACCCTGST AGTCCACGCC GTAAACGATG AGTGCTAAGT 300
 GTTAGGGGGT TTCCGCCCCCT TAGTGCTGCC AnTAACGCAT TAAGCACTCC GCCTGGGGAG 360
 35 TACGACCGCA AGGTTGAAAC TCAAAGGAAT TGACGGGGaC CCGCACAAGC GGTGGAGCAT 420
 GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC TTGACATCCT TTGACAACTC 480
 40 TAGAGATAGA GCCCTThcTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC 540
 TCGTGTCTGT AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC 600
 ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG 660
 45 ACGTCAAATC ATCATGCCCC TTATGATTGG GGCTACACAC GTGCTACAAT GGACAATACA 720
 AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT 780
 AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACC 840
 50 GTGAATACGT TCCGGGTCT TGTACACACC GCGCGTCACA CCACGAGAGT TTGTAACACC 900
 CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG 960

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TATATTCGGA ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT 1080
 GAATGTTTTAT TTAACATTCA AAAAAATGGG CCTATAGCTC AGCTGGTTAG AGCGCACGCC 1140
 5 TGATAAGCGT GAGGTCGGTG GTTCGAGTCC ACTTAGGCCC ACCATTATTT GTACATTGAA 1200
 AACTAGATAA GTAAGTAAAA TATAGATTTT ACCAAGCAAA ACCGAGTGAA TAAAGAGTTT 1260
 TAAATAAGCT TGAATTCATA AGAAATAATC GCTAGTGTTT GAAAGAACAC TCACAAGATT 1320
 10 AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG CAGACAATGA GTTAAATTAT 1380
 TTTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAT AATGAAAACG AAGCCGTATG 1440
 TGAGCGTTTG ACTTATAAGn ATGnnnGATA TGTGTAATAT CCATATCTAA AGCTAGATCT 1500
 15 AAACTTTGTT CAAAATCTTC AATCGTCTGT TTCGGTAAAT GATACATTAA ATCTAACTG 1560
 ATTGATTAA TACCTGCGTT TTTAGCATTT AACACCGAAG TGTAAATATC TTCAGTATTG 1620
 20 TGCCTTCTAC CTAAACAGA CAATAACTCC GGCTTGAATG TTTGAACGCC CATTGAAATC 1680
 CTTTTTACTC CATATTTCTC TAATAGTTGG ACTTTCTCTT TAGTTAACTC ATCAGGATTT 1740
 GCTTCAAATG TATACTCGCC TGTGATTGTA AACGTATCAC GTATT 1785

25 (2) INFORMATION FOR SEQ ID NO: 3007:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3007:

35 TGCAAAAAAC ACAATAACGA TAAATGTTCC CATTGATCCT ACAGCATCGC GAACATTTTA 60
 CCTAAGTCTT TTGTATTTTT AATTTCTTTG CTAAATCC CATAAACTAA TCCAGGTACT 120
 40 AAAAAACGA CAAGAATAAT TAATCCGACA CCGTTAATTA ATGGCGATCG TCTAGTAAGC 180
 TGCCTGTTTT AGCATTCTT AAAAACTAT GTCAGGAATG GCTGTAATAA TTAATAAAAT 240
 AATTGnGCTA TGAACGATA TTTGCCATTT TAAAAATGT GCTCTTTGTC AGAATATGTG 300
 45 AGATGTnCTC ATGGCATCAT GCATTAACT GCATCATATT TTCCTAATCT AGGATAATGA 360

(2) INFORMATION FOR SEQ ID NO: 3008:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3008:

TTGCCTTCAA ACACATACTT GTAGTCGGAT GATCACCTGT TCCAAAAGnC ATACCTGGGT 60
 5 CGAGCTCAAT GCAAAGCTCT TCATCCGCTT CTTTAGCATA TGTTTCCCAA CTAGGAACTA 120
 TTGTGAACTT CTTGACGCT CGGGAATGGA TGGAAATAGT TTTTCCATTC ATTTTCCCAA 180
 TCCGTCTCTG CAATAATTTG CTCACTGAAT TGAACGTTAT GTTGATCAAG TTCATCTAAA 240
 10 TTTAATAACT CATCTTTGAA TTTGCTGTCG CAACTGTATC ATCATAAGTG CATTTCAGTA 300
 AAATAGGCTT nGCAAnCTTA CTCCCTTATC TGGGATAAAG CCTCGGTTTT 350

(2) INFORMATION FOR SEQ ID NO: 3009:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3009:

25 TCTTATATCA CCAGGAATTA ACACTGCCTT TTGACCACTT TCTTCAATCA CTTGGCGTAC 60
 TTCTTGTCGA TCTTGTCTT CACTCGGAAG ATAGTTAATC GCTACATCTG CACCTTCTTT 120
 AGCATACGCA ATTGCTGCTG CACGCCCTAT TGCTGAGTCA CCACCTGTGA CTAAtATTTT 180
 30 ATAGCCTTGT AAGCGTTGAT GACCTTGGA AGACGTTTCG CCACAATCGG GTGCTGGCGT 240
 CATTTCAGAT TGTAAACCCG GTACCTCTTG TTCTTGTTTT TCaTAATCCG TTGTTTTAAA 300
 TTTTGTTcNa GGaTCTkGAG CkGCCaTTTT TtGACaYctC CGTATnCGCT TAATGGGTAT 360
 35 CATTTACCCC AATCTTCCTA AGG 383

(2) INFORMATION FOR SEQ ID NO: 3010:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3010:

TAATTCAACG GGAATTTTCC CTTTGAAGTT AACATAACGG TAGGCTGCTT TAACAGCTTC 60
 50 ATCATCGGGC GCTTCGACAT CTTCTAATTC ATATGCAATG CCCAATGTTT TCCACTTATG 120
 AACACCTAAC TGATGATATG GCAGAATTTT AAACTTTTCG ACGTTATCAA GAGAATTAAT 180

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TGTCGAATCC ATACCAGGTG GTTTCATATC TGACAGTTTG CGCGCGAAGT TAAAGGATGT 300
 GTGTATTAGG GCTTTCCCGG TCCATCCAAA TAnGGTTGGT CCATTAAATCC ATAAGGTTTT 360
 5 AnAATCnAAA TAATAATCCA GTCCGGTA 388

(2) INFORMATION FOR SEQ ID NO: 3011:

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3011:

ACTGCTGTAA CGTCAGTTGA TCTTTTCATT CTTGGTTTAA TTTCTGAGAC GTTACTTGGT 60
 20 TGnGChAnGC CACCAATTGC CATACCGACA GATTGGAAGA ACAATGCATC AGTTCCACCA 120
 ACACCAAAGA TGTCAACCAAG TACAACGAAA CCTACATATC CAACTGTAGA TACAATTAAA 180
 ATACCCATTG CTTTTTTTAAA TTCAGGATTA TCTGATTGAC GTnCATTTTT AGCTTTAAGT 240
 25 GAAGTAAGTG CTACACCACT AACTAATAAT ATCATGGCGA TTAAACCAAA GATAATTGA 300
 GTCATTGAAG ACCATTCACC TAAAAGATA ACGCTGGAAT AATGGTGTAC CCAACTAATT 360
 GGCATACCTG GTAGGAACT GGGCATAGGT ATTTGGATAC 400

30 (2) INFORMATION FOR SEQ ID NO: 3012:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3012:

TTATCGGATT CGTTAATACT GGCGGTTTAC GCAATAGTTT AGATGTAGAT GATAACAATG 60
 TGCCTATTAA ATTTAAAGAA GAGTTCGAAC CTAGAAAGTT TGTTTTCACT AACGGCGAAA 120
 45 TTAAATACAA TAGCAATTC GAAAAAGAAG ACGTACCGAA TGCATCAAAC CAACAAAGTG 180
 CGTCAGATTT AAGTGATGAG GAACTTCGCG GAATGGTTGC GAGTATGCAA ATGCAGGTGG 240
 CACAGTAAAC GTATTAACAA TGGGATTAGC TCAACCAAAC GCTATGTTAA CACCACAGTT 300
 50 GACTGACTGG AACTACCAA ACCAGTACTG AGGGGnCGTT AATAATGAGT GTTTCCACTT 360
 AAGCATAAAC TTTTGTGGT CTTAAACGGC ATTAGTGTGC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3013:

10 GGCTGTAATG AAAATCCAAA AGCCAAGCTT ATTTAATTCG CCTTCATGTG TGCCTGAATC 60
 AATAGTGTTT GTATCATGAC TCATGACTTA CAGCCTCCCT TTCTTTAATA CGCGCTTCTC 120
 15 TTAATCTAGC TTCAGTTTCT GCAACTTCAG CAGCAGGGAT ATGATATCCG TGATCGATTT 180
 GGAAACTGCG ATAAATCATA GTACCAAAAA TACCGAATAA ACAAATTAAT GCTGGAATTA 240
 CAGTTTCGAA AATTAAGAAG AAACCGCCGA TAGTCATAAA GATACCAATC CAGAATCCAA 300
 20 CAGGAGTAAT GGTGTCGCAT ATGGATGGCC TTGGnAATAA TGGGTTGnCC TAAGTAATGG 360
 CCGACCAAGG TCCTTTCCAn ATCCACCAA 389

(2) INFORMATION FOR SEQ ID NO: 3014:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3014:

35 AATCGCTTCG GTTAAGTGT CTAACCATTC GTAATAACA TGTGTATGAT CAAGCTGAGC 60
 TTTAATTTTT TGTGCCTCTT GTGTTTCAGC TTCAGTTAAA TCACTGCTTT CAAGTAATGG 120
 ATTGATAATA GCTTGAGCAT CTTTTACTGC TTCGACATTG ATGTCAATTT CACGCTGGAA 180
 40 TTTTTTAGTG AAAAAGTTTC GGAAAAAGAT GAAAAAGTCT TTCTCGGCGA TAAATGTGT 240
 TTGCGGCTCC TCTCGTAAAT TGTGGTTAAC AATATCAAAT TCCTGCAATT CCTAACGCAG 300
 CACTCATACT nGTTGnCAT TGCAATGATG ACGCATTAC AGGGCAACTG CTCAACACAT 360
 45 GGGCATAAAG TTCCACACTC ATAGGCAACA ATCATGGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3015:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3015:

5 ncCTATCTCT GGTGAGAGT CTTTGAGCTG AAAAATGTGA CACACAAAAT TGCAATGGnA 60
 TCAACAAATG TTTCCCATG TGGATGGTCT TGAATAAGTA TTTGGTGTTC AACTTGGTGA 120
 TTTGCCATGA CTAATACCAT GTCAATTTGTA CTTGTATCGC CATCAACAGT AATCATATTA 180
 AATGTATGGT CAGTCGAAGA TTTTAATAAT TGATGAAGTG TATTCGATTC AATCGATGCA 240
 10 TCGGTTGTTA TAAAAGCAAG CATGGTAGCC ATATTGGGT GAATCATACC TGAACCTTTG 300
 GTGCTACCAC CAATTGTAAC GGTTTACCAT CGATTTTAGT GATACAGCGA TATGTTTTGT 360
 ACAGGTATCA GTGTTAAAA 379

(2) INFORMATION FOR SEQ ID NO: 3016:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3016:

CATATAAATT GCTAACGTGC CACCATTAC TAAGGAATTG ACATCCACTT CATTTTCTTC 60
 TGAATCTTTA AAGTGACCTG TAGAAAATGT CACACTTTTA GCAACTGTAC GCATTGTCAA 120
 30 ACCTGTCTGC ATAGTAGCAA CTGCTGCGCT CGCTGATGTC ACCCCTGGTA CAATTTCAAA 180
 CGCAATATGA TGTTCAATTA GTATGTCGAC TTCTTCTTGC ACACGACCAA ATATCGCTGG 240
 ATCGCCAACT TTAAGTCTAA CAACCTTGTT ATATCGACGC GTGCTTCCAC GATACAGTCA 300
 35 TTATTTTTCT GCGGAAAAT GTTTGGAAC GGCTTTTACC AACnGGTAA TTCAGAGGCA 360
 ATCGCAATGn AAATTACGn TCACnAACGG TCATTGGATG 400

(2) INFORMATION FOR SEQ ID NO: 3017:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3017:

50 CCTTTTTCTC TTCTTTCATA TCTGCAAACG TGCATCAATT TTAGGATCTA AATCTCCAAA 60
 TGCTTCTGCA ACTGGTTCAG AGCGTTCATA ATACATACGA ACTTTTGGAT ATAACGCTTT 120

TCATTTAACT GTTCATCAGT ATATTTATCA TATGCTTTTG TTGCTTGTTT TAATTCTGCT 240
 TTAACACCAT CATCTTTTTT CGATGTCTTT GAATCATCCT TCTTACTATC GTCGTTCCCC 300
 5 ACATGCAGCA 310

(2) INFORMATION FOR SEQ ID NO: 3018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3018:

TCGCTTTGTA AATTCTGGAA CAAAGnCAGT CATGACAACA ATTCGTGTTG CACGTGCATA 60
 20 TACTAAAAGA AATAAATTA TAAATTTGC TGGATCTTAT CATGGCCATT CTGATTTAGT 120
 ATTGGTTGCA GCAGGTAGCG GCCCATCTCA GCTCGGTTCT CCAGACTCAG CTGGTGTTC 180
 AGAAAGCGTC GCACGTGGAA GTCATTACTG TACCTTTCAA TGATATTAAC GCCTATAAAG 240
 25 AAGCAATTGG AATTTTGGGG TGATGAAATT GCCGCAGTAT TAGTAGAACC AATTGTTGGT 300
 GAACTTTGGG AATGGnnAAT GCCTCAACCT GGGATTTTTA GGAAGAGGGT 350

(2) INFORMATION FOR SEQ ID NO: 3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3019:

ATATCATGTG CCAGTGAAAG CGGCACTGGn CGGATATGGC GCACATATGG ACATTATGAA 60
 40 AGAGTACCAA TTAATCATTT TAGCGCCACA AGTTGCGTCT AACTATGAAG ATATTAAGCA 120
 AGATACAGAT AGATTAGGTA TTAAATTAGC GArGACTCAA GGTGCTGAAT ATATCAAATT 180
 45 GACACGrGAT GGCCAAGCAG CCCTTGATTT CGTTCAACAA CAATTTGAAA ATTAAGAATA 240
 GGAGTTTTTC ATATGACTAA AACATTACCT GAAGGATTTT ATTTTGGTG GAGCAACAGC 300
 AGCATATCAA GCAGGAAGGT GCGACCAAAT TACGGGATGG GTTAAAGGTC GCGTGCATTG 360
 50 GGGATACGGT ATTTTAGGAA GGAAACTTA TTTGGTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3020:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3020:

10 ACGTTCGTCT TACGTTTAAC GCCATACGGT GTATTAGCAA TTATGGnCCA ACACATTATC 60
 GACAAGTGAC TTTGGCGCCA TTTGGACTTT AGGAAAAATT CTTAATCGCA TCGTACGCTG 120
 CATTAAATAC GATGTATATC ATTCACTTAA TTATTTTAAG CCTGTTAGGT ATTAGCCCAA 180
 15 TTCGCTATGT TAAAAAGACT TTGGAAGTAT TAATCTTTGC ATTACATCA CGCTCAAGCG 240
 CGGGTGCCTT ACCAATGAAT GTACCAACAC CAACCAGACG TCTAGGCGTG CCAGAAGGTA 300
 ATGnCAATTT CGCTGCGACA TTTGGAATGG CGATTGGACC AAATGGGTGG GCAAGnAATT 360
 20 A 361

(2) INFORMATION FOR SEQ ID NO: 3021:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3021:

CAATGACCAT GACCAATTGA TTTGGAACAA TGATTGACAT TGGAGCTATG CATCAAGTTT 60
 35 GTCTTTAAGA CTAATAAACC CACGAACCAT GTTAACCCCG TGGTGACCA TCACCAATTG 120
 nCTCGATCTA ATTCAGTTAA TTCAGATTCA TGTTTTTTAA ACGTTTCTTC TAAATTTAAT 180
 AAACGTGnCT TTCATATCAT TCACTTTCAT TTGTGnCCAC CTCATAAATG TATATTATCA 240
 40 TATCACTCT TATTAAAGTA TGA CTGTTGT TGGTGCTAAA AATGCTCCAA ATATTCGGTT 300
 TATTAGGCAC GATAGTTATA GAAAAACCTG ACAGTCTAAA GATGTCATAT AATCAC 356

(2) INFORMATION FOR SEQ ID NO: 3022:

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(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3022:

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GTGTTTGGTC CAATATCCAT ACCTTCTTGG nTCTGCTGGA ATTGAATCAG ATGGTACTAC 120
 AGTGATTTTG GCATCATTAG nAAAATTCTT TAGTCAACTT TAGTGTCTAC TGGTAATACA 180
 5 ATTTTATCAC CATGTTTTTC TAATAAATCT TTTGCGAGTC GGATTTTATC TTCTTCTAAT 240
 AATGAAATAC CAATTTCTTT ACCTTGCGCT TTTAAGAAAG TATAAGCCAT ACCTCCGCCG 300
 ATGATAATTT TATCAGCTAT GTTAACTAAT AA 332

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(2) INFORMATION FOR SEQ ID NO: 3023:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3023:

AAAGGTATTC CACAAGAATT AGCTTTGCAA AAATGCCAAA GCAAACAGAA GATGGnACAA 60
 TTTAAAGTgn CCTACAATCA TGAATGAGGA GGACGCGTAA GATGAGCATT CGCTACGAAT 120
 25 CGGTTGAGAA TTTATTAACT TTAATAAAAG ACAAAAAAAT CAAACCATCT GATGTTGTTA 180
 AAGATATATA TGATGCAATT GAAGAGACTG ATCCAACAAT TAAGTCTTTC TAGCGCTGGA 240
 TAAAGAnAAT GCAATCAAAA AAGCGCAAGA ATTGGATGAA TTACAGGCAA AAGATCAAT 300
 30 GGATGGCCAA T 311

(2) INFORMATION FOR SEQ ID NO: 3024:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3024:

ATTAGACATT ACAAGGTGCA GTACGTGCAA CATATTAGAC ATATTGAATT AAGTGGTCAT 60
 45 GnAAGGTATT GACAGTTAAA AAAGTTGAAC AATTAGAAGA AATCGAGGGC TTAATATTAC 120
 CTGGTGGCGA GTCTACAACG TTACGTCGAT TAATGAATTT ATATGGATTT AAAGAGGCTT 180
 TACAAAATTC AACTTTACCT ATGTTTGGTA CATGCGCnGA TTAATAGTTC TAGCGCAAGA 240
 50 TATAGTTGGT GAAGAAGGAT ACCTTAACAA GTTGAATATT ACTGTACAAC GAAACTCATT 300
 CGGTAGACAA GTTGACAGC 319

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3025:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60
 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTGGAATAA AGGTAGCATA 120
 TGTAATTGTT TGTGTTTACG TATTTCTGGT GGTAAGTTCC GTGAAACCCA ATGTCTATAT 180
 TCCCATTTAA TACGCTATTT ATAATGTGT CATGTTCTAA TAAGCTCGGT ATGACATGTG 240
 TATCATTTTG TAAAATGAAC GTTTGGATAA GGGGAGTAA CATGTGGGAT ACGTCACTCT 300
 CATCAAGCCA TG TAGATACn 320

(2) INFORMATION FOR SEQ ID NO: 3026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3026:

TCTCAACAAA TGCATCCAGT ACTTAAATTG GCATTATAGT AATTTAAGnA CAATATATCA 60
 ATATTTCTCC TTATCCAGCA ACAGCAAATT TATTGGTAAG GTGTACGATT GAACCTTTAG 120
 TCAATGAAGC AGGTACATTT GGATTGGCCA GGTGGATTTA CTTCAACTGA GCGCTTTGTG 180
 AGAATGGGCA TTTATGAAAG CAAACATTGC TCAAACAAT GATAAAGAAA TGGATTTAAT 240
 GAATGCATTT TATTTATTAG ATGCGGTAAA TATACCGATT GGAATTGTAC GTCCGCATGA 300
 TGCTGACAAT CACTATACGA TGTATCCA 328

(2) INFORMATION FOR SEQ ID NO: 3027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3027:

ATTGAAAATA TGTGTTCTnT GTAAAATTTT AATCGTTCGC CACGATGCTG TTGATAAAAA 120
 TTCAAAACT GGAGTTGATC TTCTAGTTCA ACATAATCAT CGTAATTAGA CATGTAACCT 180
 5 TTGATTAAGA TTTCAAGTAC ATGATCTTCG ATAGTATTGn TTTTAACTTG TTGTTGAGCC 240
 GCTATATCTT CCATCGTGGA ATTGTTCAAG CAATTTTGTA TAAGTAATAT AAGTTTCGATT 300
 TAATGAATGT AGGTTTCATT AT 322

(2) INFORMATION FOR SEQ ID NO: 3028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3028:

CAAGAATCTT ATACTTATCA AAATTATAC TGTGAAGCGA GTCTATTGGC TAAAAGACTC 60
 AAGGCTTATC AACAACTCG TGTGGGCTA TACATAGATA ATTCGATTCA ATCGATCATT 120
 25 TTAATACATG CATGTTGGTT GGCAATATT GAAATTGCGA TGATTAATAC AAGGnTGACA 180
 CCTAATGAGA TGACGAATCA GATGAAGTCA ATCGATGTAC AATTGATTTT CTGTACCTTG 240
 CCACTGGAAT TACGAGGGTT TCAAATTGTA TCGCTGGATG ATATTGAATT CGCCnCCGG 300
 30 GcnTATTACA ACG 313

(2) INFORMATION FOR SEQ ID NO: 3029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3029:

CTTCCAAAGA AAAGACCACA GTTTTTGACG CATCAATATG GTGCAATTTT AGAGACACTG 60
 45 TAGTTGCAGA AGATGGTTCA GTTGGACTTT GAAGACAATC GTTATACAGA AACACGCGTG 120
 CCGCTTATCC AATTAATCAC ATTGACAATA TTGTAGTACC ATCTAAAGCA GCACATCCAA 180
 ATACAATTAT TTTCTTAACT GCGGATGCAT TTGGTGTAT TCCACCGATT TCAAAGTTAA 240
 50 ATAAGACCAG CAATGTATCA TTTCTTGAGT GGTTCAC TTC TAAATAGCTG GncAGAGCGT 300
 GGTGTGACAG ACCTGACCAT CATCTCAACA TGTTCCGnGCA CCGTCTTCCG TACATCnACT 360

(2) INFORMATION FOR SEQ ID NO: 3030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3030:

TGATGGATTG GCTAGCAGGT GTTTACATTA ACTCATTAAA TGTTATTCAC TACATGCACG 60
 ATAAATACAG CTATGAACGT ATTGAAATGG CATTACATGA TACAGAAATT GTACGTACAA 120
 TGGCAACAGG TATCGCTGGT TTATCAGTAG CAGCTGACTC ATTATCTGCA ATTAAATATG 180
 CACAAGTTAA ACCAATTCGT AACGAnGAAG GTCTTGTAGT AGACTTTGAn ATCGAGGCCA 240
 CTTCCCTAAA TACGGTAACA ATGACGACCG TGTAGATGAT ATTGCAGTTG ATTTAGTAGA 300
 CGCTTCATGA CTAATTACGT GGTCAITAAA CATATCGTGA TTCAGACCTT CCATGGGnGT 360
 ATTACCATTA CTTCAACGTG GTnTCGGGTA GAAACTGGGT 400

(2) INFORMATION FOR SEQ ID NO: 3031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3031:

nGCGTTTAAT CACATCTTTT TGATAATGTT CCCTTACCAT TTCTTCATGT GCATCTGCAT 60
 AGTCTTTTCC AAATGGCAAA CTAACTGAT ATGCAACTTT TAAATAGGCA TCTATATGCG 120
 ACTCGTCAAC GATGGCAATT TCAACGTcna GTTACGCGGA CAAATTGGCA AGCGCATCAC 180
 TTTCTATGGC ATACAATTCC ATAATACCTA GTTCAAAATT CATATCTTTA AAACATAGCC 240
 ATCCAATGGA TTATCAAGTT GTTCATTTTC CGGGAAAACT nAAACGCATA AATGATTTGG 300
 AACCTTGATT TGTATGTGA 319

(2) INFORMATION FOR SEQ ID NO: 3032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3032:

5 AAGAAGTGGC AATTATGATT GATGCTCTAG CTGACAAAGG GAAAAAAGCA TTAGAAGCAT 60
 TATCTAAAAA GTCACAAGAA GAAATTGATC ATATTGTTCA TCAAATGAGC TTAGCAGCTG 120
 TTGATCAACA TATGGTGCTA GCAAAATTAG CACATGAAGA AACTGGAAGA GGTATATACG 180
 10 AAGATAAAGC GATTAAAAAT TTATACGCTT CTGAATATAT ATGGAATTCA ATAAAGACA 240
 ATAAGACAGT AGGGATTATT GGTGAAGATA AAGAAAAAGG ATTAACGTAT GTAGCGGAAC 300
 CAATTGGTGT TATTTGTGGT GTTACCGCCC AACCACCAA TCCCTACGTC CGACCACCTA 360
 15 TTTTAAAGC CGATGGATTT GCCATTAAAG ACnGGGAATC 400

(2) INFORMATION FOR SEQ ID NO: 3033:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3033:

TAGCGGTAAT CGAAATTGGG GACTAAATTT CGCAAAGCG GGTGCGACGA TATCAGAAGA 60
 30 GTATAATGTC CCTTTATTAA TGAAGTTTGA GTTACATGGA AAAACAAAG ACGTTATTGA 120
 ATTTAAGAAC AAGGTGGGTA ATTTTAATGA AAACCATGGA AGAGAAAAAG TACAATCATA 180
 TTGAATTAAA TAATGAGGTC ACTAAACGAG AGAAGATGGA TTCTTTAGTT TAGAAAAnGA 240
 35 CCnGAGCTTT AGTAGCTTAT TTAGAGGAGT AAAnGACAAA ACATCTTCTT CGACACTGAA 300
 TCG 303

(2) INFORMATION FOR SEQ ID NO: 3034:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3034:

50 CTnCGCTATT TTGTAGGACA TCTTCTAAAG TGCTAGGnGA AGAGATTATA GAATAGGCAC 60
 TATCAATACC GAAATCGTAA ACATGTTGAT AATTTTCGCC TAGACTGCCA CAAATCGCGA 120
 TGACAGGAAT ATGATATTGT TTTGCAGCTA ACGCAACGCC TGACGGGTGT TTTACCAAAG 180

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TGATGAAAAT CTGTAATGTC AAAGACGGAC ATCAATGACT TTTGTTGAAA GTTGTCTCAC 300
 AAAACGnTAA TGAATGCTGC GGCCCATGAC CGGCCAGCTG 340

(2) INFORMATION FOR SEQ ID NO: 3035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3035:

AAAGAACATG GTGTAGCAAT AGTCTCTGGA GGTGGAAGCG GACATGAACC TGCGCATGCC 60
 GGTTTTGTG CAGAAGGTAT GCTAGATGCA GCGGTTTGTG GCGAGTATTT ACATCACCTA 120
 CACCTGATAA AATATTAGAA GCTATTAAAG CAGTAGATAC TGGTGATGGT GTATTACTAG 180
 TTGTAAAAAA CTATGCAGGT GACGTGATGA ATTTGCAAAT GGCACAAGAG CTTCCAGAAA 240
 TGGAAGGTAT AAATGTTCAA ACTGTTATTG TTCGTGnCGn CATTGCTGTG ACAAACGnGT 300
 ACA 303

(2) INFORMATION FOR SEQ ID NO: 3036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3036:

GGGGAAAGTA AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT 60
 TATTGTAAAC TTTTCATTTT TTAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA 120
 CGAAAGGAAG GAAAAAATGA CnACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT 180
 TATCGCTAGT TTAnGATTGG TACCGGTAAT TCCACTACCA TTGnCTTCAG TACCAATTGT 240
 ACTTCAAAC AGTGGTATTT CTTAGCAGGG GCGATTTTAG GACGTAAATA TGGCACATTA 300
 AGTGTTATCG TCTTT 315

(2) INFORMATION FOR SEQ ID NO: 3037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3037:

5 GCACCAATTG ACGAAGGAAT ACCGAATCCC ATTGTTCCCTA AACCACCGCT TGTAACCCAT 60
 TGTCCGTGAT TTTTAAATGG ATAAAATTGA GCTGCCACACA TTTGATGTTG TCCCACGTCT 120
 GTAGTAACAA TTGCTTCACC ATTTGTAATT TTGCCGATAT ATTCGATTGT TTGTTGTGGC 180
 10 TTACAAAATA CTTGATCTTC TTCACCAAGT TTAAATGGGT GTTTCTGCTT ATTATTTTGA 240
 CAATGTTTTAA CCCAGTCACT GTGTTCTATA GTCTCAACAT TTTTATCATT TAAACCTCC 300
 AAAAAACCTT TACAGCCnG CAAAAAACC 330

15 (2) INFORMATION FOR SEQ ID NO: 3038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3038:

GTGAGTCCAC ATAATAACTT TGACGTCCTG TTAATGTTCT AAAAGGTACT AGACGTTCTA 60
 TATTCGTTGT AAATGGTGAA TATCGTCGAC CTTGTTTATT TGAACCTGGG AATACTGCTG 120
 30 TCGGTATTAC TTCTCGTGGT TGTGAAGTTA TATTTAAAAA CGAAATTTTC TCAGCAGCGC 180
 TGTGCTAGA AATATCTTTT AACGGCATT CAGTTTGTTT TCGAGATCT TCATATGGAT 240
 TTTTGTGnAT AATThACCAT TCGTAGCAGA TGGAAATACT TGAGTATnGG CATCAGCGAC 300
 35 ATTGACGTGC TGTATCAATA CGTGGACGAT TCGC 334

(2) INFORMATION FOR SEQ ID NO: 3039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3039:

GGTCTGATCG TGGTGAATGA AAAAGGTTCT TCTCTGTAAT GAATTATCTC TTACCGATGC 60
 50 AAGATATTAT GAGCATGCAT TGCTCAGCAA ACGTTGGTGA AAAAGGCGAT GTTGCAATTAT 120
 TCTTTGGTCT ATCTGGCACT GGTAAAACAA CCTTTATCGG CTGACCCACA CCGTAAACTA 180

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ATGCAAAAGC AATTAACTCTT TCCAAAGAAA AAGAnCCACA GntTTTTGGA CGCATTCAAA 300
 TATGGTGCAn TTTTAGAGAA CACTGTA 327

5 (2) INFORMATION FOR SEQ ID NO: 3040:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3040:

GTGATATTCA CGAnCGTTAT TTTCAATATT TGATAAGTAG AAAnTATGAC GATCTTCATG 60
 AACAGCATCT TGTTCCTCGT CAAATTCAAC GTCATCAAAA CGTTTGAAGA ATGTTTCATA 120
 20 TGCATCAACA GATACTTCAG TACGGTTATT TAATAATGCT TTATGTGCAG CTTGGATCTA 180
 AATGATCTTT GTAGCCTTCA ACTnAATGTC GCACTATAAA ATTCACCAAC TGAACCTGAG 240
 CCATAACTGA ATAAACCGAT TGTTTCCACC AGCTTGTGAA TCTCGATTTT CAAGTGAATG 300
 25 ATATT 305

(2) INFORMATION FOR SEQ ID NO: 3041:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3041:

GTTGTGTACC TTAAATGATC AACCGATGCA TAAGAAGAAA GTGAGACGTC ATCAAATTGG 60
 40 TGCTGTATTT CAAGATTATA CGTCATCATT ACATCCATTT CAGACTGTTA GAGAAATCTT 120
 ATTTGAAGTG ATGTGTCAAT GTGATGGACA ACCTAAAGAA GTTATGGGAA GTCCAAGCAA 180
 TTACATTGTT GGAAGAAGTC GGTCTATCTA AGGCATACAT GGATAAATAT CCTAATATGT 240
 45 TATCAGGTGG AGAGGCGCAA CGTnTGCAAT nTGCGCGTGC AATATGTATT GAACCCnGAA 300
 ATATATTTTG TTTGGAT 317

(2) INFORMATION FOR SEQ ID NO: 3042:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3042:

5 AATCTTCGAA AAATAATGCA ATGCAGATTC CGAAAAAAC AATATGATAG AAACACCTCA 60
 ATTAAATACA ACGGCTAATG ATACATCTGA TATTAGTGCA AACACAAACA GTGCGAATGT 120
 AGATAGCACA ACAAACCAA TGTCTACACA AACGAGCAAT ACCACTACAA CAGAGCCAGC 180
 10 TTCAACAAAT GAAACACCTC AACCGACGGC nATTA AAAAT CAAGCAACTG CTGCAAAAAT 240
 GCAAGTTCAA ACTGTTCTC AAGAAGCAAT TCTCAAGTAG GTTATTAAAA CACGGATGGT 300
 GCTAATAGCT TnGCAACAAC GTGGGCTTTA AAATTCTCCA ACTTTAGTTT T 351

15 (2) INFORMATION FOR SEQ ID NO: 3043:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3043:

ACGnCCCTTAC TGGnTACTTG GTTGATAAGT GTTAATCCAA ATGACGTCCT GCTACGTACA 60
 GCTTTACGAA TATTTAATGC ACGTGTGATA TTTTGAGAAA ATACACCGCC TGGCTAAACC 120
 30 ATACTCAGAA TCATTAGCTA TATCAATTGC TTCTTGATCG TCCTTCACCT TAATCACTGT 180
 TAACACTGGT CCAAATATTT CTTCTGTGC TAATTTGTGA TGATTGTCTG GCACnCAATT 240
 AATGTCGGCT CAAAGAAGAA CCCTTTATCT AATCCATTTT CAGTTAAGCG ATGACCGCCT 300
 35 GCTAAAATTT GTGCATCCG 319

(2) INFORMATION FOR SEQ ID NO: 3044:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3044:

GTCAATAAT CTAACATTTG TGTATCTGT TAATTAAGTG GntTTTACCT TAATTTGTTA 60
 50 CATTGnTCTG TATTAAATCT TTTTGTAACC ATTGGTTACT TTTTCAGGTG GAATTTCAAC 120
 ACCCATGTCA CCACGTGnCA ACCATTAAAC CATCAGACAC TTCAAGAATT TCCGCAATAT 180

AAATTCACGA ATTTCTAAAA CATCACTAGG TACGACGTAC GAAACTTGCT GCAATGAAGT 300
 CAACATTTTC TTTAATACCG AAACGGATAT CTTCAGCATC TT 342

5 (2) INFORMATION FOR SEQ ID NO: 3045:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3045:

TAATATCATG TTGTGCTTTT AGTGCTTCGG CAATTTGTTT TGTACTTACT GACCCAAACA 60
 ATTTACCACC TTCACCAGTT TTTGCTGATA CTTCAACTTC AATGTTTGAT AACGTTTCTT 120
 20 TTAATGCTTT ACATCTTCAA TTTCTTGTTG GCGTTCTTGT TTTGCACGTT TTTTCTGTAA 180
 CTCTAATTGT TTAAGGTTAC CTGGTGTGTC TTCTACAGCA TAATTCTTTT TCAATAAGAA 240
 GTTATTTGGC ATAACCTACT GGTACTTCTT TAACTTCACC TTTTTTACCT TTACCTTTAC 300
 25 CTTTAACAnC TGTGTAAAAA TTACTTTTCAT GCAGnTCACT CCTACTTAAA TGTTCGGTAA 360
 TGCCTGTTGT AATGTGCCAA CGCCnCTCGA CGTGACACCT 400

30 (2) INFORMATION FOR SEQ ID NO: 3046:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3046:

40 AATCACTGTT TCATTACTTG TTCCAAATCT GnATTCAAAC TATTGTTCAA AGATTCTAAT 60
 TCCGCTTTAT TTTTATCTTT AATCGCTTTT GTCATCGCAG CATCTTTAGn CATCGACTTn 120
 CTGTTGCAAT AGTTTAATTT TAGAACCCGC ATCTTTACTA GCCAATTTCT CTTCATAAGC 180
 45 AATTAATGAC TTCGTTAATT GCGAAAGTGT ATCTTTTTGA TTATCATTCG CTTTTGCATC 240
 TTCAAGCTTT CTCACATCTG CATTTGACAG CATTACTTGC ACTATTATCT TCAAGCGATA 300
 50 ATTTCT 306

(2) INFORMATION FOR SEQ ID NO: 3047:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3047:

ATGGATCATA TTAGCACGTA AAAGAAAATT CTGTTTCATTA TGAAGAAGTG CCAGAnGTTG	60
AATTTAAACG CACATATGTA TGTGAAGATA TGTCTAAATG TATTTGTTTA TACAACGCAC	120
CTGATGAAGA AGCGGTAnTC GCGCGCGCAA AGCAGTTGAT ACACCGATTG ATGGCATCGA	180
AAAACTTTAA TAAGACAACA AGTTGATGAG ATATATGTAT ATAGGTTTGG CATGGATTTC	240
GATTGCAnTT ATTAGAATAG CTCAATGCTA TAAATGTAAG TAGTTGATAT TGAGGAACTA	300
ATGAAC	306

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(2) INFORMATION FOR SEQ ID NO: 3048:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3048:

GACAGGCTAC GAGATATTTT AAACAAATTT ACATCAAATC CAGTATTAGG TGTTATTGCA	60
GGTATCGTTG TAACTATTTT AATACAAAGT AGTTCAGGTA CGACATTATC ACAATCGGAC	120
TGGTAACnCT GGATTTATGA CATTGAAACA AGCCATTGGA GTGATAATGG GTGCTAATAT	180
CGGAACAnCG GTAACGTCAT TTATTATCGG TATAGATTTA GGCGAATATG CAATGCCAAT	240
TTTAGCATTa GGTGCATTCT TGAATCTTTT TCTTTAAACG CTCTAAA	287

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(2) INFORMATION FOR SEQ ID NO: 3049:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3049:

CATATAAATA GCGnTACATC GCGCCATTCT TGATCTGnAC ATATCTTTCT TAGGTCCAAC	60
CGTGAATGAT TACGTCCATG ATAACGTACA AACGCAATTT CATTGTGAT TCGATTGACT	120
AAAGGTACAC TGCCATCTTT CACTTGTGGT TCATCAACTA CTGCATGAAT GATTTGATGT	180

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AATTCTACAC ACATTGGAAA GCTTGTAATG CTGTCTTACA TACAAATATA TTGATATTTG 300
 TGCATGCACT CAACCAGGCG GAAATGACCA TACCATGCTA ATTTTCTGGT AnGAAGGCCT 360
 5 ACATATCTAA A 371

(2) INFORMATION FOR SEQ ID NO: 3050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3050:

CGCCAAATAA AGATAATACA CGTATTGGTG AAGATATAAC TGTRAACTGCA CATATCTTAA 60
 20 TTGATGGCGA AACAACGCCG ATTACGAAAA CAGCAACATA TAAAGTAGTA AGAACTGTAC 120
 CGAAACATGT CTTTGAAACA GCCAGAGGTG TTTTATACCC AGGTGTTTCA GATATGTATG 180
 ATGCGAAACA nTATGTTAGG CCAGTAAATA ATTCTTGTCG ACAnATGCGC AACATTGAAT 240
 25 TTCCAATTTG TTGGAnCATA TGGGCTAACA AGGTGTTTAG GCATATCTAC TCGTCTTATT 300
 GGGTGCATAT GTAATGGCAA GCA 323

(2) INFORMATION FOR SEQ ID NO: 3051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3051:

CCGnACCAAT CGGTTTACAG TTCATTGGTA AACCATTTCG ATGAAAAAAC GTTATATCGT 60
 GTCGCTTATC AATATGAAAC ACAATACAAT TTACATGACG TTTATGAAAA ATTATAAGGA 120
 GTGGAAATCA TGCATTTTGA AACAGTTATA GACTTGnGTT CACGTAGAGT TAAAAACGGA 180
 45 CTCAAAAATG TTTCTCCATC ACCAGCGCAT TInGAGCAGA ACCTAACTCA AATACGAATG 240
 GATCGCTTA GCATATCCAG TGCTTACCAG TTGTTAATAA GCGTGCGTAG ACGGGCATGC 300
 GTGCTGCAAT GCCTAAATAG GAACG 325

(2) INFORMATION FOR SEQ ID NO: 3052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3052:

CTTTTAATCG	CTTGAAACT	ATAGGTAAGA	CAATACAAGT	AGCTACAAAG	CCATATATTA	60
CTGTTAATTG	ACCTATGAAA	AAATATCCGC	TAACGGGTGC	CGTCAATCCT	GCGATAGCAA	120
TACCAATAAA	AAGTACAGTC	CACGAAGGAT	AAACATTTTC	AAGTGAAAAA	TCTTTTAAAT	180
ATTTTATTGA	AAAAATAATC	ATATGCGTCA	TAATTCACAC	AAGGCATAAA	ATCCAAATAG	240
GCGTATTAAG	CTATTGTAAA	GTTTGTTACT	AAAAAATGTT	TTAAATAGTG	TnCTAAAAAG	300
CCGGCATGAA	AATGTGTGAC	CTGATGAACT	GAGGCTGTTA	TTGTCTTCAC	TTATTAAATT	360
TGTCTAGTCT	AAAGGTGATC	CAATCAGAAG	CAAGTCCGCA			400

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(2) INFORMATION FOR SEQ ID NO: 3053:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3053:

AATGAGATGC	GAAGGATGAT	CAGAGAAAAA	GTCTCTCAAT	CAGGTGTGAA	AGTCAGATGG	60
TTATCACAAC	TTTGGCGTAC	GTTTTCGATA	TAATGCACTA	GGTGATTTAA	ATACGAGCAA	120
TATTGTTTCT	TCAAAGAAA	GTTTCGGTAT	TACTGAAGTG	TGAAATCTGT	CTCTATGCAT	180
GCCGGATCGA	CATTAGCATT	ACTAATCCAG	AGAAAGCAAA	AGGTATTGTG	TATACACCAG	240
AACATTGCCA	GCGAAAAGTA	AATGGTCACA	GCTGTAGAnC	AAGGTATTTA	TAATGGGGGC	300
GGTAAAGCAG	AAGGCCCCCTA	TGTAGCATTT	CnTAAAGnTG	GGAAAAGGTA	AAGCAGCATT	360
ATCGGTG						367

45

(2) INFORMATION FOR SEQ ID NO: 3054:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3054:

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TnATTTATCT nAGCTCATGA CATGATGGCT GTTCACATTG CAAGGCGTTG ATGATnAAAT 120
 AAGGAAAGGC ATTAGGAAAA AGCCACAGGG AAAACATTTT AGCAGCAGGT TCTTGAATC 180
 5 ATATATTCAA GTTCAACAAG CGAATGCTGT TAAATTGCCC TTTGGATGAC AATCAATTCTG 240
 ATATCGTTTT AAATGAAGCA ATGTTAACAA TGTTACCCAT CGCCATAAAG GAAAAAGCAT 300
 TACGCGAGTA CTACCGAGTC TAAAGCCTGG GGGTATCTGT TAACACATGA TATTGTCATC 360
 10 GTTAATGAAT CACATGCCAC AC 382

(2) INFORMATION FOR SEQ ID NO: 3055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3055:

CTTAAGATTA GGTGTGCTTA ATTAGTACTG GCTGGGAACG ATAAAGGCAT ATTGCAAAAA 60
 25 ATAGAACATC CATATCCATT AAATGTATTT ACGCTAAATA TTGnCGACTT ATATTTTTAG 120
 ACATAGAGAA GAGACAAGAC AATTTTAAAC GATGCAACGA CAGTTAGGCT GAGGCAGTTA 180
 AAACAAATAT TTGATACACA TGTTGnCAGA TAAAAGTCAG TGTTCCCATC AAATGChAAT 240
 30 TTTGTACTAC TAAAAGCTCA GCAGCGCAAC AATTAGGACA ATACGTATAT GAACAAGGGA 300
 TTTAAACCTC GCTTTT 316

(2) INFORMATION FOR SEQ ID NO: 3056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3056:

GTTCACCATC CGTTTATTTT AATGAAAAA TCGACAAAAA TGGTCGTGAA AACTATGATG 60
 CAACAATTAT TCCAAACCGT GGTGCATGGT TAGAATATGA AACAGATGCT AAAGATGTTG 120
 TATACGTACG TATTGATAGA ACACGTAAAC TACCATTAAC AGTATTGTTA CGTGCATTAG 180
 50 GGTTCCTCAAG CGACCAAGAA ATTGTTGACC TTTAAGTGAC AATGAATATT ACGTATACTT 240
 AGAGAAAGAC nGCACTGAAA ACACTGACCA GCGTATTAGA ATCATGACGT TACGTCCAGT 300

CTTAGCAGCG TGGGnCGTAT

380

(2) INFORMATION FOR SEQ ID NO: 3057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3057:

TATGTGATGG ACTTAAAAAA ACGAACTCAA TTAATACAAT GGGCTCAAGA AAAAGAAGAA 60
 CGATTTATTA TAGAAGATGA TTATGATTCC GAGTTTAGAT ATTCGGCAA ACCCATTCCA 120
 GCAATTCAAG GTCTATATTC AAGAGGAGAA AAAGTGATTT ATATCAGTAC ATTTTGCAAA 180
 GTCTATTTTT CCTAGCTGTT CGAGTTGGCA TATATGGTGT TACCCTATTC TATnATGGAA 240
 AAAATATCAT TTCTnCAAAA TCCACCATTG GAAGGGCAAC ACTGGTAACC TGTTTCATAT 300
 GGCAAAACCT TATTGGCAAC GTTTnAT 327

(2) INFORMATION FOR SEQ ID NO: 3058:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3058:

CGAAAAAGGA GAATGAAACA TGAGGTAATA CAACATTACA TGCAACAACA ATTTATGCGT 60
 GTAAGACATA ATGGAAAGCA GCTATGGCTG GAGATGGGCA AGTAACGCTT GGTTCACAA 120
 GTCATCATGA AACAAACGGC AAGAAAAGTG CGACGTTTAT ATGAAGTAAA TGTTAGCTGG 180
 TTTGCGAGTA TGTAGCAGAT GCGTTTACTT ATTTGAAAAA TTCGAAACAA nATTACAACA 240
 GTTTAGTGGT AACTTAGAAA GAGCnGCTGT TGAATTGGCA CAAG 284

(2) INFORMATION FOR SEQ ID NO: 3059:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

AAAGAAGCGG ATGAAGAGCT TTGCATTGAG CTCGACCCAG GSTATGGCTTT TGGAACAGGT 60
 GATCATCCGA CTACAAGTAT GTGTTTGAAG GCAATAGAAA CATATGTATT GCCACAGCAT 120
 5 TCAGTAATTG ATGTTGGTAC TGGCTCAGGT ATATTAAGTA TTGCAAGTCA TCTAATCGGT 180
 GTAAACGTA TTAAAGCGTT GGATATTGAT GnaATGGCAG TGAGTGTAGC TAGAAGAAA 240
 CTTCAGAAGA natCATTGTG AACGTTGAAT TGGAAGCTGT TCCAGGTAA CATATTGGAA 300
 10 AG 302

(2) INFORMATION FOR SEQ ID NO: 3060:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3060:

TTTTTAANGA CACATTGnGC TGTGTTTAAT GCATGAAAGG AACCACTGAC ATGCATnAAA 60
 25 TCTTTGAATG GTTCTTTATC AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTTAAATCAA 120
 TATAATTCAA AAAGGTCGA GGATATGAAA TCACATCTTC GACCCTTTAT TTACTATTTT 180
 AATTCAGCCA CACGCAAACG GTTATTTGCT CTCTCTAAAG CTCTTTCGGC TCTATGGAAT 240
 30 ATCAGTATTG TCGTCAATCA TTTTCCAAGT GAGACTCTGC TCTTGCTTTG GCTAATTTAG 300
 CTCTTTCAAC ATCAATTTCT CTGTCAGTTC 330

(2) INFORMATION FOR SEQ ID NO: 3061:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3061:

CGATCAATCA ATATAATTCA CGGCGCAAAA CGTTTATTTA GCATGTTCTT GCAGACTCTG 60
 AAAGTGGCAT TAAACCTTCC ATTAAGATTT TTACCATTCT AGGCATTAAT ACCATTACTG 120
 CAGCCATTGA CATTCCTAAA TTAATGATGT CTCCAGGTTT GTAACCTGCT AACACACCAA 180
 50 TACCTAamCC TAAAATTAAG CCGACAAATA TAGACTCTCC AAATGCGCCA AAACGTTTTT 240
 GAATTGnTTC AGGATCAGCA TCTAACTnat TCAGACCGGG TACTTTTTGT AACAAATTTAA 300

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(2) INFORMATION FOR SEQ ID NO: 3062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3062:

TATAAAATCA ATGATTTTAA CAAATAAAAA CGTACCGCAA ATACTGCAAA TAACAGCAAA 60
 TACTAGTTTT AATAAAATAT GACCGGTTGG AAAGAACAAT AAAGCAATTA AAATACCTAG 120
 TTTAGCCCAT TCCATCGTTC CAGCTGTAGT CGGACTAACA AACTTATTTT GCATCATTG 180
 TTGGCATTAT CAAGCCTGCT GAAAGCCAAC GAACTTCCAG CAATTAAAAT ACTCATCGTC 240
 CTTGGTATTC GGGCTTGGAG AATAAAATGA TTCCGCTGGT GACTCAGTTG AAATGTAGTG 300
 AAATCTTTGA ATTGGATAGT TnCACTGCAC ACCTGATGGn AnCAACGGAA 350

(2) INFORMATION FOR SEQ ID NO: 3063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3063:

TTAGTGATTT TAACGTGTAT CGGTAATTTT AAATAAATGT TTAATGCTTT TGAAAATACA 60
 GTTCTAACCG AAGACGTCGG GTACACTGAA TCACCGGAAA CGCCAAGGTC TTTTATTAAA 120
 CCTTGTTTAC TATATTGCAT ATACTGTGGA TGCTGTCGCA ACACATTGAT TTGATAAGGA 180
 TGTGTTGGTA ATAAAATAAA ATCTTTGGGT ATCTCTGATA TATCTATGTC TGCTAATTGG 240
 ATACnACACT TTCTCAACCT GGATCCTTCC TTTTACCTnC CACCATAGCC GCGTGGAnCA 300
 GGAAACCATC CTGGGATGCA CCAGCCAAAA TAAATGCCAA TT 342

(2) INFORMATION FOR SEQ ID NO: 3064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTCCAGCTCC AGAACCAAAC TTAACAGTAT TATGGTCAGT ACGTTTACCT GACAACTTCA 60
 AAACATACTG TGCAAAAATG AGTATTAAAA CAAGTTCTAT CCAATATGAA AATGATGACA 120
 5 TTATGCGTGA AAGCTATGGC GATGACTATG GTATCGCnTG TTGTGTATCA GCGATGACAA 180
 TTGGTAAACA AATGCAATTC TTCGGTGCAC GTGCGAACTT AGCnAAAACC TTACTTTACG 240
 CTATCCATGG TGGTAAGATT GAAAATCTGG TGCACAAGTG GGCCCAACCT CCGAGGGATT 300
 10 nACCAGCGGA GTAATT 316

(2) INFORMATION FOR SEQ ID NO: 3065:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3065:

TGATTGCGTG GATCAGCAAC TTCAAAGATT AACAAATAAT ATTACTTGGG CAGATAACCG 60
 25 CGCTGCAAAA TATGCAACAG TAATAAATGA AGTGCAATGAT GGGCAATGCG ATTTACCAGC 120
 GnACAAGCAC AnCGGTTTCA TCCTATGTCG CGATTAGCGA AGATTTTTGG ATGAAACATG 180
 ATGGCCAGAT GTATTTCCAC GTACTGCTAA GTTTGCAGAT ATTAAACAT ACATTTCTAT 240
 30 CATTATTGAT ACATATATCA TTGATTATTC CATGGCTTCC GChACAGGGA TGTTAATTAG 300
 AACATAGATT GGAGTGAGGC AT 322

(2) INFORMATION FOR SEQ ID NO: 3066:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3066:

45 TATAAAGAAT CCTGCCTTAC CTAAGAACAC TTGTCTTGTC GTTAAGACTG ACTCTAGACT 60
 CTTATGTTTA TTATCAACCG TTAATAAACT TACCATCAAG AGTGACCTA CCCATACTGA 120
 CAGTGCAGTA TAGAATGGTG TCATACCTGA ACCATAATCC TTAAGTGGGA AAACATCAAC 180
 50 AGTCTTCTTA TTAATAGATT GCAATAATAC CCGCTGCTTT TTCAAATCAT TCTATGGTTC 240
 GATTAATTGT CGACGCATCA TCTTGTCAT TCTTGAAATT TATTCGCTTT TCAACTTTCA 300

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CACGCTGACA TAC

373

(2) INFORMATION FOR SEQ ID NO: 3067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3067:

15	TTCAGAGTTC GGAACATAAG GCGCTACAAT GTTGTGTTGC CAGTAGTTGA CTGAATATGC	60
	GTTTGTAACA AGCTTTTTTC GATTCTAGTC AACAGTAATT AAATTTATGA TATGGGCAAT	120
	ACTTTGTAAT ACTAATATTA AATGGCGACT TTATTTCACT ATGTTATAAG AGTGCCATTT	180
20	GTTGATAAAG GnATACTAAA GGGTATCGTT TGAATTTTA GTAAC TAGAT ATGTTCCGGT	240
	ATAGACCGnA TTGTGGATAC GTAAATTTAA TGnATGAAT TTAAAATGA AAACATGACA	300
	TTAAATGAAT C	311

(2) INFORMATION FOR SEQ ID NO: 3068:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3068:

35	TATGATTATC TAGTAAGTAA ATTGCTGACG CGCCGAATAC CGCAAAGAAT ATAAAGCAAA	60
	CTAACGCCGG GACAAAAAGT ACACCTAGGA ATAAATTCTT TAATCGTACG TCCTTTTGAC	120
40	ACACGTGCAA TAAnATACCT ACAAATGGGT GCCCAGGnTA TCCACCATGG CCCAGTAAAA	180
	GATTGTCCAA TTTTGTAACC ATTGGGAATT TTTGACCACC TGTCGGAATG CGTAAACTCA	240
45	TACTTAAAGA AATTTGCATT ATAATTACCT AGACC	275

(2) INFORMATION FOR SEQ ID NO: 3069:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

AAATGGGTTT TGTGACATTA ACGTCTACAA AAGATGGTTC AGAAGAAACA CACGAGGCTG 60
 ATGGTGTATT CATCTATATT GGTATGAAAC CATTACAGC GCCATTTAAA GACTTAGGTA 120
 5 TTACAAATGA TGTGGTTTAT ATTGTAACAA AAGATGATAT GACAACATCA GTACCAGGTA 180
 TTTTTCAGC AGGAGATGTT CGCGACAAAG GTTTACGCCA AATTGTCACT GCTACTGGCG 240
 ATGGTAGTAT TGCAGCnCAA GTGCAGGGAA TATATTGACA TTAACGATCA GCCTAAnTCC 300
 10 GAGCnGATTA GATGTGAGCG G 321

(2) INFORMATION FOR SEQ ID NO: 3070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3070:

GTTTGACCTG CATATTTGAC AGTCATAACC TTTGTATCAC CATTATATTA ATATCAAAAT 60
 25 CTTGGAACGT GTTATTTGAG nTGACATTTA ACTTCGCAGC ATTATCAGCT GTTGAACCTG 120
 ATGTATACGT TCGCAACCC ATAActATCT GTGTTACAAT GCACCAAACG CACCTCCACC 180
 AGCTACATTA GATGGGCAGC TTCGCCCTTG AGCTGATTGG TTTAGATGAT TGTGATACGA 240
 30 TCCAATTTGA AGCCAAATnG TACTTAAGCA CAATCCTACT GCGGACCGTT TAACCCTGTT 300
 TCACCTATAC ACTGnTGAAA GGCAAACCGT ACCACTCACC ATTTCCATGC CTTCCATATT 360
 35 TGGTTACCAA ATTTACTTTT CCCnGAAAAA TGAAACTCTT 400

(2) INFORMATION FOR SEQ ID NO: 3071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3071:

TGGCCATTG TCATTGCATT TTTACCGTGG GTGTTGATTA TTATTCCTTA CTTACTATTT 60
 50 AAATCGGATA CACTAAATAT TATTCATACG GGTGATAATA TTGCACGAGG TCTAGGTGTA 120
 AGGTTAAnCA GAGAACGTTT AATATTATTC TTTATCGCAG TGATGTTATC ATCTGCTGCT 180
 GTAGCATAGC AGGTTCAATT TCGTTTATCG GATTAATGGG TCCGCATATT GCCAnACGTA 240

(2) INFORMATION FOR SEQ ID NO: 3072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3072:

GACTCCCTGC AGGTCGACGT CTAGAGGATC CCCCCACAGC AATTCACCTA TACATGTAAC 60
 AGTGTGAAAT AATAACGTCA CAACGGCATA ATACACATTG CAACGTCCCA ACAACATATC 120
 ATAGAATCGT AACGGCATGA CATCAACACC AAACCTGGGC TATAACACCA TAACAGCGCA 180
 ACGCCACATC ATAGGCACTA CATCAAGTCG CATCGTAGCA CCAGCACATC AAAGTAACAT 240
 GGGCATCAAC ATCAAACCGG TCTATAACAC CATAACACCG GCAATGCCAC ATTCATAGGC 300
 ACTACATCAA GTCGGCATC 319

(2) INFORMATION FOR SEQ ID NO: 3073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3073:

ATATACGCTT ATCAGCTGGA GCTCAATAGA TGGAGGATGA TTATGGGGCT ACCGGTTCTG 60
 TCTATAGCAC TGGTCTATCA GCTATGTGGA TTACAATCGG TTTAACATTA GGTGCTTATA 120
 TAAATTACTT TGTTGTGCT CCTAGACTTC GTGTTTATAC CGAATTAGCT GGAGATGCAA 180
 TTACATTACC AGATTTCTTT AAAAATCGTT TAAACGATAA AAATAATGTG TTAAAGATTA 240
 TTTCTGGATT GATTATCGTA GTATTCTTTA CATTATATAC nn 282

(2) INFORMATION FOR SEQ ID NO: 3074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3074:

AATCGAnAAA TCATGGATGT ACTTGAATCA AATGCAAACA GCGAAGTGTh TTGAATTGCA 120
 TGGTAGCGTT ATAGACGAGC CAGTAGAAAT TCAATCAATT AAAGTATATG TTCCTAACGA 180
 5 TGATGAAGGT CGTACGACAA CTGTAATTGG TAATGCTTTC CCTGACTCAG AAGTTAAATG 240
 CATTACACCA GCAGATATCA TkGCTTCAAT GAGTTACTTC TTTAACTTAT TAAGCGGtAT 300
 TGGGtATACA GATGATATTG GACCATTaGG TAACCGTCGT TTACGTTcTG tAGGkGGaAT 360
 10 TACTACmAAA CCaATTCCGT ATcGTTTTAT CCAAGA 396

(2) INFORMATION FOR SEQ ID NO: 3075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3075:

ACCTACATTT GCAGTTGTCG GTGTATAACC GGCTGGTGTT GAAAACTCTA CACTATAAGT 60
 25 TCCATTGCTT AAACCAAGTGA ACTGATATTT ACCATTTTCA TCTGTTGTCG TACGATCTAA 120
 TTCTTTACCG TTACTATCTT TAAGAATGAC ATAAACACCT TTAATCCCTT TTTCAATTGGC 180
 30 ATCTTGTTTA CCATCTTTAT TTGTATCTCC CATACATAGT CACCTAGATT ATATTChTTT 240
 GGGCGCCATA GCAGTTGATG AGCATTCAACA TTGAAAAACT ATTGACCACT ATATTAGTTT 300
 GCAGTGCTAA GnATAACATT TCCATACGTG ACATACTGAT AGACTGTGAG TGATGTATGC 360
 35 GCTGnTGCTC ATAACG 376

(2) INFORMATION FOR SEQ ID NO: 3076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3076:

TTACATCACC AATTAGACGT TATCCTGATT TAACAGTTCA TCGTTTAATC CGTAAGTATT 60
 50 TAATTGAGAA ATCAATGGAT AACAAAGAAG TGAAGCGTTG GGAAGACAAA TTGCCTGAGT 120
 TAGCTGAACA TACTTCTAAA CGTGAACGTC GTGCTATTGA GGCAGAACGT GATACTGATG 180
 AATTGAAAAA AGCAGAATAT ATGATTCAAC ATATTGGTGA TGAATTTGAA GGTAAATGTCA 240

AAnGChGnGA TATACGTTTG AGGCGCAATG C

331

(2) INFORMATION FOR SEQ ID NO: 3077:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3077:

AATCATATGC ATCGATTTC	AGCAACAGCA ACCATTCATC	CTATGTCCCA TTAGCAAATT	60
TTTTGGATGA AACATGAATG	GCAAGATGTA TTTCAACGTA	CTGCTAATTT GCAGATATTA	120
AAACATACnT TTCTATCATT	ATTGATACAT ATATCATGAT	TATTCATGGC TTCCGCAACA	180
GGATGTTTAT TTAGAAACAT	TAGATTGGGA TGTTGAGGCA	TAGAACTGCT GGGTATTTCC	240
AAGGAAATGT TGCCGGAATT	ATTCCAACAA CTATTGATGT	AAGTATGAAA GAACGTATGC	300
AACATAATGG GCTAATAAAG	TACACCGTnT GTTAATGGTG	CnATG	345

(2) INFORMATION FOR SEQ ID NO: 3078:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3078:

GATTATCAAG CGATTGATCA	AGTATCATCA TTGTTGAAAG	AAAAATATGG CATTGCACAT	60
TCAACGTTGC AAATTGAAAA	CTTGCAATTG AATCCATTAG	ATGAGCCATA CTTGACAAA	120
TTAACATAAA TAAACATTG	TAGCGCCTAA AACATTAATC	TATGTCATAG GCGCACGTTT	180
CGTTTTTATAC TTATGTTGCA	TCATTTAAAT GATTTTCGTC	AATTTCTTTG ATGCTATCTA	240
CATCTAACAC GAGGTAACT	TGCGTTGATT TTGATAAAGT	GATCATAGCT TTTAGTACTT	300
GAGGATTTTT ATTGTTGCTG	TTACGAATGT GGTGATGTTT	AATGCGGGAC AGTAATTTAA	360
GTTGTTTTTT TACAATTGAG	AGTGTGATAT TTCGATTCGG		400

(2) INFORMATION FOR SEQ ID NO: 3079:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3079:

5 AAACGTTTAA TATACACTTT TACACGTCGC CTTCATTGAA GCGAATTGCC ATAACCTTCA 60
 CATTATATAT AGTTCTTTCC ATATAAATGT CCAAATTTTT AGAACAACGC AATAATAAC 120
 CATCCACCTA ACTTATCAAA AATTAAAGTG GATGGTTTTT CATTTTCATT TATATTTATA 180
 10 TTAGTGTTAA TCCAATCATA GATTTATCTA TATGCACTGC TCTATACaTT TCCTCaTTTA 240
 ATTTGcyTTA CTTTCATTTA TATCATTATC AGAACACTTG GCGTGTCATC GnTATTATTT 300
 CGCATCTTTG AnACGTTTA 319

15 (2) INFORMATION FOR SEQ ID NO: 3080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3080:

TCAAATGCAT CTAGGnCACA TTATTCTATT TGGGCATTCT TAGTGCTGTT CTTATTTGCG 60
 GCTTTAACGT CATCTATTTT TTTATTAGAA TTAAATGTTT CTAAC TTCAC GAAGAATGAC 120
 30 AATACAAAAC GTAAAAAAGT CGCAGTGATC GGTAGTATTT TAGTATTTAT CATTAGTATT 180
 CCAGCAACCT TATCnTTTGG TATCCTAAAA GATGTAAGAT CGGTGCGGGA ACGATTTTTG 240
 ATAATAAGGA TTCCACCGTT CGAATGTAAT GAAGCCATAA GCGGG 285

35 (2) INFORMATION FOR SEQ ID NO: 3081:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3081:

ATCATAGCGT TTCTCCTAAA AATTACGATT AATCAAAGTA TGCCATTATT TAAC TTTAGT 60
 TTCTTCAGAA TTATTTGCCC CATTATCATG TTTTCTTCT TTATTAACAG CATTTTATC 120
 50 ATTTTAAACA AGATACAATT TACCAATTAA TGGGCGGTGT GCGTGCTGGT ATGGGTTATA 180
 CTGGTTCACA CGATTTAAGA GAATTACGCG AAGAAGCACA ATTTACACGT ATGGGTCCTG 240

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CATTCTAATT AAGATAAAGG AGAACGACAA ATATGGGAAA TGGCAAAGGA CCAAGAGTTA 360
 ATCCTTGTCT TAGGACTTTG GTAGGCCATT ACACCCATTA 400

(2) INFORMATION FOR SEQ ID NO: 3082:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3082:

TGAATTTGCT CCAAATAAAA ATACAATTGC CATTAAAATC ACCAGATATT ACAAGTGGCA 60
 ACATGTTAGA AACACCGTTC ATTAAGTGTT TATAGAATGC TTTACCTGGG CTTATTTCTT 120
 GACTGTCATT TGAGTTACCT GGCAACAAAA GGTTTACGAC TTGTATCTAA TGAATACCAT 180
 CTGCTACTGG TnCTTCTACG ACATTTTAC CATCGAnCG GTCCGTCTCA ACATGTACAT 240
 CAGCAGCA 248

(2) INFORMATION FOR SEQ ID NO: 3083:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3083:

TACTAAAGGT TTAAATCAAA AATGGCTAGG TATCGTATTT GCGATTTTAA TTACAATTAC 60
 ATTTGCATTT GTATTAAACA CAGTGCAATC TAATACAATT GCGGAGTCGT TAAATACGCA 120
 ATATAATATT AGTCCAGTAA TCACAGGTAT TATTTTAGCA ATCGTAACAG CTATTATTAT 180
 ATTTGGTGGT GTACGTAGTA TTGCTACGTA TCCTCGTTAA TGTACCGATA TGGCTATCAT 240
 TACATGGTAT GGTTTAGTAA TAATGCTATT AATTTAGACC AATTGTCCnA TGATAGGACG 300
 ATATAAAAGG CATTGGnACG ACAAGnACTG GTGCGCTGAG gGCTCGGTCT CCAGGACAAC 360
 GGGGTATC 368

(2) INFORMATION FOR SEQ ID NO: 3084:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3084:

5 TTGGACTTTA TAAAGTTACT AAGTTGTAGA TTATCCTGGT AAAGAAGATA TTGCGGTTGT 60
 ACAAGTTGAA GAAAAATCAA CACAACCAAA AGGTAGAAAA TTCAAAGATT TCACTAGTAA 120
 ATTTAATATA GCATCAGAAG CTAAAGAAAA TGAACCTATA TCAGTCATTG GTTATCCAAA 180
 10 TCCTAATGGA ATAACTACAA ATGTATGAAT CAACTGGTAA AGTATTATCA GTGAATGGGA 240
 TATAGTGnAT CGGATn 256

(2) INFORMATION FOR SEQ ID NO: 3085:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3085:

25 ATATGCATAT GCTTCTTTAG GTGAACGAAT ATCTGGTTCA GATACGATTT CAATTAGCGG 60
 TGTACCTTGA CGGTTCAAGT CAACTAATGA ATACTCCACC TTTATGTGTT GACTTACCAG 120
 CATCTTCTTC CATGTGAAGA CGAGTAATAC CGATTTCGnTT TGTTCACCG TCGACTTCGA 180
 30 TATCGATATA TCCCATTTCA CCAATTGGGT TGATCAATTG AGAATTTGAT AGCTTTGGGA 240
 TATCGGGATA GAATAGTCTA CGGTCAACTA GATCnGGTGC GAnTCCATAT TTAGTGCCAT 300
 GCAGCACGCA T 311

(2) INFORMATION FOR SEQ ID NO: 3086:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3086:

45 ATGTAAATGA TCATCCTTCA TAATAACAAC GATTACTGAT CTTGATCATG ATTTTGAACA 60
 ATAACAACTG CTTTATTAAT ACCTTGATA CGCTCGAGnC ATGCCAACCT CTGACAACTC 120
 50 AATCCTAAAC CCTCGAATCT TAAC TTGTTT GTCCTTTT CGA TATAAATAAT CTATGTTGCC 180
 ATCGGGTAAC AAACGAACGA TATCACCCT TCCTATACAT CAGCTGATTT ATATTTGAAT 240

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(2) INFORMATION FOR SEQ ID NO: 3087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3087:

GTAAAGATTT CAATTCATCA TCTTTAAATA AACTTAATGG TAATTnGTTA TACChAATAA 60
 AGCCTTCTGG ACACCTTCCTT TAGACCGACG ACCGTCTTAG CTAATGTCTGA TTTCCCTGAC 120
 CCTGATTCAC CGACAATGCC TAATGTTTCG CCTTTTCTAA TAGCCAAGTT AATATCATAA 180
 CTGCTCGGTA TGGGCTGCCC CTCGGTGATG TGTAATCCAC GCTCCACGCG ATCGATTTTA 240
 ATAAAATATC ATGGTT 256

(2) INFORMATION FOR SEQ ID NO: 3088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3088:

AAGGTTATTT GAATGATCAA GGTATCCACA AAAGAGGTGC TGAAATAGAT CGACTCGTTA 60
 AAGGATGTAC AGGTGTTAAA CGTACAACTG GACAGCATCC AGGGGGTATT ATTGTAGTAC 120
 CTGATTACAT GGATATTTAT GATTTTACGC CGATACAATA TCCTGCCGAT GATCAAAATT 180
 CAGCATGGAT GACGACACAT TTGATTTCCC TTCCTnTCAT GATATGTATT AAAACCTGAT 240
 AAACHTGGAC ACGTGATCCC ACCATGATCG ATGCCTCCAG ATTATCAGGA ATGATCCAAA 300
 ACCATACCTG AGATGTAAGA GTATCAGTAT TAGACnC 337

(2) INFORMATION FOR SEQ ID NO: 3089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3089:

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120
 AAACCTCGAA GGTATTAAACA GCGAAGTATT AGAATATGCC GAAATTCAAG AATTTGATCA 180
 5 AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAATTCATT AAATGTATnA CTACATGCAC 240
 GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300
 GGA 303

10 (2) INFORMATION FOR SEQ ID NO: 3090:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60
 GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTACA AATACTGAAC CAGCGTTCAT 120
 25 GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180
 TAATTCCTAA TKTATGTGGG ATTAACTTG GAAATTTTCA TLAATGTAAC TTCATCAAAC 240
 CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300
 30 ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGGACGT ACTGAATGGA CCCTTTCTCG 360
 GnGTGTATCT GCAAGGTCAA TTTTCATTnT CAGGCATGGT 400

35 (2) INFORMATION FOR SEQ ID NO: 3091:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

45 TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60
 TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120
 GATAGTCACG TAATGGATTT TGTGTGTCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180
 50 GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAATCATA 240
 CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

(2) INFORMATION FOR SEQ ID NO: 3092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

CGACACCTCA ATAATCATAT CGTAATGTTT AACTTTTCCT GATTTAAATG TAATTTTCATT 60
 TCCATTGATA GCATTAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC 120
 ATCAAGTATA GGTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA 180
 TAAAGTAGGG TGTAACCAC GTTCATAAA GATTTCAAGG AACTCCAATG GAACATAACC 240
 TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA 300
 TCCAGGGCCT CCAAATTCC nAGGGGAAAn GGTAATATCC ACCTTCCAAG GCCAAGGGCC 360
 AATTGGCACC TGGCCACCCA GGGnCTTAAA AAGGGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 3093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

TTATACCCGn CAAATTCATA AATATAGTnC CTTTTCAATA GATTGATATG TATGTCTAAA 60
 TGTATCGATT AACTTTGCTA ATGCTGCTTC ATCTAATGGT CGGTCTGCTA ATTTTAAAAA 120
 TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTC TTTAGATGAT GGTTCCGTTA 180
 AGCCACATGC TTAAATGCA CTTTGTGTG CTACTTCACC ACATTTTTTC GTGTCTGCCA 240
 ACGTACCATC AA 252

(2) INFORMATION FOR SEQ ID NO: 3094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60
 AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120
 5 TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180
 AGGTCAATAA TAAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240
 GGCCGAGGTA CAAAAAATGT TGAGCATTTT AAAGTATAAA CTTATCGACA CGnTTGTGTG 300
 10 CAGTTTTTCAT GTTT 314

(2) INFORMATION FOR SEQ ID NO: 3095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60
 25 ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAA CGTATTTAGA AAATGCCACG 120
 CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180
 ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAnAAGTT GGACCCTTTG 240
 30 AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300
 GCTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

(2) INFORMATION FOR SEQ ID NO: 3096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60
 ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120
 TACATACTTT TGAAGTAGCT GTCTCATTTG TTGATTCATG TAAATGACAT CATGCTCCAT 180
 50 TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240
 ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTTC GTCCATATCC ACGGATGGCG 300

ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 3097:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

15

ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC 60
 CAATAATCCC nCAGGATATA CGTGGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG 120
 ATGCACTTAC AATTTTAAAT AGATTTTAA GACCTGTGTG GTTTTGTACA ATTAATGTGA 180
 CATGACTAGG TCTTGCACGT TTATATGCAT CTTCACTACT GAGTTTTTTG GTTGATTn 240
 GTTATGATTT AATACGGCTA ATTCT 265

(2) INFORMATION FOR SEQ ID NO: 3098:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

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CTAATGTATC AGTTTGGCAT GAATCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT 60
 TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG 120
 ACCATTCTTT TTCCTTTTTC TCTTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT 180
 CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGA 240
 TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTC TGACCTTTTA 300
 AAATCATTnA CTGTCAnCAG A 321

45

(2) INFORMATION FOR SEQ ID NO: 3099:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60
 AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATTT TGTATTACCT GAAGTTTAA 120
 5 TTTCAACTGA TAATAATGGG ACATTTTAA CTTATACAGT TAAAAGGGAA AGTTTACTG 180
 TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240
 CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276

(2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAAACGTT 60
 GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120
 25 GCAAnGTTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180
 AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

(2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

nCGATATAAC AAGTTTGTTA GACTTAAAGG TGCGATCCA GCGATATTTG GTCGTGTGCA 60
 AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120
 ATCAGCGAGC GChAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180
 45 AAGTGTGGAC ATTTTCTACA GGTCACTTTT AAAGATTCAG AAGAAAATGA AGTGGGATGG 240
 TCCATTCCTT AAGT 254

(2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

5 CAATCACTCA TGTAGTAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA 60
 ATGGCATAAT CTTCAThTGT AATGTTTAAAT TTACCGCCAn TAACAGATAA GATATGTTGC 120
 ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCACTCA AGATGAATTT 180
 10 ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT 240

(2) INFORMATION FOR SEQ ID NO: 3103:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

20 GTTGTAACCT TCAATTGTTT AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC 60
 AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG 120
 25 AATTTTACTT GAATCAGGTG CTGARACATA TCGAGTTGAA GATACAATGA ACCGTATCGC 180
 ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCACT TCAACTGCAA TTATTTTTTC 240
 ATTAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG 300
 30 AANGTGCGAA TAAGCGGGGn AATTCTTC 328

(2) INFORMATION FOR SEQ ID NO: 3104:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

40 TTTTGCTTTG TCGGCTAATA ATCTAATGTT CGTGGAACCG nAACCAGAGA TATTACAAAT 60
 45 ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG 120
 CTGATTTAAG GCGGCATTGC AAACTATTTC GCCACGAATC CTGAACGTCC TTTGCCAGCT 180
 ACAAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACCTCA TCCGCTTCAA 240
 50 CATGTGACAA AGTCACTTTA ATCnA 265

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60
 ACTGGAACTA CTAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120
 nGTATTGGAC GTGGATCACT TGTTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180
 AAGGTAAAGA TTTATCTGAC AAATTGATCG TTACTAACTC AATCGATGAA ACGTTTGTGA 240
 CCT 243

(2) INFORMATION FOR SEQ ID NO: 3106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60
 AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGGnG CCCAAACACA TCTAGATGCT 120
 TTACTAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180
 CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

(2) INFORMATION FOR SEQ ID NO: 3107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60
 CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTGAACGT GTCCAAAATA 120
 GCGGnTAGAn ATTCTTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

(2) INFORMATION FOR SEQ ID NO: 3108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60
 TCTAATTGGA TACAAATGTAA ACAAATGGT GATTGTAT TATAGATAAT AAACATTCGn 120
 TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180
 CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240
 AGTATTATGC AAGTACT 257

(2) INFORMATION FOR SEQ ID NO: 3109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCACT GAATCTTGCA ATGCCTTTTG 60
 TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120
 ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180
 TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

(2) INFORMATION FOR SEQ ID NO: 3110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTTAATTGGG AAAnCAGGTA AAAAGGATGG 60
 AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCCnCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240
 CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300
 5 CnAAGCGCGT ATTAGCACTA GCCGAA 326

(2) INFORMATION FOR SEQ ID NO: 3111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTTATCA 60
 20 ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120
 ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180
 ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT NAATTTTTTA 240
 25 TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

(2) INFORMATION FOR SEQ ID NO: 3112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTTAA CACAAGGnTT CGAACAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60
 40 AGCATTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120
 TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180
 GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTA 240
 45 TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300
 CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

(2) INFORMATION FOR SEQ ID NO: 3113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTCGAATC CCTCTTCCTC 60
 5 CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT 120
 ATTTACCTTT TTTATTTGTC TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG 180
 CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAAATATACAT AGCAAAATGT CGTTGTTGTT 240
 10 TTGTGATAGA T 251

(2) INFORMATION FOR SEQ ID NO: 3114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

TTTAAGTGAA TTTCTTTGGG TTACAGAAWT TTCAACAACT TTAAAGCAGC TATAATGATG 60
 25 ATTTTCAGCT TGTACAAAGG AGAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC 120
 GCCTAATAAT AAAAAGTCTA AAAGTTGTAT TTTAAAAATA GTTCTTTAAA TTATATACCC 180
 ACCACATTTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAACCTCCA ATATTGAACT 240
 30 CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTGAGTC CACTTTTATT 300
 TGTATTGTAT AGAGAGAAAT AAAAGAAAC CTTGTTTAC AAGGTTTCTA ATACGTTATG 360
 TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACACT CCACAAGTGG 420
 35 AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCCGCCAC ACCGGCTTAA TGGTAAACAA 480
 AAAACTTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT 540
 40 CCGGGAAGGA ACGTGtTCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG 600
 AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA 660
 CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC 720
 45 GGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG 780
 ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA 840
 TAACTGGGCT AGCTGGATTG GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG 900
 50 CTTGGCTATA GCCCATTAAAT AATAAGGGCG GCTGAAGGGG ATCGAACCCT CGAATGTCGG 960

	CGAACCCACA CCAAAGGTTT TGGAGACCTC TATTCTACCG TTGAACTATG CCCCTATTAA	1080
	AAATAATAAA TGGAGGGGGG CAGATTCGAA CTGCCGAACC CGAAGGAGCG GATTTACAGT	1140
5	CCGCCGCGTT TAGCCACTTC GCTACCCCTC CATAAATGGT GCCGGCCAGA GGACTTGAAC	1200
	CCCCAACCTA CTGATTACAA GTCAGTTGCT CTACCAATTG AGCTAGGCCG GCTAAGAAAT	1260
	GGTTCAGGAC AGAGTCGAAC TGCCGACACA TGGAGCTTCA ATCCATTGCT CTACCAACTG	1320
10	AGCTACTGAA CCATAATAAA AATGTAATGA TGGCGGTCTC GACGGGAATC GAACCCGCGA	1380
	TCTCCTGCGT GACAGGCAGG CGTGTTAACC GCTACACTAC GAGACCTATA AAATATTGCG	1440
15	GGAGGCGGAT TTGAACCACC GACCTTCGGG TTATGAGCCC GACGAGCTAC CGAACTGCTC	1500
	CATCCCGCGA TAATAAAAAA TAATGGCGGA GGAAGAGGGA TTCGAACCCC CGCGGCCCGT	1560
	TAAGGCCCTG TCGGTTTTCA AGACCGATCC CTTGAGCCGG ACTTGCGTAT TCCTCCATTA	1620
20	TTATAGGTAA ATCGCTATTA ATTATAAAAT TAAATGGCGG TCTCGACGGG AATCGAACCC	1680
	GCGATCTCCT GCGTGACAGG CAGGCGTGTT AACCGCTACA CTACGAGACC ATTAGTAAAA	1740
	CGGAGGAAGA GGGATTCGAA CCCCCGCGAG CCGTTAAGCC CCTGTCGGTT TTCAAGACCG	1800
25	ATCCCTTCAG CCGGACTTGG GTATTCCCTCC AAAATTATAT GGAaCtTGCAG GACTCGAACC	1860
	TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA	1920
	ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG	1980
30	AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG	2040
	GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAA GCAGGCGCTC TCCCAGCTGA	2100
35	GCTAAGCCCC CATAATAATT ACAGTATATC GGAAGACAG GATTGGAACC TGCGACCCCT	2160
	TGGTCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA	2220
	TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	2280
40	GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAcGgTGATC	2340
	ACTCACCGCA GGATTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	2400
	AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TGTATTCTAC	2460
45	CGCTGAACCTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACgCC GTAAGGCGCT	2520
	aGATCCTAAG TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG	2580
	GATTGGAACC TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGA GCTAATGGCT	2640
50	CTTCCATGGT GCCGGCCAGA GGAATTGAAC CCCCCAACCTA CTGATTACAA GTCAGTTGCT	2700
	CTACCAATTG AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCTGA	2760
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	AAACTGCCTG	GCAACGTTCT	ACTCTAGCGG	AACGTAAGTT	CGACTACCAT	CGACGCTAAG	2880
	GAGCTTAACT	TCTGTGTTCC	GCATGGGAAC	AGGTGTGACC	TCCTTGCTAT	AGTCACCAGA	2940
5	CATATGAATG	TAATTTATAC	ATTCAAAACT	AGATAGTAAG	TAAAAGtGnA	TTTTgctCGC	3000
	AAAACATTTA	TTTTGATTAA	GTCTTCGATC	GATTAGTATT	CGTCAGCTCC	aCATGTCACC	3060
	ATGCTTCCAC	CTCGAACCTA	TTAACCTCAT	CATCTTTGAG	GGATCTTATA	ACCGAAGTTG	3120
10	GGAAATCTCA	TCTTGAGGGG	GGCTTCATGC	TtnAgGATtT	TCAGCACTTA	TCCCGTCCAC	3180
	ACATAGCTAC	CCAGCTTATG	CnTTGGCACG	ACAACtGGTA	CACCAGAGGT	ATGTCCATCC	3240
	CGGTCTCTC	GTAATAAGGA	CAGCTCCTCT	CAAATTTCT	ACGCCCACGA	CGGATAGGGA	3300
15	cCGAACTTcT	aCGACGTTCT	GAACCCAGnC	sTGTACCGCT	TtaATGGGCG	AACAGCCCCA	3360
	CCCTTGGGAC	CGACTACAGC	CCCAGGATGC	GATGAGCCGA	CATCGAGGTG	CCAAACCTCC	3420
20	CCGTCGATGT	GAACCTTGG	GGGAGATAAG	CCTGTTATCC	CCGGGGTAGC	TTTTATCCGT	3480
	TGAGCGATGG	CCCTTCCATG	CGGAACCACC	GGATCACTAA	GTCCGTCTTT	CGACCCTGCT	3540
	CGACTTGTAG	GTCTCGCAGT	CAAGCTCCCT	TATGCCTTTA	CACTCTATGA	ATGATTTCCA	3600
25	ACCATTCTGA	GGGAACCTTT	GAGCGCCTCC	GTTACCTTTT	AGGAGGCGAC	CGCCCCAGTC	3660
	AAACTGCCCC	CCTGACACTG	TCTCCCACCA	CGATAAGTGG	TGCGGGTTAG	AAAGCCAACA	3720
	CAGCTAGGGT	AGTATCCAC	CAGCGCCTCC	ACGTAAGcTA	GCGCTCACGT	TTCAAAGGCT	3780
30	CCTACCTATC	CTGTACAAGC	TGTGCCGAAT	TTCAATATCA	GGCTACAGTA	AAGCTCCACG	3840
	GGGTCTTTCC	GTCCTGTCGC	GGGTAACCTG	CATCTTCACA	GGTACTATGA	TTTCACCGAG	3900
35	TCTCTCGTTG	AGACAGTGCC	CAAATCGTTA	CGCCTTTCTG	GCGGGTCGGA	ACTTACCCGA	3960
	CAAGGAATTT	CGCTACCTTA	GGACCGTTAT	AGTTACGGCC	GCCGTTTACT	GGGGCTTCGA	4020
	TTCGTAGCTT	CGCAGAAncT	ArCcACTCCT	CTTAACCTTC	CAGCACCGGG	CAGGCGTCag	4080
40	cCctATACAT	CACCTTACGG	TTTAGCAGAG	ACCTGTGTTT	TTGATAAACA	GTCGCTTGGG	4140
	CCTATTCACT	GCGGCTCTTC	TGGGCGTTAA	CCCTAAAGAG	CACCCCTTCT	CCCGAAGTTA	4200
	CGGGGTCATT	TTGCCGAGTT	CCTTAACGAG	AGTTCGCTCG	CTCACCTTAG	AATTCTCATC	4260
45	TTGACTACCT	GTGTCCGTTT	GCGGTACGGG	CACCTATTTT	CTATCTAGAG	GCTTTTCTCG	4320
	GCAGTGTGAA	ATCAACGACT	CGAAGACACA	ATGTCTTCTC	CCCATCACAG	CTCAGCCTTA	4380
50	ACGAGTACCG	GATTTGCCTA	ATACTCAGCC	TTACTGCTTA	GACGTGCAAT	CCAATCGCAC	4440
	GCTTCGCCTA	TCCTACTGCG	TCCCCCATC	GATTAAAACG	ATTATAGGTG	GTACAGGAAT	4500
	ATCAACCTGT	TATCCATCGC	CTACGCCTGT	CGGCCTCAGC	TTAGGACCCG	ACTAACCCAG	4560

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	TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGCTCCA CATGTCCTTA CGATCATGCT	4680
	TCAACGCCCT TAGAACGCTC TCCTACCATT GTCCAAAGGA CAATCCACAG CTTCGGTAAT	4740
5	ATGTTTAGCC CCGGTACATT TTCGGCGCag TGCTACTCGA CTAGTGAGCT ATTACGCACT	4800
	CTTTAAATGA TGGCTGCTTC TAAGCCAACA TCCTAGTTGT CTGGGCAACG CCACATCCTT	4860
	TTCCACTTAA CATATATTTT GGGACCTTAG CTGGTGGTCT GGGCTGTTTC CCTTTCGAAC	4920
10	ACGGACCTTA TCACCCATGT TCTGACTCCC AAGTTAAATT AATTGGCATT CGGAGTTTGT	4980
	CTGAATTCGG TAACCCGAGA GGGGCCCCCTC GTCCAAACAG TGCTCTACCT CCAATAATCA	5040
15	TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA GCTATYTCCA GGTTTCGATTG	5100
	GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA ACGTAAGTCG GTTCGGTCTT	5160
	CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA	5220
20	CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT	5280
	TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT	5340
	TAACGGGCTC TGACTIONTG TAAGCACACG GTTTCAGGTT CTATTTCACT CCCCTTCCGG	5400
25	GGTGCTTTTC ACCTTTCCTT CACGGTACTG GTTCACTATC GGTCACTAGA GAGTATTTAG	5460
	CCTTAGGAGA TGGTCTCTCC AGATTCCGAC GGAATTCAC GTGCTCCGTC GTACTIONGGA	5520
	TCCACTCAAG AGAGACAACA TTTTCGACTA CAGGATTATT ACCTTCTTTG ATTCATCTTT	5580
30	CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT ACAACCCCAA	5640
	CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA GGAATCGAA	5700
35	TTTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG CCTTCTGATA	5760
	TGCTATGTAT TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCGGAA	5820
	ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT	5880
40	CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC	5940
	ATCCTACAGG AAACGCGTTA TTAATCTTGT gaGTGTTCTT TCGAACACTA GCGATTATTT	6000
	CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA	6060
45	TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA	6120
	AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC	6180
	AATATGTCAC ATTATTCGCG ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG	6240
50	AGTGATCCA GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT	6300
	GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC	6360
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ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480
 GAGAACAACCT TTATGGGATT TGCTTGaCCT CGCgGGTTCG cTkGCCTTTG TAATGTCCAA 6540
 5 TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

(2) INFORMATION FOR SEQ ID NO: 3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60
 20 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120
 TGTAAATTGTT TGTGTTTACG TATTTCTGGT GTAAGTTCCG TGAAACCAAT GTCTATATTC 180
 CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240
 25 TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCAn TCCCCnCCAA 300
 GCCCATnGAG GTACCTTTAA TTTTA 325

(2) INFORMATION FOR SEQ ID NO: 3116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

CCGnTTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60
 40 GnTTTACCTA CTAAATTTGA GGCGGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTCA 120
 GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180
 45 TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

(2) INFORMATION FOR SEQ ID NO: 3117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGThTTTT GAAATGATTG CGGCGATGTT GGCGACAGTT AAAGTAGGTG GCATCTTATA 60
 5 TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120
 TAACTGCAGT CATGTCTTAC GGC GTTgNAA TTGAAACGAC ATTACCAGTC ATTCAATTGG 180
 10 AAAATGCTAA AGGCTTTGTT GAATCAAAGG 210

(2) INFORMATION FOR SEQ ID NO: 3118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60
 GTTGCCATTC AACACTTGAT TAATTTCACT TAACTTTGA CGCGCTGCTT GTAATTTTGG 120
 25 GGTGTACGCA TTAAACGAAC GGnCGTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180
 GTTCTAAATT GCGTTTCCAA GTTThAAGCG GCGCTTATCT GGTGT 225

(2) INFORMATION FOR SEQ ID NO: 3119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTAG 60
 CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120
 GAGTGCGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180
 45 GTGTGTTGAT GnCGAnCACA ACCCCTCCGA ACACGCTTAA TG 222

(2) INFORMATION FOR SEQ ID NO: 3120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60
 5 GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120
 TACGATTCTT GTTTATATGC CATATATCAC ATCTTATTTT ATGGACGCGT GCTATCGGCG 180
 TACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240
 10 ACTTTG 246

(2) INFORMATION FOR SEQ ID NO: 3121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

CAAATACCTT CTCAACnTTG TACTTTTTTGC CTAATTGAGC TGCACGAATT GCTGCAACGT 60
 25 ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACCTAC 120
 CATGTTTTAC CCCTCCATTA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180
 CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGAKrtGct 240
 30 AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTTGAGC AATACGGCCA 300
 ATTCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360
 35 TGAACCGATA TTA CTGATTG TGCATnnGCA CCTTnCAT 399

(2) INFORMATION FOR SEQ ID NO: 3122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60
 TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120
 50 ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180
 AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

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(2) INFORMATION FOR SEQ ID NO: 3123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

5	GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT	60
10	AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAATCGGC GAATATCTGA ATTCAAACC	120
15	AGCGATTATC ACAGCAATTA TTTAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG	180
20	TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCACT AGCTTGCTTA ATGATGCACT	240
25	TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA	300
30	TCGTnGGCCn ACGTTAACTA ATTCnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA	360
35	GTACGCCAAC TGCCACGA	378

(2) INFORMATION FOR SEQ ID NO: 3124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

35	TATTGCAAGA AATGAACTGC TGATTTTTAT AGTTTTAGTG GTCATAAAAT GCTTGGACCA	60
40	ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG	120
45	TTCGGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC	180
50	TACTAAATTT GCAGGTCGGG TTAATCCCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG	240
55	CnAGGAAGCC T	251

(2) INFORMATION FOR SEQ ID NO: 3125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

5 CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA 60
 TCCATACGTT CGATTTTACT CTTGCGATTT TTAATGTTAG TTGCAATTC ACGTTGAACT 120
 AATTCTTTCA TTACGAATGG TTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT 180
 TGGTACCATT TCCAGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA 233

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(2) INFORMATION FOR SEQ ID NO: 3126:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGACCTT GTTGnCTCC ATTGGCAATG 60
 TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTTG ACGTGCTTTA TTTTACAGCA 120
 25 TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC 180
 AATCACATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCTTGAT AACTTTGCAC 240
 TGTGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA 300
 30 TGTCTTAACA TTATCGACAA CGGTGCCTTG TAACCCCTTCT GTCAATGTCA GTTGTTCAAC 360
 TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA 413

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(2) INFORMATION FOR SEQ ID NO: 3127:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

45 GTCGTAAATA CTGAACAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA 60
 CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG 120
 50 TANATCATCT TCTACATACA TAGGTAATTT TATGSCGATT CCTCATGGAG CATCCTGTAA 180
 AAAGTTTTAC AATCACATGT GCTTATTTT 209

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(2) INFORMATION FOR SEQ ID NO: 3128:

(A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

10 TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC 60
 TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTTGGTAT 120
 ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG 180
 15 CCTTCnAAAA ATATGCTGAA AGnC 204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA 60
 30 AATCTTAACT TATCGAAGTA TCCTGTTTTT TCTGCAACAC CAATACCAAT CATCACTGCT 120
 AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTTAAT CGTATTCTTC TTATCATCGT 180
 AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC 239

35

(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT 60
 AATATATTCT CTnGTCTCAA CCTTAATCGT ATACTTCAGA CGTCTGTTTG TAGACAATAA 120
 50 AGTCATTCAC GTCTTCATAT GTCATCANAT GTTTATCATG ATATGATGAT ATATAATCGG 180
 TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG 240
 CTGAGAGCTG TGTATCAGT 259

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60
 TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120
 CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180
 CTTGTnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

(2) INFORMATION FOR SEQ ID NO: 3132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGnATCATC TGCTGCTGTA GcnTAGCAGG TTCAATTTCA TTTATCGGAT 60
 TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAAGTTG TATTAACCAA 120
 TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180
 TTACAACCAG GTGGGGTTCC AGC 203

(2) INFORMATION FOR SEQ ID NO: 3133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGGTA GCTGGCACAG ATATTACGAA 60
 TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120
 AGGTTATGTC AAAGTGAATT ATGTTTTTcn AGTGCTAATT CTGCTGTAA GGTGACACAT 180
 TCAAAATACT GTACCTAAGG A 201

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60
 CGAAAGAGGT ACCGnCGAAT ATTTCAAGG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120
 AATCATCATT CTTTATGCAT TAGGATTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180
 AGCGGAGGTA TTTTAAAATT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60
 GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTCGG TGTTAGCGGT GGAGTGCAAn 120
 TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180
 CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCAnTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60
 AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTTGA 120
 ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180
 TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

ATTGGGAAAT GTTCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG 60
 GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAATTGnA 120
 AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT 180
 TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA 240
 AGAATCCTGC CTTACCTAAG 260

(2) INFORMATION FOR SEQ ID NO: 3138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTGTGATTA TCATTGCTT 60
 TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCATT ACTTTCATA TTATCTTCAA 120
 GCGATAATTT CTTAACTGCA CTTACCATT GCTCAATTGC TTCTGCTAT TGTCATTGCA 180
 TATCGGAGTA GTAGGAAGTG CnGAATTCGG CA 212

(2) INFORMATION FOR SEQ ID NO: 3139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT 60
 TGAATGTTG CGACGCTTAG ATCAGAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA 120
 TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA 180

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300
 GAATATGGTA CAAATGTTTT AACAAATGGCA CAAAGATGCA ATTGAAACCA GGTnCAACGT 360
 5 GTGTTAnTAC AGG 373

(2) INFORMATION FOR SEQ ID NO: 3140:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60
 20 TCGTTTTTGTGA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120
 CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180
 ACCnTGCCCC AACTAAATG GCATTGGGTA AAACCAnTG 220

(2) INFORMATION FOR SEQ ID NO: 3141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60
 ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120
 40 TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

(2) INFORMATION FOR SEQ ID NO: 3142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTTAGC ATTTGGTTTA ACAACnGGT GTTGCAATAT CCCCACTTAA GGTCTGTATA 60

ATTCATTTT TATGTTCTC GATAACTTGT ATTGCTGCTT GTTTTCCTCC ATCTGTCAAT 180
 CCATCATTTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60
 ACTGACTGAG CCATAAAATG CGAAAGTTAC TCGCCCATAT AGACTGATTA ATCATATGTC 120
 ACCATTGGAT TTGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180
 AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGT TTTGAAATGG GCCCACGGGC 240
 TTGTTTTAAT CAAAATTAAA AAATTGTGGT nCTTGGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60
 CAGTAAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120
 GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCtATAGT ATTTGTAACC ATCTTTTAGT 180
 TGATaAATGC CACGCGCATC TGTTATTGCG TCATTTTtag GTAcAAATG AATTTkGAGA 240
 TTTCTCaCaT TATCAGGTAC TTTAAATAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300
 TCAGCAATCG TATCATTAGT ATCAGCATT TtGATAATAA CATTtGTTGC GCCTTGACCG 360
 TTTTtagTAG TCATTGTATT AAATCAAGGT TAATTcAGAA TTCGGATTtA CTGTTAATGC 420
 TTTCTCGATA CCATTAAAAAT CGCCATGGTC ATTcGTATCA GTTCCAGTAT ACGGCCTAAT 480
 GCAATACATT TGCCTGTGcn TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

(A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

10 ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTC 60
 ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120
 TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180
 15 TAACCATAGT TTGGTTGGAT CCAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240
 TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCCTGGTA ACCATGGTGG TGGTAATAAC 300
 CC 302

20

(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

30

CAGGAATAGG ATCATTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60
 CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCTT 120
 35 CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180
 AACCAATCCA CTTTCTACCT GGTTTCGGGT AAATTTTAC CTCCATACCA GGGnCTCCC 240
 CCTTTTTTGG GCCAAAATAG GAAAAAGAG GCGGGGAAA TCCTCCCCC AATTCCnTTC 300
 40 CTGGCCCTGG AGGTTTCCAC CTAAATTTTT TT 332

40

(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

50

GAGAGTGGTT AACAAGCAAA TAGAAATAAT TAAAAATGCA GATGCAGATG CATCGGCGAA 60

55

CnCCAAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180
 TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTGGCC TTGGATTTT AAGATATTGG 60
 TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120
 CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180
 TTTTGTTCa GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60
 TTATGGCTAT CATTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120
 TTGTTCTAT GATAGGTCAC GATTATTAAa AGTGCATTTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60
 TCTGGCGGTA CCATTACAG GTACCGCAGC TTATTAAAGC AACATCACGG GCAATGTTAT 120

A

181

(2) INFORMATION FOR SEQ ID NO: 3151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTTAATTG AGCGACATAC TCTTCTGTTA GCTCTGCTAC TTTTAAAT AGAGCGATTG 60
 ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120
 CTAATAAAT AATTCGAAT GCTATCATTG GTTGTTTCAA CAGCTTGATG CT 172

(2) INFORMATION FOR SEQ ID NO: 3152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTTAT AAGCGATATA GATTTGCGAT GTTGCATTTA TTAAACCTAA 60
 TAATGGTAAA CGACAAGTGT GACTGTTACT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120
 AAATCAACCA AAGTAGGTA TTTGAATNTT GGAATAATG AGACATAGCG AGAGTGTATA 180
 TGCAATACGA CAGTACTNTA AATTAAGAG 209

(2) INFORMATION FOR SEQ ID NO: 3153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60
 TTGCCTAAAG GTTCAATCGT TAAACCTTCC AATAAATTTG CTGTTGCTGG ATAAGGAGAA 120
 ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG 60
 GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA 120
 ACTTAAGAGC AATGTTTGCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTCGGA 180
 AACTTTACAA TATTTGTTGC GGATGATTAT TTAACTTTTC GAGAATGTTG ATGGCACAGT 240
 CCACTATAnC AATCAGTATC GCAATGG 267

(2) INFORMATION FOR SEQ ID NO: 3155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCCCTC AAGAAGCAAA 60
 TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT 120
 TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA 180
 AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG 240
 GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT 300
 TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA 360
 AATTTTACAG TGACAGATAA gTGAAAYCAG GGgATTATTT TmCacGAgTT ACCAGATatT 420
 TACTGGTAAT GGAGACGTGG GATTATTCTA ATTCAnATAA TACGATGCCA ATTGCAGACA 480
 TTAAAAGTAC 490

(2) INFORMATION FOR SEQ ID NO: 3156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

CCTTCAGTAC CTTGTAATAG TTAnTTAAAT GTTCCGATCA TCGTGTAAGT TGATTCATCA 60
 5 TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT 120
 TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTTTTTC AGATAGCATC ATTGGTGGAT 180
 10 TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT 240
 TGGCGCACAA TCCnTGCAAC GT 262

(2) INFORMATION FOR SEQ ID NO: 3157:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT 60
 25 TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTGAGCTT CTGCTGTCGT TTTAGCCATT 120
 GGGTTTTTCAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA 170

(2) INFORMATION FOR SEQ ID NO: 3158:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

40 CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA 60
 ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT 120
 ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG 180
 45 CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG 240
 GCAGTTTATA GACATACATT GTGnCTTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG 300
 TACAGTAAGT An 312

50

(2) INFORMATION FOR SEQ ID NO: 3159:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs

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- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

10

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60
AATATCTAAT GTTTAAATC TATCGTCGCA AGATGCTTCC TGTAAATTAT CAGTGCCATT 120
TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

25

CTTGTTTCATT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60
CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATTT 120
CACTGGTAAT ATTTCTGTTCA TTAATCTGA TTGAGGGAAT TCCGCCCATC CAGAGTCCC 180
CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

30

(2) INFORMATION FOR SEQ ID NO: 3161:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

45

GCACAGGTAG CGGTAGTGGC GGTCTATGA TGACTTTGGT AATCTAAAGC AAAATGTACG 60
ATAATAATAA ACGTCGTTTC GTTCTCTGA TGTAGCAGGG GCAGTGAAGA AACAAGATTA 120
TTGAATTGTT GATTTCTTGA AGATATAAAA ATTCAAGAAT GGTCTAGGA TTCCTAAGGT 180
GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240
CTCTTTTGGG TCAGTTTGG AGTTTGTGTT GTCGGCTGTC GGATTnTCGT ATGTAGGAAC 300
GGCTGTTTAC TThCGTGAT G 321

50

(2) INFORMATION FOR SEQ ID NO: 3162:

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- (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

10

AACATTTGAG CAATATCAAG AAACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60

TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGTT TATTGCGGCG 120

ACACTTTTAC GAGGCGTGCA CTTTATACAA GTGCCanCG 159

15

(2) INFORMATION FOR SEQ ID NO: 3163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

25

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60

TTTTTAAGCT TGAATTTAA CAAATCATAA GCCGTATGAA TATTTAAATA TGCCACCATG 120

ATTGAATGGC CCCTTTCTAT TAGTTanGTT TTGTGCG 157

30

(2) INFORMATION FOR SEQ ID NO: 3164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

40

TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60

ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCTAT AGGTATTTCa TCAGCAGGnG 120

45

TTGTTGATGA ACAAAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180

ATTTTAAGGA TTATTAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

5 AGAAACACTT CTATTGAATC GTCTTACTGC TGTTCCTCTAT TTATAACACT TCGTATTGAA 60
 TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTTCTAATGCCTG GATCCTTTAT 120
 ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

(2) INFORMATION FOR SEQ ID NO: 3166:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

20 ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60
 CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120
 25 AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

(2) INFORMATION FOR SEQ ID NO: 3167:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

35 TGTGGGGGAA ACCTGCACAG CAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60
 40 TAAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120
 ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

(2) INFORMATION FOR SEQ ID NO: 3168:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

55

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120
 GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

(2) INFORMATION FOR SEQ ID NO: 3169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGAAAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60
 ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAAA CTGCATGCTT GCTCGATTGG 120
 CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAATT TAGTATGTCA AATGTCCCAA 180
 TCAnTAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60
 TCTAATTCTT GATGGAGGTG AAAACTGTTA ATTTTCATGTC CAGTAATGAT GATAGGCTGC 120
 TTGCGTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180
 GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTTTCAG AGATTGCGAC ATCGATTGGT 240
 AAATGTAAAt GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTTCG 300
 GTTGTTGCAT TTTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTCG 360
 ATAGTCGTCA AATGTACCnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

5 TAGAAGGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TCGCCCAATT GCAGTGTGGA 60
 ACGAGCGACC AGAATCACTA TTTAATTACT TTAAACAGCT GTTGCACAA GTTACGAATC 120
 CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180
 10 AAGGTAACCTT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCGG 240
 TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTAAATT AACTTATTTA 300
 TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360
 15 TGGAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

(2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

ACATAATTTA AAATAATATT ACATTGTAA TGGnCACCAA GTAACGTTTC GGTTGCTTGG 60
 30 TGTTTTTTGG TATGAATTAC TTTCTGTTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120
 ATTAAGATTT AATTACAAAC GGAACTAAA TGTAATAGAA TAAACT 166

(2) INFORMATION FOR SEQ ID NO: 3173:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

45 ATAATGAGAn TGTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60
 CGAAAGACCC AACTCCAGGG ACCGCCGGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120
 GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

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(2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

5 CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60
AACGTTTGAA TTTAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120
TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

10 (2) INFORMATION FOR SEQ ID NO: 3175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

20 TATTTGAAGA TGGCTGTGTA CAAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60
ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCnA GTATGTCGTC AGAGAAGATA 120
CACCTAATCG CTAATTAATG AGGTTTGGA ACAT 154

25 (2) INFORMATION FOR SEQ ID NO: 3176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCTTCAG CCCATACGnT 60
GCGAAAGGTT TATTAATTTC TTCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120
40 ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180
GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CGGTGCAATG 240
GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGGTTATTC TGTTGAAGTA 300
45 ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360
CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420
50 CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

(2) INFORMATION FOR SEQ ID NO: 3177:

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- (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

10 TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AnTTGTCATC TGTGCTGGTG 60
 CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTTAGTAT CTAAAACTT GAAAATATTC 120
 AAATCAATTG TTGGTGAAGT AATGGCATCA 150

15 (2) INFORMATION FOR SEQ ID NO: 3178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

25 TTACTCTATC TTGATTTGAC GAAATACTAT TAnGCTAATA TCGATATTTT AAAAACGAGA 60
 TGATGTTCCA AAGCAAGCCA TTTCGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120
 30 TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

40 CTTCGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60
 ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120
 45 TTAAAGCAGA TTTACGTATG TCTACAAGTT TAnTTGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCCnTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60
 5 GGTGTATTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCATTCA 120
 TGATTGGGGC GATTTCGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180
 GTATTTATTT GGGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240
 10 TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

(2) INFORMATION FOR SEQ ID NO: 3181:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60
 25 ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120
 CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180
 CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACCTA CCGGTTCAAC TTGGTCGATG 240
 30 TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTTG 300
 TThCACCGnT ThCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

(2) INFORMATION FOR SEQ ID NO: 3182:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

45 TACCAACACG TACACCTTCT AAAATAACTG CATTTGCACC GTnTTAATAC ATCATCCTCG 60
 TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120
 ACATGTACAT TTTTACCACT TGTAGCACG 149

(2) INFORMATION FOR SEQ ID NO: 3183:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

10

GCGGTGCCGG TGTTGCAATT GCGCAGTGG TGTTGGTAGC ATGTGGTCTT TCAATCAATG 60
TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120
ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

25

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTTGTTTATA ATTCTCTGTT AAAGAACGAC 60
TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAAACAGT GACATTTTCT CAATCGGCGT 120
ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCCAC GCTAGTCGnC 180

30

(2) INFORMATION FOR SEQ ID NO: 3185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

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GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60
CCGTGCTACA ATCGGGnCAA GTTGGTAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120
CCGGCACGTT CAAGATGGGA AAGGTATCCG 150

45

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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GAATTTThAGG TGAATCAGAA GATTAACGCT GTTGCCTCCT AAGCTAACAG ATACTGGTTC 60
 GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTTAATAAA ACCGTAACTC GAGCATTATT 120
 5 AGAGGAAGCT AACCAAAGCA GGTTTA 146

(2) INFORMATION FOR SEQ ID NO: 3187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60
 20 AAATGGTGTC ATGTATTCAA CAGTCTGTTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120
 AAGGTCGGAC CGTTTGCGCA ATTGAGACCA GGCGCGCAAT TAGGG 165

(2) INFORMATION FOR SEQ ID NO: 3188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60
 35 ACATTCTTTG GTGTAACGn AACCAATTTT ATTGGTGCC ACCACTAGTT ATTGGAATCC 120
 TGTGTTCTTT ATTCCATTG TATTAGCACC AATTGTTAAC GTATGG 166

(2) INFORMATION FOR SEQ ID NO: 3189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

AACCCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60
 50 GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTTATCTA ATTGATCCTT ACCAGTTTGA 120

(2) INFORMATION FOR SEQ ID NO: 3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTGGGAAA AATTTTTTAA CCCCCCTTAA 60
 AATTCCCCGG AAAAAGGAAA CCCGGGTTTT TAAAAAAAC CCGGGGTTCC CAAAAATTTT 120
 TTGGGAAAGG GAAAGGAAAA AAGGGTTAAA AAATTTTGG GAAAAACCG GGGCCAAAAA 180
 AAAGGGTTTT TTTCCCCTTA AAAAAAATTT AA 212

(2) INFORMATION FOR SEQ ID NO: 3191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TTGCCCTAC AACGATAGCT AATGATTTAT 60
 ATTGTAAACT CAAATGACCT TGTGAATAC CTCTGACAC AAGCGCGCGA CATGCTGCAA 120
 AGTTTTGCGC TAAACCAACG GCAGCAAC 148

(2) INFORMATION FOR SEQ ID NO: 3192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTTA TTAAACCAGC TGCTTCTAAT AGTTTAAGTG 60
 CACGTGCTTG GTTTGACACA TCATTTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120
 TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCAGG GATGGCTCTT AAATATATGT 180
 TACGTGATAA TTTCTCGAaA AATGGCTTCC CT 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTGGATACT GGTATATTC AGCTGCACCG 60
 CAAGCAACTT CTATTGATGG CCnAACTGCC TTTTACCTC AAGCAATGGG TATGGTAGTT 120
 GTTGCAGTCA TTTATGGCTT T 141

(2) INFORMATION FOR SEQ ID NO: 3194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACGTTT TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCG TGGCGGAATG 60
 GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120
 GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAA ACCTCAGCCT 180
 TCCAAGCTGA TGTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240
 ATTGAAAAC GAATGACAAT ATGTCAACGT TAATTCCAAA AACGTAAC TAAGTTACAA 300
 ACATTATTTA GTATTTATGA GCTAATCAA CATCATAATT TTTATGGAGA GTTTGATCCT 360
 GGCTCAGGAT GAACGCTGGC GGCCTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420
 GCTTGCTTCT CTGaTGTTAG CGGCGGACGG GTGAGTAACA CGTGGaTAAC CTACCTATAA 480
 GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540
 CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600
 GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660
 CACTGGAAC GAGACACGGT CCAGACTCcT ACGGGAGGCA GCAGTAGGGA ATCTTCCGCA 720
 ATGGGCGAAA GCcTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780
 CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAAGTGTGC ACATCTTGAC GGTACCTAAT 840
 CAGAAAGCCA CGGCTAAcAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAAACT GGAAACTTG AGTGCAGAAG AGGAAAGTGG 1020
 AATTCCATGT GTAGCGGTGA AATGCCGAGA GATATGGAGG AACACCAGTG GCGAAGGCGA 1080
 5 CTTTCTGGTC TGTAAGTGAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140
 CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG 1200
 TGCTgGCATA ACGCATTAAAG CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260
 10 AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

(2) INFORMATION FOR SEQ ID NO: 3195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60
 25 GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTCG TGCTAACAAT 120
 CGATGGTTTA CnAAACCTTA 140

(2) INFORMATION FOR SEQ ID NO: 3196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60
 GCATTTGTCTG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120
 45 CTTTACCAAC GntAATATTG TTGTC 145

(2) INFORMATION FOR SEQ ID NO: 3197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGTGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GSTATGGGAAT 60
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCh 240
 CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300
 10 TnTTCAGCTG 310

(2) INFORMATION FOR SEQ ID NO: 3198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60
 25 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120
 AATTGAATCA GCTTTTnTCG 140

(2) INFORMATION FOR SEQ ID NO: 3199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

TGGTGATTTT AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAT TATTTGTTG 60
 40 TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTTGTTAA 120
 AACCAGTGAT TGCAACCTGC CATTACAnG GAAAATTACC TAATAAGTGG CGTATTTACC 180
 45 AGTC 184

(2) INFORMATION FOR SEQ ID NO: 3200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTTC 120
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

(2) INFORMATION FOR SEQ ID NO: 3201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60
 20 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAGATA CGTAATGTnT 120
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

(2) INFORMATION FOR SEQ ID NO: 3202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAAGTGT 60
 35 AAAACGAGTG AATTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180
 AAAGTCCGAT TC 192

(2) INFORMATION FOR SEQ ID NO: 3203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTGT ATTGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAGC 120
 ATCTTATAGC GTGATAGCCA TCGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180
 5 TAAGCAGTAC ACACCAGTAA CATTTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60
 20 TTTAATTACG NAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTGTGTC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TCGCATTAT 60
 35 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACC TTCAGTG CTTACTGGT 120
 CATCTAAATG ATTTT TAGCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60
 50 GACTTTCAGT CGTAACGTTT ACAAAC TTAA GCGCACGTCA NATGAAGCAT CGTGTAGACC 120

(2) INFORMATION FOR SEQ ID NO: 3207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60
 AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GntTAATGAA TGCATTAAGA 120
 AGCTGCAAGA ACTTATAAGT GTGCA 145

(2) INFORMATION FOR SEQ ID NO: 3208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnaAT CACACTTAGC 60
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTTATCAA CGGTATATGA AGGGGATTG 120
 GAAGATGCGT T 131

(2) INFORMATION FOR SEQ ID NO: 3209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60
 CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTCTGT AACAGCGCCA 120
 TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

(2) INFORMATION FOR SEQ ID NO: 3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60
10 AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120
AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

ATGCATACTG TATGTGTTCC AGCATATACA ATTTTnCCA TCTTTAATGA CAACTGTACC 60
25 ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTTGATCTC 120
GGTAAAATTA ATTCTGC 137

30 (2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

40 ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60
AACAAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120
45 AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180
ATTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT 239

(2) INFORMATION FOR SEQ ID NO: 3213:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60
 5 TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120
 TCAAAAGTCT TGATATTTGA TACCCACGCT 150

(2) INFORMATION FOR SEQ ID NO: 3214:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

20 CTAAGCATTG GTTTAACTA ATGTTTCTAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT 60
 nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120
 TTACGATATT ATTAACAAC TGTcTATCAT TAACGAAAGC AATTAACAAG AGTACTTGTT 180
 25 GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240
 TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300
 TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360
 30 TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

(2) INFORMATION FOR SEQ ID NO: 3215:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60
 45 CAGATAATTT AGATAAATAA TTAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120
 ATAACTAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180
 50 TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT 240
 GACATCATTA AGAATATAAA TGCCTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA 300
 ATTTTTCAAT AACAAATGCG CCACTAAAAC TCAAAATTTT CACCACCAAC ATCCAAATTA 360

55

(2) INFORMATION FOR SEQ ID NO: 3216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120
 CTTGCTTTAT GCTATGGGTT TTTCAAACCTT AAA 153

(2) INFORMATION FOR SEQ ID NO: 3217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TG TAGACCCA TCAATTGCAG 60
 CCATTACATA TGCGGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120
 AnATAAAATT ATTACATC 138

(2) INFORMATION FOR SEQ ID NO: 3218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60
 TTATGcmTTT TaTTGcmCma GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTCGATGGG CCAAACACAA 240
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTTGA TTAAACAAAT TTATATGAAG 300

AACAACGTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTT GAAACAATAT GGAGAAGCAG 420
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGCAGC 480
 5 ATATGCA 487

(2) INFORMATION FOR SEQ ID NO: 3219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

(2) INFORMATION FOR SEQ ID NO: 3220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTGC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCnGG 60
 35 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180
 40 TATGTAATTG TTTTGTGGTT ACG 203

(2) INFORMATION FOR SEQ ID NO: 3221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTGAGA 60

GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240
 5 TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCTCA 300
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCnGGGG TACACCTGGT CCACTTCATC 360
 A 361

10

(2) INFORMATION FOR SEQ ID NO: 3222:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120
 25 GTGCGTACAA GAATTAATCA AGGTTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60
 40 AATACATCTC CAACATTTGC CTTnAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120
 TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

55

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCTAAGC ATATTTCTGA 120

TGATTTAACA CATTATGAAA CGAGA 145

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60

CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120

TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60

TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120

CATCTANTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CanAAATTCG TCATTCAGTT TCAACTTTAT 60

CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120

TTATCTGGCA ATAATCGTTG 140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60
 TGACTTGCTT GATAAATAGC AACAAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

(2) INFORMATION FOR SEQ ID NO: 3229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60
 ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GntTCTACA 119

(2) INFORMATION FOR SEQ ID NO: 3230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60
 CTAAATGTTG GAAAAATTTT TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCTACAA 120
 GAGCAGGG 128

(2) INFORMATION FOR SEQ ID NO: 3231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60
 AAGTATCGTG TACAAGTTAT GAATGANTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120
 TTC 123

(2) INFORMATION FOR SEQ ID NO: 3232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAAC 60
 CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA TTAGGACATA 120
 TAAATTCATC ATTAAGTTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180
 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACTAAT AAGTGGCGTT TTATTAAAAT 240
 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAAATAACC 300
 GAAGLATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360
 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420
 TTAAGTTGGC CATTTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480
 GTTTTAGAAA AACTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540
 CTTTCGGAAT AATCATCAAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTtaCGGG 600
 TCTGTTTTCT AATTTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720
 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTGAAT 780
 TTTTCGTTCAA TTTTCGATTCG TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840
 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900
 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020
 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080
 TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140
 CGCTATCAGG TATCGTTTCA ACAATTTTCAT TAACATATCG CGAAATATCA ATTTGAGGAA 1200

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500
 ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560
 10 CTGCTGTTTT TTTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTAA ATAATTTGAA 1620
 TATGGrAAAT GTATTaWTct CTCATTTGTA TAGATT 1656

(2) INFORMATION FOR SEQ ID NO: 3233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

TTGCTCATAA ATCTTTTCTT GCGGCTCTGA ACACTATCTT CTATTCTGTC GGAATTTTTT 60
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120
 GGTAATCCA 130

(2) INFORMATION FOR SEQ ID NO: 3234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCCTGGG 60
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120
 45 AA 122

(2) INFORMATION FOR SEQ ID NO: 3235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAAC TG CTACTATTGA 60
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAGC ATTACATGCA TGAACCCAGT 120
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTG CAGnTTCCAC ATG 173

10 (2) INFORMATION FOR SEQ ID NO: 3236:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60
 AGCGATTANA AAGCATTAT CAAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120
 CA 122

(2) INFORMATION FOR SEQ ID NO: 3237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

35 TTTTTTGCCC AAAATTTTTG GGTTTTTTTT GGGTTAAAGG AAAAAAATT TTAAAGGGG 60
 GGGGGGGGTC CCCC AAAAT TTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120
 40 CCCCCCCCCT TTGAAAACC CCTTAAAAA ATTTAAAGGT TAAATTGGAA AAAAAAATT 180
 AA 182

(2) INFORMATION FOR SEQ ID NO: 3238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGANGTTC GACAACGTAT TGTGGCAGAT GTTGCACTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60
 GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60
 AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120
 AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60
 TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT 120
 GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60
10 TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60
25 GTTGTATATAG TCTAACAATG GTTGGCTCCT CTTATTTTAT GTGCTAAAAA TTTATAGGCA 120
ATTTTATTAC AACAAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATT 180
30 AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60
45 CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120
ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

(2) INFORMATION FOR SEQ ID NO: 3245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

5 GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTTAA AATTTGGAGA TTATGTGTGG 60
TGTTCAGTA TCGGTTCAAT AATTGATATT GCGGCACCGT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTTGTTACA TACGCATGAT 60
20 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTGnCC AATTGTTACT ACCGTTC 117

(2) INFORMATION FOR SEQ ID NO: 3247:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACAnCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60
35 AGCCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60
50 ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120
CnTTTGGTCC TGCCA 135

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTACATG CCATCTGAAT CTCTAATTTT 60
 AAAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60
 TCTAGTATTC CAAGTTGAAA AAACTTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120
 GA 122

(2) INFORMATION FOR SEQ ID NO: 3251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60
 CAAATTCATC AATCACAAAT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120
 CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60
 5 TGTAAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

(2) INFORMATION FOR SEQ ID NO: 3253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60
 20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120
 GTAACGGCAC TATATTGAAA 140

(2) INFORMATION FOR SEQ ID NO: 3254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60
 35 TTTCTCTTCT ATTTAAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120
 CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC ATACGTAGCA 180
 40 ATGAAATCAT CTAATTGTGC TTTAACCTWT TCTTGTGTAC CTGcAATGAT GCGTGCTTGg 240
 ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300
 TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACChA ATAACCAAAC ATCTAAGGCA 360
 45 GTTGTAAGCG GChACTTCCG CTTGTTATC AGChACAAG 399

(2) INFORMATION FOR SEQ ID NO: 3255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAAC 60
5 GAAGCTATCG TCTCACTAnC CTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAATTC AGTTAGTAAA 60
20 AAGTCTGTGA GTAAGGGTGT ATGGAAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAAGTGT ACATCGTCTA ATAATAAGTT 60
35 GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60
50 GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 124 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG 60
10 CACCTTGCCAT ACTTTTAAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC 120
GnTT 124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

TACCAATGTA TATCCATATA CTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT 60
25 TTTGCTTGAT TAAAACTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG 120
TACAATAAT 130

30

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCTTAA TTTTTTAATT AAATTTTGA 60
ATTAAAAAAG GAAAAAATCC AAAGGTTAAT TTTAAAAAA GCCCAAGGTT TTAAAAATTC 120
CCCCAACCAA AAAGGGGGGG AAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG 180
45 GGGCCCTCCC TTGGGGGTTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA 240
ATTGGGGGTT GGGGCCCTGG GGGAAAATT TTGCCCTTC CCAAGGGGTT TTTTAAACC 300
CGGATTTTTG GAAAAAATA AGCCCATTTT CCCCCCAACC CnAAAGCCCA GTTCCCGCCC 360
50 ATTTCCCGG GGTAAACCCTG CCCCACCGG GGCCATTTT 400

(2) INFORMATION FOR SEQ ID NO: 3262:

55

(A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTGGATGT TGAGAGACGT 60
 GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120
 GCGACGGCTG ATGG 134

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25 TTTTTTCTG TTGGTACTTG TTTTGTGGTT GGCGATTGTG GTGTGTCTGA nTTAGTAGAT 60
 TGCATTGGTT GTGGCGTGTG TGCTTGATGG AGGTGTTGTC ACTTT 105

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40 GTTCCATCAT TCCCACnAT ATCCAACATG TGGGCTACTG CAATGCTTTA GCGGTCAATG 60
 CCTCATCATC ATCAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

(2) INFORMATION FOR SEQ ID NO: 3265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTCGCCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

TTACCTTTAA AATAAnGTTT TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG

60

GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA

104

(2) INFORMATION FOR SEQ ID NO: 3267:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACAAACAT GCAAATGGTT CAAGTATCAT

60

ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA

117

(2) INFORMATION FOR SEQ ID NO: 3268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC

60

AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C

101

(2) INFORMATION FOR SEQ ID NO: 3269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

5 CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60
 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120
 ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGT TTTAGCCTGC nGCTGCCTCG 180
 GGGTTTTCTT TAAATTAATG nAACCGC 207

(2) INFORMATION FOR SEQ ID NO: 3270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

20 ATATTCGCAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTAC AGTGATAAAA 60
 GGGCTTGGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

(2) INFORMATION FOR SEQ ID NO: 3271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

35 TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60
 GATCAGCACC AGATATTGCA GGTAAAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120
 TT 122

(2) INFORMATION FOR SEQ ID NO: 3272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

50 GAAGGATGAT GATTCCGAGC AnCTTCTTGC AGAAGAnGCG GnAATAACGT GACATATTGT 60

TGCGAGCGCT TGACAATCTA TTCITTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTTGA TTTTtTGAAA ATAAAGCAGT 240
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTTACTT TGTACATTAT TGTAATTTCA 60
 GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTCGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60
 TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAACtGGT AAGCCATTAC 120
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240
 nTGATGTGCG AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

45 (2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60
 CCGGCGATAT CTGGCATCTT TTATTTTCGGC ATTTTTTCAA ATCATGGTTA TTCCAGTTTG 120
 5 GCGGCTTAAA AATTCnTT 138

(2) INFORMATION FOR SEQ ID NO: 3276:

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GnATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60
 20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

(2) INFORMATION FOR SEQ ID NO: 3277:

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCTG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTATC GTGTGGCATT 60
 35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACCTGTT GCGAGTATTT CCGGTCTCGT 120
 CATT 124

(2) INFORMATION FOR SEQ ID NO: 3278:

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60
 50 CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

(2) INFORMATION FOR SEQ ID NO: 3279:

(A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60
 GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60
 TTCGTTCCCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

40 ACTATGTTTG AAAAAATCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60
 ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

55 ACTTGGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

(2) INFORMATION FOR SEQ ID NO: 3283:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

15 AAATGACGAT AGAGTCAGGT ATTAATCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60
TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

(2) INFORMATION FOR SEQ ID NO: 3284:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

30 TTAAGAAACC GAGCAGCGCA TAAncCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60
CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

(2) INFORMATION FOR SEQ ID NO: 3285:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

45 TAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAC GGCTGTTTTA 60
AAGCATCCTC CCATAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

(2) INFORMATION FOR SEQ ID NO: 3286:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60
 5 TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

(2) INFORMATION FOR SEQ ID NO: 3287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCnAG AACCCATTTT TTGAATATTT 120
 CACCACTCGA ATCATCAATA C 141

(2) INFORMATION FOR SEQ ID NO: 3288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60
 35 GCGGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

(2) INFORMATION FOR SEQ ID NO: 3289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAGCA 60
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

(2) INFORMATION FOR SEQ ID NO: 3290:

(A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTT AAGCGATGAT TGCAATTAGA 60
 CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTATATT GGAGATGGTT AAAATGCTAA 60
 AACTCAACAT GAGTAACCAA AATATTGCCC TTA AAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60
 40 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

55

GCGCGTAATA CCTGCACTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

(2) INFORMATION FOR SEQ ID NO: 3294:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

15

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT

60

AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n

111

(2) INFORMATION FOR SEQ ID NO: 3295:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

30

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTGTCCG AATCCCCATC CTGCACCTGA

60

TAATAAGGCG AATAGCAAGT TGGTCCCGT nGGGAAGCCA CTTGA

105

(2) INFORMATION FOR SEQ ID NO: 3296:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

45

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTGCCATG GCATGATAGT CCAGATACAT

60

GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTAAAAACCT GCGGGTTGGT TAAACCATTT

120

AACCTAAATG GGTTCOAAGG GTTAACGCGG TTAAATGTT TGAAAGGTT TnCCCAGTTT

180

CCAAAAAGTT TTTnATTCCC C

201

50

(2) INFORMATION FOR SEQ ID NO: 3297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTTCTCTGA 60
10 GAAATATTTT CATCTTTTAC ATTTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA 120
TCTTGTAATT CTCTTGAAAC ATCATACATC TkGGCCACAT TTTCAGCACC TkGAATCATT 180
GATGGGTCGC TCATTTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT 240
15 TCGTACACAG AATGCGGTCTG TTTGATTTTC CAAGGTGCTC GACTTGTACT TTCAACACCA 300
CCTGCAATAT ATACCTTGCC AGCTCCGGCT TGGATCATGC GACATGCATA TTGaACACTT 360
TCAAGTCCAG ACCCACATTG cCGATCGTT GTGaGCCAG TATTGAAGCT TAAGC 415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC 60
CCATTTAGGT GCATCGACCA ACTGCCCGAC GAAAAGCCAT TTTGAAAACC AGAAGATGC 120
35 CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG 164

(2) INFORMATION FOR SEQ ID NO: 3299:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTITT TAAATGCGAT GTGTGGCTTC 60
TACATAACGG GAAATTTTAA GTTTTATGAA TcACATATC AATTGC 106

50

(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCANTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60
CATTTAAGGA AGCGATTAC AATCGAGAAC ACAAAGTACA AC 102

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAAAT GATATTGGCG 60
CACCGTATAA CCATGTCAAA GTACCATTTC TAATCAGTCA TTGGCGCAAT GGCTGCCCTA 120
GCGTTCA 127

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTGAAACGT CCATGGACCC AATTGATTAA 60
TTGGnTGTA CTCGGTCAAT GGTATATCC TAAATGCACT GGCCTGCTGG TGTTCTTCTG 120
GGCGTTGCTT CGGAAAT 137

(2) INFORMATION FOR SEQ ID NO: 3303:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATLATT 300
 TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTCCGTT 360
 10 AAAAGCGTTG GCACAATCCA CAATGCCAAG TGCCAAAGT 399

(2) INFORMATION FOR SEQ ID NO: 3304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

(2) INFORMATION FOR SEQ ID NO: 3305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTACCCTA TTTTGTAAA TGGAACATGG 60
 AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTTGCGTA TTCATTCCAG 120
 40 CTTTGTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180
 TTATGTCCAG TTGGACGCCA GA 202

(2) INFORMATION FOR SEQ ID NO: 3306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60
 AACTACTCCC GACAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTCGTTA CCTGCGCCTT CTTTTGCGG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60
 35 ATGGTTTCGCA ATAATTTTAA AATACCTTCC GCTACATTG ATTTAAAGCT GGTTGCGCAN 120
 TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCCTTTTA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60
 50 GGAAACGGAC ATTCAAAAGG GATTTAGTTC ATCCCAGATG GATTTCAATT TGGGGAATTC 120
 CATTTGGA 128

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCACACGA CATCTGTAGC TGGTATTGAT 60
 CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60
 CAGCGATTTCG GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60
 AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120
 TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60
GCACAGTTAA ATGATGCCAA AG 82

(2) INFORMATION FOR SEQ ID NO: 3314:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60
TTATCAAAAT AGTGAGGGGC GTCATCA 87

(2) INFORMATION FOR SEQ ID NO: 3315:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCATTT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60
TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120
TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGTnTA TTAGCAACTT GGAAGTGCCA 60
TTGTTAAATT CAGCTGTCTG TTACATTTCA ACCATAGTCT TTCACAAT 108

(2) INFORMATION FOR SEQ ID NO: 3317:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT 60
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA 120
AAGATGATGC ATTAAATGCA CG 142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT 60
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA 120
AGAGCGAGTG ACTTAGGTCA AACACAGAG CAAGGCCAAT GGAAGCCAGT TATTCATGAT 180
GCAATCAGCG ATAGTTTAGT ACTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT 240
AAGAAGTGGG ACTTAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA 300
ATTACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA 360
GATGGGATAT CATCGTCCAA TCCnAC 386

35

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

ACAAATGAATG ACATGATTCG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA 60
ATCGCCGGTC ATAATGTTTC TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT 120
GGC 123

50

(2) INFORMATION FOR SEQ ID NO: 3320:

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- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

GGCGAACTGT CAATTGCCCG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGT 60
 AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

GCGCCGGTTT TAACAGGTAA TTTAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60
 AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60
 TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

TGCCAAATGT TCCCATAATT TCATTACGAN TCTTAAGTAG GTGGCTATCA TTACGATCGG 60

55

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCATAAAA TAATAGTTGA 180
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300
 TAGTGCCAAA CGTTGTTTCA TACCCCGGA CAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360
 TTCTAAATCA ACTAATTTAA GCTGTGCGTT AATCTCTTCA 400

10

(2) INFORMATION FOR SEQ ID NO: 3324:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGnATCC TAATGTATTT 60
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25

(2) INFORMATION FOR SEQ ID NO: 3325:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

TCTGAANTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60
 TCCTGAAATC CGCTAATCTG AACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40

(2) INFORMATION FOR SEQ ID NO: 3326:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

TGTACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60
 TAGCCTTCTT CATTAAACC 78

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60
ATATTCACTA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCCGCGGT GGTTTCCGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60
CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60
TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

(2) INFORMATION FOR SEQ ID NO: 3331:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTAA TAACTCATA CCAAATCCTG
GGCATCTCTT

(2) INFORMATION FOR SEQ ID NO: 3332:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

CCTTGGGCAC CTTCAATTG CATATTACGA CGTTTTGCAG CTTGGTTCAA TTGGCAATAA
CTACACCTAG TGCAGTTGGA TC

(2) INFORMATION FOR SEQ ID NO: 3333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA
AAAACAAGTA TATTGA

(2) INFORMATION FOR SEQ ID NO: 3334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

5 TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTTCCCTGGC 60
ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60
20 CATACGAGTA AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3336:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60
CATAGGAGAA AACAGG 76

35 (2) INFORMATION FOR SEQ ID NO: 3337:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTGA CTAAAAAATG TATTTAAATA 60
AGTAGTACCT AA 72

50 (2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTAAATATGC 60

10

TGTCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

25

TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTAAATGAAT GTCITCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

40

ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTAATCCTT GGTIGCTCTT TATTTATTT AAATTGTAGA 60

55

ACCTAGA 67

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTAC AAGCATCAAT CCATTAAATTA ATAATTCCAT TAAATGTAGA 60
 TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TCGCGATATC 60
 ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGaAATGA 120
 AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180
 AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240
 CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300
 TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360
 CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60
 TCGCAGTGGT AATTTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

- (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10 CGGGAGGTGT TAAntCTTCA CAAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60
 TCGGTTTCAGG TGCCACAGGA AGTGATTcAG GTAGCnAAGG GTTATCTGAT ATTTTGAAC 120
 CTGCATTAAg TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180
 15 ACAATATTCT TAAAGATGCT GCATTAAcGC GCAGATTtAA TGAAGTGCTT GTTAATGAAC 240
 CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTcG CGAAAAATTC GAAGAACACC 300
 ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360
 20 TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420
 TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAAACTGG AGAACGAATT TCTG 474

25 (2) INFORMATION FOR SEQ ID NO: 3346:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35 AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60
 TTAG 64

40 (2) INFORMATION FOR SEQ ID NO: 3347:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50 AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAACAAAT 60
 GTTTTAAGTT GTTGATTtAA AATATTAAT 89

55 (2) INFORMATION FOR SEQ ID NO: 3348:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10 ATAACCTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTTCTTT 60
AAAGAACAAT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT 107

(2) INFORMATION FOR SEQ ID NO: 3349:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25 CAACGCATCC TGCATTITTA CCTATTCTCG AATCACCGGT AATTAGTACA CCAACACCGT 60
AAACATCTAC TAAA 74

(2) INFORMATION FOR SEQ ID NO: 3350:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40 AGATGCACCT ACTTCTAACT GTCGCCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG 60
TA 62

(2) INFORMATION FOR SEQ ID NO: 3351:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55 GCTGCAAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT 60

(2) INFORMATION FOR SEQ ID NO: 3352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTCGAT ATAGAACATC TAGCGACGTC GATTGCAAG GTTGAACCAT 60
 CTACATTAGG TGAGGAA 77

(2) INFORMATION FOR SEQ ID NO: 3353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

(2) INFORMATION FOR SEQ ID NO: 3354:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

(2) INFORMATION FOR SEQ ID NO: 3355:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATACC TTTAGGGTTA CTACCAGGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA

(2) INFORMATION FOR SEQ ID NO: 3357:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCAGCCCTT TGAATATGGG AACTCAAAC GATCTACTGG CTGATGTAAT

TACCCCTGTT TTGATTG

(2) INFORMATION FOR SEQ ID NO: 3358:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA

(2) INFORMATION FOR SEQ ID NO: 3359:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA

(2) INFORMATION FOR SEQ ID NO: 3360:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25 GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTCGCT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50 CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTTAA TCGGTTGATT AAAAGTGGCA AAGCACGTGC ACATACGA

58

10

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

20

TTTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT

58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTACTTT GTAATTCAG TAACAGTTGA TCATCATG

58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC

58

(2) INFORMATION FOR SEQ ID NO: 3368:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA

58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG

58

(2) INFORMATION FOR SEQ ID NO: 3370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA

60

TTGACGGC

68

(2) INFORMATION FOR SEQ ID NO: 3371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

ATTACCAACA GCGAAATAT TGAAAAGCTG TAAAAAGCT GGTGCAsmCm TACTTGGATT

60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT

120

TGCACTTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG

180

CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA KCACTTTTAA CGACCAGTTA

240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT

300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA

360

(2) INFORMATION FOR SEQ ID NO: 3372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCAACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA

58

(2) INFORMATION FOR SEQ ID NO: 3373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG

57

(2) INFORMATION FOR SEQ ID NO: 3374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATTT CTTTCGTG

57

(2) INFORMATION FOR SEQ ID NO: 3375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA

60

ACTAACAGAC

70

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG

57

(2) INFORMATION FOR SEQ ID NO: 3377:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG
 CTCGCATCCA

60

70

(2) INFORMATION FOR SEQ ID NO: 3378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT

56

(2) INFORMATION FOR SEQ ID NO: 3379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC

56

(2) INFORMATION FOR SEQ ID NO: 3380:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10 ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35 GAACACACAG GCAACCCAAA GCAGTGACGG CGAAANTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

50 NGTATGTGAA AACTATTTGG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

- (i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

25 TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

- (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTAAAT TATTTCTATT TGCTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

TCTTAACTGC A 71

40

(2) INFORMATION FOR SEQ ID NO: 3387:

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

10 TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCAACTTT TGTTCG 56

(2) INFORMATION FOR SEQ ID NO: 3389:

- (i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTTATTAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

35 AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

50 CAAACGCAAT AGCTGGTGAC TTAAGTGGG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

- (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 55 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTATTAC AAAAGCCAAC TGTAT

55

10

(2) INFORMATION FOR SEQ ID NO: 3393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATTCCATAACGGA TCAATGGCAG GATTG

55

(2) INFORMATION FOR SEQ ID NO: 3394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC

55

35

(2) INFORMATION FOR SEQ ID NO: 3395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCAAT TGTTGGTACA GGTTATGGAA CACGTTGCAG CACGTGATTG TGGTGCGG

58

(2) INFORMATION FOR SEQ ID NO: 3396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

5 (2) INFORMATION FOR SEQ ID NO: 3397:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

30

(2) INFORMATION FOR SEQ ID NO: 3399:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

55

(2) INFORMATION FOR SEQ ID NO: 3401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG

55

(2) INFORMATION FOR SEQ ID NO: 3402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG

54

(2) INFORMATION FOR SEQ ID NO: 3403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT

58

(2) INFORMATION FOR SEQ ID NO: 3404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT

60

TGTCT

65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:

AAATTTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC

(2) INFORMATION FOR SEQ ID NO: 3406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:

TCGATTTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC

(2) INFORMATION FOR SEQ ID NO: 3407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:

AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT

TAAAGATTAG AAGG

(2) INFORMATION FOR SEQ ID NO: 3408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

TGATTTTACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT

AGTGCTCA

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

54

(2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

54

(2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

53

(2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA

60

TCA

63

(2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10 ACTACCATTG CTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC 53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC 60

TT 62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG 55

(2) INFORMATION FOR SEQ ID NO: 3416:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG 53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

55

- (C) STRANDEDNESS: double .
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA

59

10

(2) INFORMATION FOR SEQ ID NO: 3418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20

CGTGTCACC ATCACCAATT GTCGATCTA ATTCAGTAAT TCAGATTCAT GTT

53

(2) INFORMATION FOR SEQ ID NO: 3419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT

55

35

(2) INFORMATION FOR SEQ ID NO: 3420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45

TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG

53

(2) INFORMATION FOR SEQ ID NO: 3421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATRA TAAAACTTA GACCATTCAC 60
5 CCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTTAAG TCGCAATAGT AGCGGCCGTT TCTT 54

20 (2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

30 CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

40 ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

45 (2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTCAAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

52

(2) INFORMATION FOR SEQ ID NO: 3427:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT

52

(2) INFORMATION FOR SEQ ID NO: 3428:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

52

(2) INFORMATION FOR SEQ ID NO: 3429:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAGGT ATTATGGCGG CA

52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTCTTTTTT TTATAAAAAT CTTATGCTTT 60
TTAACTAATT GTAAGA 76

(2) INFORMATION FOR SEQ ID NO: 3431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGGTAAGTC GTATTAGAAC TAAAGCGGCT 60

(2) INFORMATION FOR SEQ ID NO: 3432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

(2) INFORMATION FOR SEQ ID NO: 3433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTAAATTT 60
TAAATTTT 69

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:
 GATCGCTATC CATTAGCTAA ATTAAACGT TCAAACCTCAG GTACATGTTA C

(2) INFORMATION FOR SEQ ID NO: 3435:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:
 TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

(2) INFORMATION FOR SEQ ID NO: 3436:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:
 ATTAAAGCCA ACATTAATTT ATCCACTATT AACAATAACG GCTACAGGCT TATTAATGAT
 TTATACCTTT

(2) INFORMATION FOR SEQ ID NO: 3437:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:
 TTTGTTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTCTTAG A

(2) INFORMATION FOR SEQ ID NO: 3438:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10 GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G 51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A 51

(2) INFORMATION FOR SEQ ID NO: 3440:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35 CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA 55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAACCAG TGTGTAAAAC CGGA ACTACT 60

50 ATGAGGGGCA TGAAAGT 77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA

55

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(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACTTTG GGATAAAGGT GATGCCCAAA CTTTCCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

45

ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC

50

(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

50

5

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATTGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

15

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTCCTCA TCTCTCTACT

60

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(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

40

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

55

TTATCACGGT ATATGAGGGG ATTTGAGG

88

(2) INFORMATION FOR SEQ ID NO: 3451:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

15

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

(2) INFORMATION FOR SEQ ID NO: 3452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GGCCTGGATT ATCAAGTTTG

60

GGTA

64

30

(2) INFORMATION FOR SEQ ID NO: 3453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

45

AAGAATAAGT A

131

(2) INFORMATION FOR SEQ ID NO: 3454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGA AGAAGCGCA

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

(2) INFORMATION FOR SEQ ID NO: 3459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC

(2) INFORMATION FOR SEQ ID NO: 3460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG
CAAAAGCT

(2) INFORMATION FOR SEQ ID NO: 3461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

(2) INFORMATION FOR SEQ ID NO: 3462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:

ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT

(2) INFORMATION FOR SEQ ID NO: 3464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:

TCTTTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT

(2) INFORMATION FOR SEQ ID NO: 3465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:

AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTG CCGACA

(2) INFORMATION FOR SEQ ID NO: 3466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:

ACATCCGAAA GATGACTTGT TTAAAAAAGC AGAGCATGAT TTGCTTACTA TGATTACACG
 CGG

(2) INFORMATION FOR SEQ ID NO: 3467:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCTTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25 (2) INFORMATION FOR SEQ ID NO: 3469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

35 TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

50 CCCTGTTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

5 TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT 50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT 54

(2) INFORMATION FOR SEQ ID NO: 3473:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

30 TAATAGGCAT TCCCATTAGG TGCCTCGACA ACTGCAACGC AAGCATTGTA AACAGA 56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA 55

45 (2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GGC GAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAAnCATTTCG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG

50

(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTTCAG CTGCTAACGA GTTCTGTGA CTGTTTCATGT CTATCACTTT GCGTTCCTC

60

(2) INFORMATION FOR SEQ ID NO: 3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC

(2) INFORMATION FOR SEQ ID NO: 3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTTCTGT TGTAGAACAA
GA

(2) INFORMATION FOR SEQ ID NO: 3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T

(2) INFORMATION FOR SEQ ID NO: 3483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG

(2) INFORMATION FOR SEQ ID NO: 3485:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG

(2) INFORMATION FOR SEQ ID NO: 3486:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG

(2) INFORMATION FOR SEQ ID NO: 3487:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTGTGAT CACACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT
 AATGTAA

(2) INFORMATION FOR SEQ ID NO: 3488:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10

TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTTCG CCACCTTCAC CACTATATTT TCCCATGGTC

60

25

(2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC

50

(2) INFORMATION FOR SEQ ID NO: 3491:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT

52

50

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACTCTTC TAATGGGATA ATCTCTTCAT GT

52

5

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

20

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

30

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

45

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACC GGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG

56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AAACACGTA

59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT

55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

ANTGTACACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA

50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

(2) INFORMATION FOR SEQ ID NO: 3501:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

(2) INFORMATION FOR SEQ ID NO: 3502:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

(2) INFORMATION FOR SEQ ID NO: 3503:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GGC GGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

(2) INFORMATION FOR SEQ ID NO: 3504:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA

(2) INFORMATION FOR SEQ ID NO: 3506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTAAAA T

(2) INFORMATION FOR SEQ ID NO: 3507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT

TTAA

(2) INFORMATION FOR SEQ ID NO: 3508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT

(2) INFORMATION FOR SEQ ID NO: 3509:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

10

CAGATGCAAA TTGACATGGT CATCAACATC nGtnCATTAA AAGATGGACG

50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTCGATTCC CACCGCCACA TCATGATATT TATTCATAGA

60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG

94

25

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT AACTGAAAA ATGGGTAATG GTGCAAACAT AGTA

54

(2) INFORMATION FOR SEQ ID NO: 3512:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

50

CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn

50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC 58

10

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20

GTGTTCTGTGTC TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC 60
AATCTG 66

25

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35

ATGCCACTGA TAATGChnCT GAACTTATTG ATGACTTCTC ATTAGACTAT 50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC 50

50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATGAAG GTGATTGGA TCGCTATCCG TTAGCTAAAT TTAAACGTT C 50

(2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60
GTGATTTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGG 57

20

(2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

30 TGGTGGAGGT TTTGTTTTTT CCGTGTCGGT TTTTGTTC GTCTTGGTTT CTTTGTTC 60
TGTGTTCTCT TT 72

35

(2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

45 ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC

59

(2) INFORMATION FOR SEQ ID NO: 3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGTTACA

50

(2) INFORMATION FOR SEQ ID NO: 3527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT T TGATGCAGGC CT

52

(2) INFORMATION FOR SEQ ID NO: 3528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAA

50

(2) INFORMATION FOR SEQ ID NO: 3529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

5

(2) INFORMATION FOR SEQ ID NO: 3530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

30

GAATGCAAAA TCCATTTGTA AGGAnATCGA ATGGTTTAGT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

55

(2) INFORMATION FOR SEQ ID NO: 3534:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGCCA GTTTAATTGA CGAGTGGCGT AA 52

(2) INFORMATION FOR SEQ ID NO: 3535:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60
 CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120
 ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180
 CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTAGCAAG TGTGTACAT GTTCGTGATG 240
 TAGATGGTGA AAAAAGTGCA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAACAA 300
 TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360
 TGCTTGGACA ACCTTCTTAT TTCCAATTC CAGAGGTTAT 400

(2) INFORMATION FOR SEQ ID NO: 3536:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60
 GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120
 AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360
 5 CGTTTTCAAT ATTTTAAATG CTCATTTACA TAAGTAAACT CTGCTTTAAA ATAATTTAAC 420
 TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGA 480
 GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTTA 540
 10 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCAAT 660
 15 TACAAAAGTA AACTCCGCTT TAATTTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 780
 ATGTTAAATA AACATTCAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960
 TTAATCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA 1020
 25 CCCGGGaaCG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGeTCC AGCTTCATGT 1080
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

30 (2) INFORMATION FOR SEQ ID NO: 3537:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

40 GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAaGTTG AAACATCAAC ATTAGGTGAA 120
 45 GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180
 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240
 TTACCATTTC TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300
 50 ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360
 TATCTAAGAT ACTGGCGaG ATTGTCACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420
 ACCC 424

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG TTAAAAGGTA AACAAGGTCG TTTCCGTCAA AACTTACTTG GTAAACGTGT 60
 TGACTATTCA GGACGTTTCA TTATTGCAGT AGGTCCAAGC TTGAAAATGT ACCAATGTGG 120
 TTTACCAAAA GAAATGGCAC TTGAACTATT TAAACCATTG GTAATGAAAG AATTAGTTCA 180
 ACGTGAAATT GCAACTAACA TTAAAAATGC GAAGAGTAAA ATCGAACGTA TGGATGATGA 240
 AGTTTGGGAC GTATTGGAAG AAGTAATTAG AGAACATCCT GTATTACTTA ACCGTGCACC 300
 AACACTTCAT AGACTTGGTA TTCAAGCATT TGAACCAACT TTAGTTGAAA GGTCGTGCGA 360
 TTCGTCTACA TCCACTTGTA ACAACAGCTT ATAACGCTGA 400

(2) INFORMATION FOR SEQ ID NO: 3539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG TTATTTTGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT TCCCATGCCG 60
 AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC GCTAGAGTAG 120
 AACGTTGCCA GGCAAATGAC AAATCGGAGA ATTAGCTCAG CTGGGAGAGC ATCTGCCTTA 180
 CAAGCAGAGG GTCGGCGGTT CGAACCCGTC ATTCTCCACC ATTTATTCTT AGATATAGCC 240
 GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT AGGTTGGGGG TTCAAGTCCT 300
 CTGGCCGGCA CCATCTTTTG AGCCATTAGC TCAGCTGGTA GAGCATCTGA CTTTAAATCA 360
 GAGGGTCAGA GGTTCGAATC CTCTATGGCT CATTACGATT TAATTTTAT ATTTAGCAAA 420
 ATAATGCAGA AGTAGTTCAG CGGTAGAATA CAACCTTGCC AAGGTTGGGG TCGCGGGTTC 480
 GAATCCCGTC TTCTGCTCCA TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC 540
 TTAAAATCCT GCGGTGAGAG ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT 600
 AGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCTGA 660

5 GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780
 TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840
 10 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900
 CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960
 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTATGAG AGAGTTTGAT CCTGGCTCAG 1020
 GATGAACGCT GCGGCGGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080
 TCTCTGaTGT TAGCGGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140
 15 GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

(2) INFORMATION FOR SEQ ID NO: 3540:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60
 30 CTTAACGAGT ACCGGATTTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120
 GCACGCTTCG CCTATCCTAC TCGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180
 GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240
 35 CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300
 GTCTTTCGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360
 TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCtC ACAGCTTCGG 420
 40 TaATATGTTT AGCCCCGGTA CATTTTCGGC GCaGTGTCAC TCGACTAGTG AGCTATTACG 480
 CACTCTTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGChAC 540
 ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGhTTCC 600
 45 C 601

(2) INFORMATION FOR SEQ ID NO: 3541:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GCnAGGACCT TnCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCnC 60
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCTGTA GATGTTGGGT 120
 TAAGTCCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC ATCATTAAGT TGGGCACTCT 180
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300
 nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420
 TGTACACACC GCCCCTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAAGTTT GAATGTTTGT TCATTCAAAT 660
 25 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720
 CGAGTCCACT TAGGCCCACC ATTAATTTAA TACCTATTTG GGGGCTTAGC TCAGCTGGGA 780
 GAGCGCCTGC TTTGCACGCA GGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTATT 840
 30 TGTACATTGA AAAC TAGATA AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960
 CTCACAAGAT TAATAACGCG TTTAAATCTT TTTATAAAAG AACGTAACTT CATGTTAACG 1020
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140
 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200
 40 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

(2) INFORMATION FOR SEQ ID NO: 3542:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:

CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120
 CATCTGCCTT ACAAGCAGAG GGTCCGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180
 5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240
 GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300
 ACTTTTAATC AGAGGGTCAG AGGTTGCAAT CCTCTATGGC TCATTACGAT TTAATTTTTA 360
 10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAATAAC AGTTAATTAT ACCGGTGGTC GGGGTGCAAC 60
 25 CGCACTCCAC AAGTGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120
 CTTAATGGTA AACAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180
 CACCTATACC TCGTTCCGGG aAGGAACTGg TTcTAAAGT TGAACTACTC CCGCAAATAT 240
 30 TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300
 CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360
 35 CCTATACCTC GTTCCGGGAA GGAckTGTTt CTAAAGTTG AACTACTCCC GCATAAACCT 420
 GGAGGCGGCA ACCGGATTG AACC GG TGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480
 TGGCTATGcG CcAATAACTG GGCTAGCTGG ATTCGAACCA ACGAGTGACG GATmAAAGTC 540
 40 CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600
 CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660
 GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720
 45 TGCCCCATT aAAAAATaaTA ATkGGAGGGG GGCAGATTcG AAntGCCGAA CCCGAAGGAG 780
 CGGGATTTAC ATTCCGCCGG GTTT 804

(2) INFORMATION FOR SEQ ID NO: 3544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCCT AGGCGGTGGC TGTGAGCTTG 120
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 10 GTGTTGGCTT ATTACCGAGT GGCAGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240
 CATCGCATAA GTTTGATKAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360
 15 GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3545:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

25 CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60
 30 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120
 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCTTTT CGAACACGGA CCTTATCACC 300
 CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTCTGGAG TTTGTCTGAA TTCGGTAACC 360
 CGAGAGGGGC cCCTCGTCCA AACAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420
 40 CCCTAAAGCT AATTCGGAGA GAACCAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

(2) INFORMATION FOR SEQ ID NO: 3546:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120
 CTGTTACAGG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180
 5 GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTGCTTCA CAGTGACATG 240
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GCGGCTTTGn GCGACACGGG 300
 TAAAAAAGC AGGCGAGTTC TATACACCAC AACAAATATC TAAGATACTG GCGAGATTGT 360
 10 CACAGACGGT AAAGATAANT ACGTCACGTG TATGACCCAA 400

(2) INFORMATION FOR SEQ ID NO: 3547:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TCGGCTCAT CGCATCCATT TTTGCCTGG 120
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTTCTTGA 180
 CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTGCGCTCT CGCTTACTCA TTTAGCTCTA 240
 30 CTAAACTCGT TCGGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTTCAC TCGCCAAGC 300
 CATTTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAA AGAGACCTTG 360
 35 CGGTCTCAAT GCGGCTCATC GCATCCANTT TTTGCCTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3548:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 50 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 GTGTTGGCTT ATTACCGAGT GCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

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TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTAC GTGATACAGA 360
TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60
AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA TTCCAGCTTC 120
ATGTAGTCGA GTTGCACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180
CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240
GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300
AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360
CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60
TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120
TGAACCGCAT GGTTCAAAAG TGAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180
TGCAATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240
AGGGTGATCG GCCCACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300
GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360
TCGGATCGTA AACTCTGTT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:

(A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

10	ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA	60
	ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCACTTTT GAATGTTTAT	120
	TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TGCGAGCGCT TGACAATCTA	180
15	TTCTTTTTTA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC	240
	TTTTGTAAAT GAGCATTGGA TTTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA	300
	AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAAAATAT AGATTTTACC AAGCAAAACC	360
20	GAGTGAATAA AGAGTTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTTCGAA	420
	GAACACTCAC AAGATTAATA ACGCGTTTTAA ATCTTTTTAT AAAAGANAAC GTTTAGCAGA	480
25	CAATGAGTTA AATTATTTTA AAGCAG	506

(2) INFORMATION FOR SEQ ID NO: 3552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

35	AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT	60
	CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA	120
40	AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA	180
	GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA	240
45	AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC	300
	GAGCGAACTC TCGTTAAGGA ACTCGGCAAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC	360
	TCTTTAGGGT TAACGCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA	420
50	AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG	480
	GAAGGTTAAG AGGAGTGGTT AGCTTCTGCG AActAcGaAT CGAAGCCCCA GTAAACGGCG	540
55	GCCGTAAC TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA	600

GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 720
 GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT 780
 5 AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC 840
 ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA 900
 10 AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATT C ATAGAGTGTA 960
 AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT 1020
 AGTGATCCGG TGGTTCGCA TGAAGGGCC ATCGCTCAAC GGATAAAGC TACCCCGGGG 1080
 15 ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGCA CCTCGATGTC 1140
 GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 1200
 CGGTACrMGg CTGGGTTcAG AACGTCGTGA GaCAGTTcCG TCCCTATCCG TCGTGGGCGT 1260
 20 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 1320
 TACCAgTTGT CGTGCCAAcG cAThAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA 1380
 AAcAThCThA AGCATGAAGC CCCCTCAAG ATGAGATTT C CCAACTTCGG TTATAAGATC 1440
 25 CCTCAAAGAT GATGAGGTTA ATAGGTTcGA GGTGGAAGCA TGGTGACATG TgGGAGCTGA 1500
 CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA 1560
 CTTACTATCT AGTTTTGAAT GTATAAATTA CATTcATATG TCTGGTGA CT ATAGCAAGGA 1620
 30 GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG 1680
 AACTTACGTT CCGTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTTGgTTAA 1740
 35 AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT 1800
 AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 1860
 TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT 1920
 40 CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA 1980
 CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG 2040
 AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA 2100
 45 CCGGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCAC TTATA 2160
 GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA 2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60
 AATAAGCTTG AATTCATAAG AAATAATCGC TAGTGTTTGA AAGAACACTC ACAAGATTAA 120
 10 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180
 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300
 15 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360
 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGAAGAGCC 420
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGACTCTCT ATACGGAGTT ACaAAGGmCG 480
 20 ACATTtGACG AaTCATCTGG gAAAGwTGaT CCAAGGAA 518

(2) INFORMATION FOR SEQ ID NO: 3554:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

30 AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60
 CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120
 35 TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGGCAT GGAACAGGT GTGACCTCCT 180
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240
 40 AGTGATTTTG CTTGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420
 45 CACTTAatCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAAA TTTCTACGC 540
 CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCCAGA 587

(2) INFORMATION FOR SEQ ID NO: 3555:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

	GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT	60
10	GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG	120
	CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT	180
	GAGTCGGAAT CACTGTCTGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT	240
15	GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG	300
	CTATCTGGAA TCTGGAGTCA CTGTCGGAAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT	360
20	ATCTGGAATC CGAGTTCATG GTCTGAGTCG GGaATCGCT	399

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

	ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT	60
	ACAACCCCAA CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA	120
35	GGGAATCGAA TTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG	180
	CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACATG CTGGGTTTCC	240
40	CCATTTCGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG	300
	TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT	360
	CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT	400

45

(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 657 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:

5 ACAA¹CTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT 120
 CAAAT²TTTCCT ACGCCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180
 CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT 240
 GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA 300
 10 AGCCTGTTAT CCCC³GGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360
 CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420
 CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTC⁴T GAGGGAACtT TGAGCGCCTC 480
 15 CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC 540
 ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600
 CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

30 GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60
 TGGTATTACT GTTG⁵CAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120
 35 GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCTG 180
 CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240
 CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG 300
 40 AAAAAGTGGG TAATGGTGCA GAACATACTA AGACAATTAA TGTGTTCGT GGTCAAATA 360
 ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACAAACACAT GGAAACGGCC 120
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATAACAACGT 180
 5 AACAAACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300
 10 AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360
 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

(2) INFORMATION FOR SEQ ID NO: 3560:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTCTAAGC GACCAATGTT 120
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCATTATT TCATTAGTAT TCTTACCAGG 180
 30 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240
 TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTCCGT GTCGCAATTA 360
 35 GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TCGATGATT 420
 GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480
 CGATT 485

40

(2) INFORMATION FOR SEQ ID NO: 3561:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60
 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

55

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240
 AGGCATATGT TGTACCTATG ATGGTGAAG AGCCTTCAGT TGTGCTGCA GCTAGTTATG 300
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAACGGT ATCTTCTGAA CGTATTATGA 360
 TAGGTCAAAT CGTCTTTGAT GCGTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420
 10 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463

(2) INFORMATION FOR SEQ ID NO: 3562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60
 TTAATCTTGG TGCGGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120
 25 TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG 180
 TTTTCAATGT ACAATTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240
 CAAATGCTCA TTTACAAAAG TAACTCCGC TTTAATTTTT CTTAATGCAT TGTCTAACAA 300
 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360
 AAAAATATTT GAATGTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCg 420
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480
 TCCGATACGG CTACCTTGCT ACGACTTCAC CCAATCATT TGTCCACCT TCGACGGCTA 540
 GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240
 5 TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360
 10 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAgCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60
 TAGTTGCCAT CATTAAAGTTG GGCACCTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120
 25 TGGGGATGAC GTCAAATCAT CATGCCCTT ATGATTTGGG CTACACACGT GCTACAATGG 180
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300
 30 ATGCTACGGT GAATACGTTT CCGGGTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360
 GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTT GTAGCTATTT GTAACCTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTTGA 120
 45 ATTCAATACA ATTGGTGTG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180
 50 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAAAG CTCATTGGTT 240
 TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

(2) INFORMATION FOR SEQ ID NO: 3566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CATATTTTAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60
 CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120
 CACCTATTGC ACGATTCGTT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGSTA 180
 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGTCACTCAG CAATCTATCT GTTGAAGACA 240
 TTGATTTGAT CGAATTGAAC GAAGCATTTC CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTCATCCAT 360
 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTACTTAA TGAAATGGGT AGACGTCCCG 420

(2) INFORMATION FOR SEQ ID NO: 3567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTT 60
 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TATTATTTAC 180
 AAATATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTTATAC CCGTGAGGTC 240
 GGGGGTTTGA TCCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300
 TAGCTCAGTT GGTAGAGCT AACGGCTCAT AACCGTTTCG TCGCAGGTTT GAGTCCTGCA 360
 GGTCCCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT 60
10 TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTT GCGATTCCGT 120
GTTTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA AGCAATAGAA 180
GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT 240
15 ACCGCAAAAA CAGTTGTCTC TGGATATATAC ACACCTGATT GTTTTAATCC TTGTCTGACA 300
TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATTA AAACCGCTTG ATGCGCCACC 360
ACAAGCCCCA CATTTCAAGT GATGGCATGG NTGTGGGTTn 400

20

(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA 60
GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG 120
35 CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG 180
ATTGGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC 240
GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC 300
40 TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA 360
TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC 400

45

(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

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GTTTTATATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120
 TTTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180
 5 ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240
 CGACCGCCCC AGTCAAACCTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaa GyTAGCGCTC 360
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420
 AGTAAAGCTC CACGGGGTCT TTCCGTCTCG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540
 CG 542

(2) INFORMATION FOR SEQ ID NO: 3571:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATA 60
 aTaAAAATGT AAtGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCn GCGTGACAGG 120
 CAGGCGTGTT AACCCCTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180
 35 CACCGGACTT CGGGTTATGA GCCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240
 AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC CCGTTAAGGc CCTGTGCGTT 300
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCTCTC ATTATTATAG GTAAATCGCT 360
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420
 CAGGCAGGCG TGTTAACCGC TACTACTACG GACCATTAGT AAAACGGAGG AAGAGGGATT 480
 45 CGAACCCCGG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540
 TTGGGTATTTC CTCAAAATT ATATGGACCT TGCAGGACTC GAACCTKCGA CCGAACGGTT 600
 ATGAGCCGTT AGCTCTAAC 619

50

(2) INFORMATION FOR SEQ ID NO: 3572:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

5 GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60
 GCAGAATTAA TTGATCAAGC GGTTACTTCA TTGAGCCACA AGATTTATTC AGTGCGATGA 120
 TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG 180
 10 TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240
 TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300
 AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360
 15 TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 3573:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

CAAATCGTAA CTCGCCGGTT CATTCTACAA AAGGCACGCC ATCACCATT AACGGGCTCT 60
 30 GACTACTTGT AAGCACACGG TTTCAGGTTT TATTTCACTC CCCTTCCGGG GTGCTTTTCA 120
 CCTTTCCCTC ACGGTACTGG TTCACTATCG GTCCTAGAG AGTATTTAGC CTTAGGAGAT 180
 GGTCCTCCCA GATTECGACG GAATTTACG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240
 35 GAGACAACAT TTTGCACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC 300
 GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTTA CAACCCCAAC AAGCAAGCTT 360
 GTTGGTTTGG GGCTCTTCCC ATTCGCTCG CGGCTACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3574:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1051 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

50 TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60

TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240
 5' GTCGAACCTA CGTTCCGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAT CCACACTAGC 300
 TCAGTGGTAG AGCTATCGGC TGTTAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360
 10' GCCATGGCTC cTtGGTCAAG CGGTAAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420
 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540
 15' GAATAAGCTG GAGGGGTAGC GAAGTGGCTA AACGCGGCGG ACTGTAAATC CGCTcCTTCG 600
 GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTGAA TCCAGCTAGC CCAGCCATTA 720
 20' GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840
 ACCAAATGTG GTGGGtATAT AATTAAAGA ACTATTTTTA AAATACAACT TTTAGAGCTT 900
 25' TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960
 CAAGCTGAAA ATCATCATTA TACGTGctTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATn 1020
 30' CACTTGATTA ATThnATCTA TATAATGCCT C 1051

(2) INFORMATION FOR SEQ ID NO: 3575:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

40 GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCCGT 60
 CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120
 45 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT 180
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240
 50 AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360
 AATAgTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAnGTGAA 420

(2) INFORMATION FOR SEQ ID NO: 3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

TTTGTTTCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG 60
 TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC 120
 GGGGCCCCAA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC 180
 CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GTAAGGGGCC 240
 CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC 300
 CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGGCCCAACA 360
 CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC 180
 TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA 240
 GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTACG TGCGGCTCTT CTGGGCGTTA 300
 ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA 360
 GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC 400

(2) INFORMATION FOR SEQ ID NO: 3578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60
 AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120
 TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA TGCAATGGTA 180
 10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTC 240
 AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300
 GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGTCTTC GCAATCCACG GATATACCTT 360
 15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3579:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGA GACTAGCGGG ATCGAACCGC 60
 30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120
 AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180
 CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCATA GGAGTCGAAC CCATAACCTC 240
 35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300
 ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360
 TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAAT 400

40 (2) INFORMATION FOR SEQ ID NO: 3580:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

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TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180
 AACAAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240
 5 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360
 10 CCGTCTTCCA TGC GCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGSTACGGCT TTTCCAGAAG GATTACAAGG CCAAACATT GCACGAACGA 60
 TTGCATTGCG TGC GGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180
 CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCCACA 240
 30 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAC TGCTG 300
 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120
 50 TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

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ATTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGT

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(2) INFORMATION FOR SEQ ID NO: 3583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

15	AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC	60
	TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT	120
	ATAGGCCCAT TAATTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT	180
20	CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA	240
	CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG	300
	CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAACTCTCG TGGTGTGACG	360
25	GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC	400

(2) INFORMATION FOR SEQ ID NO: 3584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

	ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCACTGAT TCCTGGTTCA CTTGGTTTAT	60
40	CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG	120
	CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTTGG AATGATTCTA TCTTTAGCGA	180
	TGTGTTTACG TGAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT	240
45	ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG	300
	ATATTTTCGA AATTCTATCT CAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC	360
50	AAACATTATT TGACAANGTG TGGGACAGAC ATGTGTTATA	400

(2) INFORMATION FOR SEQ ID NO: 3585:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC 60
10 TGTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG 120
TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG 180
ACCGATACCT GGCCTTGACC CTCTTGCTTT CGCAATCCAC GGATATACCT TAGTACCAGG 240
15 TAATTGACCA CCTTCACCAG GCTTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG 300
CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC 360
TTACTTTGGT GGCTTCCATC AACTTGTACT TCATAACGGT 400

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(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC 60
TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG 120
35 AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA 180
CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT 240
ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCCG 300
40 CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT 360
TATGGGTCCT GTAATTGATG TTCGATTGA ACATAACGAG 400

45

(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

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AGGATTCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTITTTTATT GAAAATGGTG CCGAGGACCG 240
 GAATCGAACC GGTACGTGAT CACTCACCGC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300
 CGCCACCCC GGCCTATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTTCGC GACCTATTTTC CTAATGCAGC 60
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180
 TAACTGGAAA GTCCTATTGA TGGATACTAG TAAAACCATA TTTAGTAAAT ACAGATGGAA 240
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAG 300
 ACGATATACT ACGACACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360
 35 GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCACTTAT AGATGGATCC 180
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360
 GTCTTCGGAT CGTAAAACTC TGTATTAGG GAAGAACATA 400

(2) INFORMATION FOR SEQ ID NO: 3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CCGGTGAGAA TCCctCCACC GATTGACTAA 120
 GGTtTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACag 180
 gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240
 GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300
 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360
 TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480
 AAGGAACTCG GCAAAATGAC CCCGTAAct 509

(2) INFORMATION FOR SEQ ID NO: 3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GGCCTCTCC CAGCTGAGCT AAGCCCCCAA 180
 ATAGGTATTA AATTAATGGT GGGCCTAAGT GGA CTGGAAC CACCGACCTC ACGCTTATCA 240
 GGCCTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAAATT TGAATGAACA AACATTCAAA 300
 ACTGAATACA ATATGTCACG TTATTCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360

(2) INFORMATION FOR SEQ ID NO: 3592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACTTAA CATATATTTT GGGACCTTAg CTGGTGGTCT 60
 GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120
 AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA 240
 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300
 ACGTAAGTCG GTTCGGTCct CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360
 ATCACCTGGT TTCcGsGTsT ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTTCGC 420
 TAnGGCTCCA CATTACTGGn 440

(2) INFORMATION FOR SEQ ID NO: 3593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTT TTTATTCCAT 60
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAAC TTTTCGTTGAA GTGTTAGGAA 120
 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180
 GTACAGGTTT TGGTTTATGG TCATTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240
 TTATnTACTA CCCATTcCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300
 GTAAAGAAAG TAATTCAGAT TTAAAGAAA AAGTTCAGC AAACCTTTGA TACGAAAAAA 360
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

(2) INFORMATION FOR SEQ ID NO: 3594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

	AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTTCAGT TCTCCGGGTG	60
10	TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT	120
	CCCCATTCCG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA	180
	GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
15	TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT	300
	TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATAA TTAACTCAT TGTCTGCTAA	360
	ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAaTAATC CTCTCGCTC	409

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(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

	AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT	60
	GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTAGCTGC TTCAAACAAT	120
35	ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TGCGCTTTTT CAATGCACTC	180
	GTTGCAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAAC	240
	TCATTGCTT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC	300
40	CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG	360
	GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA	400

(2) INFORMATION FOR SEQ ID NO: 3596:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

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CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCCTCCA 120
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180
 5 TCTGCTTGTA AGGCAGATGC TCTCCCAGCT GaGCTAATTC TCCAAAATAA TGA CTCTAC 240
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGcAACGTT CTACTCTAGC GGAACGTAAG 420
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540
 15 AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60
 30 TACCCAGCTA TGCCGTTGGC ACGACAATG GTACACCAGA GGTATGTCCA TCCCGGTCCT 120
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180
 GTCTCAGGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG 360
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

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CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240
 5 ATTTCTCTGTT GCTAAAACAA CAGCATGTAT GCCATTCATA ACACCTTTAT TATGTGTTGC 300
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATcGTTT GcaACCTCTT 360
 CTCCAGTTCT CTCGCCCCCTT GGCTAAATCT TTAACAT 397
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(2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCTTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC 120
 25 GTTGAGCGAT GGCCCTTCCA TCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTCTAT GAATGATTTT 240
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300
 30 TCAAAGTGCC CGCCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120
 50 GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA

400

(2) INFORMATION FOR SEQ ID NO: 3601:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

15 ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60
 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120
 AGTAAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180
 20 ATTCATAAGA AATAATCGCT AGTGTTGCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240
 AATCTTTTTA TAAAAGAACG TAACTTCATG TTAACGTTTG ACTTATAAAA ATGGTGGAAG 300
 CATAGGTTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG 360
 25 GncGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 3602:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

40 GCTGTCTGAG TCGGAATCAC TGTnGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60
 GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120
 AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180
 45 GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240
 TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300
 TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT 360
 50 CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

(2) INFORMATION FOR SEQ ID NO: 3603:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTCGCAATG AGATTGAT CGTnTTTGTC 60
 10 CACTACAATA TCTAATAGTT TTAATTTAAG TCCAGCATTG AAAAAAGTG CTGCCAGTTG 120
 AGCGCCCATG GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC 180
 AATTTAGTTG AGGATAAGAT AACCATTAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA 240
 15 ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT 300
 TAAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG 360
 AAAGCmGaAT CTCCAGTcaA AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT 420
 20 TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT 480
 AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CTnTCTCAC 529

25

(2) INFORMATION FOR SEQ ID NO: 3604:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

35 CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGC AAGCGATTGG TCGTCCTAAA 60
 ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTG TGTAATTAAA 120
 GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAT TGTAATACG 180
 40 TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA 240
 GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA 300
 CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA 360
 45 TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG 399

(2) INFORMATION FOR SEQ ID NO: 3605:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT 60
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCCT 120
 CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180
 10 CGACCAAATA CTAACGCCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTTAC TCCCCTTCCG 360
 15 GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3606:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60
 TAAAAACATA TCGCCCCGTA GCTCAATTGG ATAGAGCGTT TGA CTACGGA TCAAGAGGTT 120
 30 ATGGGTTTCA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180
 ACTTGGTTTG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240
 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300
 35 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAACTATA TAAGGCGGTG TAGCTCAGCT 360
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

(2) INFORMATION FOR SEQ ID NO: 3607:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

50 GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60
 GTTTCCTTTC CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCCTTTTA 240
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCTT TTCGAACACT AGCGATTATT 300
5 TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC GGTTTTGCTT GGTAAAATCT 360
ATATTTTACT TACTTATCTA GTTTnCAATG TACAAATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60
TGCAAAAnAGC CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA TTAATGGTGG 120
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCT AACCAGCTGA 180
25 GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGC CCACCTTCGA 360
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTGGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAAnTTCAAT CAGCAGAAGA ACTAGGACAT 60
45 GGCGCTTTTA AAATTATTGA AACACATGCA TTAAGATG TACAAGCAGT ATTGGGTTTT 120
CATAATGACC CATCGCGTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180
GCAGTAGATC GTTTTGAGTT TCATATTAAA GGCGTGGGTG GTCATGCTGC AAACCAGAAC 240
50 AATGCAACGA TCCAGTTATT GTGTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360

(2) INFORMATION FOR SEQ ID NO: 3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

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AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT      60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC      120
CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA      180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA      240
TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT      300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATGA ATTAACTCA TTGTCTGCTA      360
AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT      400

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(2) INFORMATION FOR SEQ ID NO: 3611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

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GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTC AACCGCCGAC      60
CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATT AAAACTGCCT      120
GGCAACGTTT TACTCTAGCG GAANTAGTT GNACTACCAT CGACGCTAAG GAGCTTAACT      180
TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG      240
TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA      300
TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC      360
CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT      400

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(2) INFORMATION FOR SEQ ID NO: 3612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTATATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180
 10 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300
 15 GNGCCTCCGT TACCTTTTAG GAGGCGACCG CCCCAGTCAA ACTGCCCCGCC TGACACTGTC 360
 TCCCACCACG ATAAGTGTCn GGGGTTTAGA AAGCCAACAC 400

(2) INFORMATION FOR SEQ ID NO: 3613:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240
 35 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300
 TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTTAT 360
 40 CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420
 TTATCAGGCG TCGCTCTAA CCAGCTGAGC TATAGGCCCA TTTTTTTGaa TGTAAATAA 480
 ACATTCA 487

(2) INFORMATION FOR SEQ ID NO: 3614:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG 60
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120
 5 CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360
 CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GcnAGTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3615:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300
 35 TCTTTTCTCG TTTCTGCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 360
 TTACTTTTTTA TTTTGACGTT TAGGCATAAA AAAAAGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 3616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TrGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60
 ATTCACTCGG TTTTGCTTGG KAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120
 55 CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTAAACCAAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGnGATCCAG CCGCACCTTC CGATACGGCT 300
 ACCTTGTTAC GACTTCACCC CAATCATTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360
 5 TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

(2) INFORMATION FOR SEQ ID NO: 3617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 60
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAT TTCTTTTATG 120
 TCAAGCGCTC GCATAAGCAA TATCATTITA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCGGAAT 240
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTACGACT 300
 TCAnCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360
 30 TCGGGTGTGA CAACTCTCG TGGTGTGACG GCGGGTGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60
 45 ATACTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTGCGAGA 120
 ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TATGTTGTGT TTGCGCTTGT 180
 CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCAATAG TACTAATTTG TGCAATGTTT 300
 GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA 60
 CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC 120
 TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180
 ACCCGTCTTT CGCTACTCAC ACCGGCATTC TCACCTCTAA GCGCTCCACA TGTCCTTACG 240
 ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300
 CGGTAATATG TTTAGCCCCG GTACATTTTC GGCGCAGTGT CACTCGACTA GTGAGCTATT 360
 ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

(2) INFORMATION FOR SEQ ID NO: 3620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TAAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60
 CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120
 GGGGGGCTTC ATGCTTAGAT GCTTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180
 ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240
 AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300
 CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360
 CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

(2) INFORMATION FOR SEQ ID NO: 3621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTT GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240
 TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAACTGCC TGGCAACGTT CTA CTCTAGC 300
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGT 475

(2) INFORMATION FOR SEQ ID NO: 3622:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60
 AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120
 CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGGCGTT 240
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAACTTT 300
 40 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360
 TTTAAGTCAG TCGCTAAAGA TTGTGGAAAG TAAGATCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3623:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CASACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTCCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300
 TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360
 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

(2) INFORMATION FOR SEQ ID NO: 3624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCTG AACCGCCGAC 60
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120
 25 GGCAACGTTT TACTCTAGCG GAANTAAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTCTG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 30 TAATTTATAC ATTCAAACCT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTTGTGACC TCTAACAGCA 60
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCCTCC TGATTCGTGT 180
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTAAACACC CATTCGTTTT 240
 55 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

(2) INFORMATION FOR SEQ ID NO: 3626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60
 TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120
 AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180
 GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240
 TTCCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300
 TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360
 CCTATCTTCC GCTCCATAAT TTAATATTTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420
 CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

(2) INFORMATION FOR SEQ ID NO: 3627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 60
 AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT 120
 TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 180
 TTCTCGTTTC GTCAGATTCA AACGTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTGC 240
 TTTTtATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300
 CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360
 GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3628:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60
 CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120
 ATTTCTTACG ACCCAGCAGG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAAGTCTTG GGGGAGATAA 300
 GCCTGTTATC CCCGGGGTAG CTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360
 20 CCGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

(2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

35 TTTATAAATA TCCAGTCTG AACGCGATTG CCATAACGGA TCAATGGCAG GATTGAAAGG 60
 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTCATCTTC 240
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360
 45 CThTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TTTAAGTTGT nGATTTAAAA TATTAATAAA GTGTAAATTT GACTATTGAn ATTCKrACaA 60
 ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120
 5 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240
 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTATG 300
 10 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATTATATTT 480
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

20 (2) INFORMATION FOR SEQ ID NO: 3631:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAACTGAGC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGCGC AATATGTAAG AATAAATGGT 120
 35 GGAGAATGAC GGGTTGGAAC CGCCGACCCT CTGCTTGTA GGCAGATGCT CTCCCAGCTG 180
 AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTCG 240
 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTTCGGC ATGGGAACAG GTGTGACCTC 300
 40 CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAAACTAG ATAGTAAGTA 360
 AAAGTGATTT GCTTCGCAA ACATTTATTT TGATTAAGTC 400

45 (2) INFORMATION FOR SEQ ID NO: 3632:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120
 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 180
 5 CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAn GCCCCCAaAT AGGTATTAAA 360
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

(2) INFORMATION FOR SEQ ID NO: 3633:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60
 25 TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120
 GCGGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACTTCGG 240
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360
 35 CCAAGGChAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

(2) INFORMATION FOR SEQ ID NO: 3634:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTG GAACCGCCGA 60
 50 CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120
 TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180
 55 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTGTCAGCT CCACATGTCA CCATGCTTCC 360
 ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60
 TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAAA GAGACCTTGC 180
 GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240
 CGTAAGTTGG GCTACCATCG ACGTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 300
 CTTTCCTCTT CTTGGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT 360
 TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTAGTCAA GCGCTCGCAT ACTGATTTTC 60
 AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120
 TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180
 TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240
 ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
 GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTCAACCCA nTCATTTGTh CCACCTTCGA 360
 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

10 AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGAATGTTA AATAAACATT 60
 CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180
 15 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240
 CGGGTGTTAC AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300
 ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360
 20 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3638:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

35 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAGTAAGT CGAnCTACCA 60
 TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 180
 40 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360
 45 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

(2) INFORMATION FOR SEQ ID NO: 3639:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAAGCAGC GATAAAAATA 60
 ATCGCAATCG CTGGCAAACCT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCTGA TAGCGTTGTA TAGCCAACGA 180
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240
 ACAAATCTCC ATAAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360
 ATAaTGACCA TTTCCCAAaT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420
 15 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480
 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAnGTC GTAATTTCTT 540
 GATAGCCGGA T 551

20 (2) INFORMATION FOR SEQ ID NO: 3640:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACCTGAT CCAACTTACA 60
 CTACCAATAG AAACCTTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120
 35 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180
 TCCTATCATC CAAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240
 TCTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300
 40 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360
 TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

45 (2) INFORMATION FOR SEQ ID NO: 3641:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGCAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240
 CTAAGCTGAG GCCGACAGnG TAGGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300
 AATCGTTTTA ATCGATGGGG GGrCGCATAG GATAGCGGAA CGTTGCGATT GGATTGCACG 360
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

(2) INFORMATION FOR SEQ ID NO: 3642:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTA TAATCTTGTA 60
 25 CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180
 TTTCACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240
 30 ATCGCGCTGG CATTTCTGCT GGCACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360
 CAAATGGka ATCATCGCCA TTAAtATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420
 35 TAATGACATT GCCTTCATG 439

(2) INFORMATION FOR SEQ ID NO: 3643:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTGT CTTGGTAAAA 60
 50 TCTATATTTT ACTTACTTAT CTAGTTTTCa ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAAA 180

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GCGTGCGCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300
 CTGAATACAA TATGTCACGT TATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnc GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTGGGATCG TAAAACTCTG 60
 20 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240
 25 AACCGTGGAG GGTCAATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

(2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC 60
 TTTCTTTGTG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120
 45 CAATGCGGCT CATCGCATCC ACTTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 180
 TncGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAAATnAT ACATTCAAAA CTAGATAGTA 300
 50 AGTAAAAGTG GATTTTGCTT CGCAAACAT TTATTTTGGG TTAAGTCTTC GATCGGATTA 360
 GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAATATA GATTTTACCA AGCAAACCG AGTGAATAAA GAGTTTAAAA 60
 TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120
 GTTTAAATCT TTTTATAAAA GAACGTAAC TCACTGTTAAC GTTTGACTTA TAAAAATGGT 180
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC CTTGGCACTA GAAGCCrATG 240
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300
 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420
 TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480
 GGGTnTGTA GACACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600
 TGaGTACGAC GGAGCACGTG AAATTCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660
 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720
 gGAAGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

(2) INFORMATION FOR SEQ ID NO: 3647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120
 AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTGGCTTA GAAGCAGCCA TCATTTAAAG 180
 AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240
 ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

(2) INFORMATION FOR SEQ ID NO: 3648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

15	GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGAATTCCA TGTGTAGCGG	60
	TGAAATGCCG AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC	120
	TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC	180
20	GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCTT TAGTGCTGCA GCTAACGCAT	240
	TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC	300
	CCGCACAAGC GgTGGaGCAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC	360
25	TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCCT TCGGGGGACA AAGTGACAAG	420
	TGGTGCATGG TGTCGTCAAC TCCTGTCTGT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC	480
30	GCACCCTTAA GCCTTAGTTT nCATCATTAA GTTGGGCACT C	521

(2) INFORMATION FOR SEQ ID NO: 3649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

40	CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTCAT ATTCAATGGT CTCATCTTGT	60
	TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC	120
45	ATACGTGTTT TAACACGTTT GTATCCCATT GCATCCCATA ATTGGAATGG ACCAAGTTTC	180
	CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT	240
50	ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT	300
	TCGTCTTGcG CATTGAATAT GGTATCAaG TTATGCACTA aGTCTTTATT AAATTCATTT	360
55	AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT	400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGn CCGTTAAGGC 60
 CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120
 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180
 TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG 240
 AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT 300
 TCAGCCGGAC TTGGGTATTC CTCCAAAT ATATGGACCT TGCAGGACTC GAACCTGCGA 360
 CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTTGCGCTA AATGCAACCA TGCATGGTAA 60
 AAACTTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120
 GTCCATTTAA TCATTTGACG ATTCACTTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180
 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240
 GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTG AATGATTCAT ATATGATGGC 300
 AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360
 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC 60
 5 GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120
 AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180
 TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240
 10 TCCCAAGTTA AATTAAATTG CATTTCGGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300
 CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360
 ATTTTCGGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

(2) INFORMATION FOR SEQ ID NO: 3653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCGGTCC TCCATTCAGT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60
 TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGCTCCA 120
 30 CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTTAC 240
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300
 35 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360
 CGTACTCAAG NATCCACTCA AGAGAGACAA CATTTTCGAC 400

(2) INFORMATION FOR SEQ ID NO: 3654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

AAAGGTCCTA AATATAATTT TACAACTAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60
 CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

GCGCTCTCCC AGCTGAGCTA AGCCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCCTA 300
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAAA TCGATCAAAT CATCGATGAA GCGAAACATA 60
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120
 TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360
 30 GACCATGACG AAATTGTAAG AGCGAGTGGG ATTAACCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480
GGGTCTGGGG CTTGGGTTCC GGTTCCTGGG CTGGGACTTG GGTTCCTGGGA 530

5

(2) INFORMATION FOR SEQ ID NO: 3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

15

GTTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60
GTTGATCTGT CCCGATTTGT TGGTAAACGG TTGATTAATG AAAATGTTTCG CGAAGGGATT 120
CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180
GAAACAAATT ATCATTGCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240
CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300
ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360
GGATTCATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

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(2) INFORMATION FOR SEQ ID NO: 3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

40

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60
GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTGGCTTG GAGTAATAAA 120
AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180
GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240
GAATTTGGTG GTACTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300
ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAGAAA AACTTTCTCA ACAGCAAATT 360
CmATTTCAAC AACGGAAAAA TCGCmACGTA TCTATATAAG GmGCGAACAG CTATGTGGTA 420
ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

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TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCAGT 660
 5 AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60
 20 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120
 TGGTGGCAGG CTATATTTCa GGTGCTTGGA TTACGCAACT TATAACAGTA TTTAATGTCA 180
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240
 25 TTGGTGCGAC ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300
 CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAAnGTG 360
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCAAA CCTACTGATT 60
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120
 45 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180
 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240
 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300
 50 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA 360
 GTGATTTTgTn TTTCGCAAAA CATTATTTT GGATTAAGTC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

10 TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG 60
 GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTT ATTTTTCTTA CCGACAAGAA 120
 TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT 180
 15 TTTTAACCAA AATTTGATTA AAAAAGTGGC TGGCAACGTT CTACTCTAGC GGAACGTAAG 240
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 300
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 360
 20 AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3662:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTGGAATG 60
 35 CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAC GCTTTTTGAT CAATTTTTTA 120
 TCGTCTTTTG TAATTTTCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT 180
 TGTAATTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG 240
 40 TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA 300
 ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA 360
 CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAACTA 420
 ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG 480
 ATGACGTGTA CAAGCGCCGC ACGTTTTGCA GCGATTGAGC CGGCTAAACT AGCTAAGATA 540
 50 GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGATKGTGCT GTTTAAGCTA 600
 ATTAAATCTT GTTGATAAAA TTCTTGTAAG ATACCAATCG TCGCACTTGA ACTTTGAACT 660

AGCATTAAAT TGGCTTnAAA TC

742

(2) INFORMATION FOR SEQ ID NO: 3663:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

15 ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT 60
 TTTACTTACT TATCTAGTTT TCAATGTACA ATTCTTTTTT AGTCAAGCGC TCGCATACTG 120
 CTTTATTTTC AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT AATTTTTCTT 180
 20 AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG 240
 CAATATCACT TTAACCAAAA AATATTTGAA TGTTAAATAA ACATTCaAA CTGAATACAA 300
 TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG 360
 25 GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3664:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTCTTTT TTCAATTATTA TCCATTATTT TTTCACCGCC 60
 40 AAAACGAATT TCATGATGTT AATTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT 120
 ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAkACATCAT TTAAAAGGAG 180
 CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AktGCTAGTA GTTGACTGAA 240
 45 TGAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCAAA CACAGAGAAT 300
 TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCAACA CAGAGAATTT 360
 CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCAACACA GAGAATTTCTG 420
 50 AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT 480
 CCCaattTCT ACAGACAATG CAAGTTGGCG GGGCCCAAC ACAGAAGCTG ACGAAAAGTC 540

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TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTCC TGTGCTAAA ACAACAGCAT GTATGCCATT CATAACACCT TTATTATGTG 60

TTGCTGCACG ATGAATATCT ACTTGGGCCA ATACAGAAGC ACGTTCCATT CGTTTGGCAA 120

CCTCTTCTCC AGTTCTCTCG CCCCTTGCTA AATCTTTAAC ATCAATTTTCG CCTTGAACCTT 180

TAACAACGGA CGCTGTTGCA TGATTGGATA AAATACTCAT TAAAATGTCG CTTTGGGAA 240

TCATTTTTT AAAAATGCAG TTATGGCCTC TAAAATCGTA TTAAGCATAT TAGCGCCCAT 300

AGCATCTTTC GATCAACAA ATACTTTTAA AGATAGTAAC TGtTGctCAG GrAATGTaKc 360

matCGCTATA CGtTGGTAAC CACCACCACG CGCTTTAATA GGAA 404

(2) INFORMATION FOR SEQ ID NO: 3666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCAG TAGCAATTAT TGAACGATAT TAGGCTATCT AGTCGGCATA TTTGTAAAAC 60

AAGATCCAAT TAAATATCAA CAGGAATAAC GAATAATATA AAAGAGGTTG GGACATAAAT 120

CCCTAAAAAA ACAGCAGTAA GATAATTTTC AATTAGAAAA TATCTTACTG CTGTTCTCTA 180

TTTATACAAT ACTTCGTATT GAATGGCTTC GCTTTCCTAG GGTGCCGTCT CAGCCTCGGT 240

CTTCGACTGG CACTGCTCCC TCAGGAGTCT CGCCATTAAT ACTACGTATT AACGTGTAAT 300

TTTACTTTGA AATACTTTAA AAAAATAAGA CACTTTGCCC AACTTGCACA TAAATGTAAA 360

ATTCAATAAA ATAAATTTCT GTGTGGATC CCTnCGTATA 400

(2) INFORMATION FOR SEQ ID NO: 3667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

	CCAACAAATC TGTCTGTGCG ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC	60
10	CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA	120
	ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC	180
	CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG	240
15	GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA	300
	CCTTTTAAAG TATTACGTAA TGTGTGTTG CGGTTTACAT CTTACCCAAA GTGCTAATGC	360
20	GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT	400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

	ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT	60
	AACATGACAT AACTCATGAC TGGGTTTCCC CATTGCGAAA TCTCTGGATC AAAGCTTACT	120
35	TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG	180
	CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT	240
40	TAATCTTGTG AGTGTCTTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT	300
	AAAACCTCTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT	360
	TTTCAATGTA CAATTTCTTT TTAGTCAAGC GCTCGCATAA	400

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(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

5 GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTGCG 180
 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCTATA 240
 GAGTGTAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCAN GGTGAAAGA 300
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360
 CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

(2) INFORMATION FOR SEQ ID NO: 3670:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

25 ATACTTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATCTTTC 60
 TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120
 GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTG 180
 30 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 240
 CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAGT CTTCCGATCG ATTAGTATTC 360
 35 CGTCAGTCC ACATGTCACC ATGCTTCCAC CTCGAACTT 400

(2) INFORMATION FOR SEQ ID NO: 3671:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

50 CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60
 TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120
 AAATTTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180
 TAAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

55

TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACChA nAGGnAGAAT 360
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCTG AGAAAGAACG 60
 TAAATTTAAT cCTGATTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120
 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300
 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAGGA GACTCGATTG TAGAAAAAGA 420
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAAATCTA 60
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120
 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCAGC TGAGCTAAGC CCCCAnAG 180
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240
 TGCGCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAACTG 300
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTCCGAAT ATATCCTTAG 360
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA 60
 GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT 120
 ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT 180
 ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA 240
 TCAGTAAGTA AACAGTGGTG GGTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA 300
 TTGGAGATG GAAATGATT ATGTACGCCA TTAACGTCAA ATTCTTTTGG CGTAAATGTC 360
 TTTGTACCAA GTCAACAATC ATATACCACT AGTCCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCTGA ACCGCCGACC 60
 CTCTGCTTGT AAGGCAGATG CTCTCCAGC TGAGCTAATT CTCCGATTTA AAACGCTG 120
 GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTGCTTCGC AAAACATTTA 300
 TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT 360
 CGGACCTATT AACCTCATCA ACCTTGAGGG nTCTTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 3676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

5 TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60
 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180
 10 GCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCCTGT ACCACCTATA ATCGTTTTAA 240
 TCGATGGGGG GACGCATAGG ATAnGCGAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3677:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

25 AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60
 TATTTTTCTT CTACTTTTGT TTTTCTGCG GCAATTTGTT GGTCAGTCGC ATCACCATTG 120
 30 TTAATAACAT TTTGTGCATT TGTGATTCT GTTGACCCG CACGTTTAGC ATTTTCATAT 180
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAT 300
 TGCTTGCATT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360
 TACTGTTCTT AATGGGCTTT TGAATAATA GCATTAGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3678:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 648 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

50 ACAGTCAATT GntCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

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AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAATATT GCGGGAGGCG GATTTGAACC 240
 ACCGTA CTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300
 5 AAATAATGGC GGAGGAAGAG GGATTCTGAAC CCCC CGGCC CGTTAAGGCC tGTCGGTTTT 360
 CAAGACCGAT CCTTCAGCC GGACTTGGGT ATTCTCCAT TATTATAGGT AAATCGCTAT 420
 10 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480
 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540
 ACCCCCGCGA GCGGTTAAGC CCTGTGCGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

(2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60
 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120
 30 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTCCGAT GACAGCTTCT 180
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTTGTGC AATTCAAACG TGTACTTTCC 300
 ACCGTTTTTC ATTTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360
 TTCAATAAGT TGTTTTCTCA ATTTAAATC AAGTTCTTTC 400

40 (2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAAnTAAG 60
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCTT 120

55

TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300
 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360
 CGCTTGGCTT CTnTCCTCTC CTTCCGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTAGCTCT ACTAAACTCG TTGCGCTCTT 60
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCCGCAAG CCATTTTTCT TTGTGTTTAC 120
 TTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180
 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300
 AAACGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

TTGAACATGT TGAATCTAAT GAAATTCTTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTGAGTAT AACGAGATTT 180
 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240
 TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

(2) INFORMATION FOR SEQ ID NO: 3683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

TTGGAATTC TCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTCGGT 60
 CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT 120
 CTACGACCAA ATACTAAACG CCCTATTGAG ACTCGCTTTC GCTACGGCTC CACATTTACT 180
 GCTTAACCTT GCATCAAATC GTAACGCGC GGTTCATTCT ACAAAGGCA CGCCATCACC 240
 CATTACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCTTC 300
 CGGGGTGCTT TTCACCTTTC CCTCAGGTA CTGGGTTTAC TATCGGTCAC TANGAGAGTA 360
 TTTAAGCCTT ANGAGATGGT CCTCCAGAT TCCCAGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

GATnTATGAT GAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT 60
 TCACTTATAC TTCTAGTCAC AGATTnAAAT AATCAAAAGT GCACATTATT AAAATATCAA 120
 TTTCACACTC AATGCGGCTC ATCGCATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG 180
 GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTcTT GACTTgTGAC AATCGCTTGC 240
 TTCTTTCTCT TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC GTTGCCTCT 300
 TTTCTCGTTT CGTCAGATT AAACGTTTTT ACTTCGCCAA GCCATTTTTT TTTGTGTTTA 360
 CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG 420
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA 480
 CTTGTGACAA TCGCTTGCTT CTnTCCTCTC CTTGGGCTCT CGGTTACT 528

(2) INFORMATION FOR SEQ ID NO: 3685:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180
 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240
 TTCAGTGC GA TGATTCGTGA AATTGAAACG CAAGATTTCTG ATATAGAGCA TCTAGCGACG 300
 GCGATTGCGA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360
 CTGTTCA GCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3686:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCCTT CTTCCGGTGGT 60
 GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240
 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360
 GATTTTAAAT TATTgAAAAA AAACCATATA CAGGTGCAAC GGT 403

(2) INFORMATION FOR SEQ ID NO: 3687:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCGCGGAT AATAAAAAAT AATGGCGGAG 60
 GAAGAGGGAT TCGAACCCCC GCGGCCCCGT AAGGnCCTGT CGGTTTTCAA GACCGATCCC 120
 5 TTCAGCCGGA CTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240
 ACCGCTACAC TACGAGACCA TTAGTAAAAC GGAGGAAGAG GGATTGGAAC CCCC GCGAGC 300
 10 CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360
 AAATTATATG GACCTTGACG GACTCGAACC TGCAGCCGAA CGGTATGAGC CGTAGCnCTA 420
 ACCACTGGGC TAAAGTCCTA ATATAATTT 449

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TCnATAATGC 60
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120
 30 TGCTTACGGT GCATTACACG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240
 TGAATTAGAT TGTGACATTT TAGTACCAGC GGCTATTTC AACC AAATTA CAGAAGACAA 300
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

40 (2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAT TTGAATGAAC 60
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATCCGC ATCTTCTGAA GAAGATGTTT 120

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CGACTTCACC CCAATCATT GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240
 CGGCTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360
 TGCAGACTAC AATCCGAAC GAGAACHACT TTATGGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

GCnGCGTTTT AGGCCCATTC GGTTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60
 TGAACCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180
 25 CAACTGAGCT ACTGAACCAT AATAAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300
 TTGCGGGAGG CGGATTTGAA CCACCGaCTT CGGGTTATGA GCCCGACGAG CTACCGAACT 360
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC 420
 CCGTTAAGGC CCTGTGCGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480
 ATTATTATAG GTAnATCGCT ATTAAATTATA AnATTAAAT GGCGGTCTCG ACGGGAATCG 540
 35 AACCCGCGGA TCT 553

(2) INFORMATION FOR SEQ ID NO: 3691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTGTG ACAATCGCTT GCTTCTTTCC 120
 TCTTCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300
 ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAATACAG ATTGAGTATA 60
 20 TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAACA TATCGCGAAA 180
 TATCATTTTG AGAATTCTAA CGAATTCCT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240
 25 ATTTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60
 TTTTATTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACACATGC 120
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTCTTAG ATTGTGCTTT 180
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCa ATAACAGGTG TTACTACTTT 240
 ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300
 50 ACCAGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTTGGT GTTCCGGCT CGCTTGGTAC 360
 TTCTGGTGTC GGTGGTGTG GGTGTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCCGT 420

(2) INFORMATION FOR SEQ ID NO: 3694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60
 ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120
 ATTAGCTACG GTTTCCTCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCACTG 240
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360
 AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCTGTGTC 60
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA 180
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240
 CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTAGCG CCTTGTAATT CTAAAGTTTC 300
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360
 TTGGTATAAC TTAATTTcnc CTTTTCTTC ATCnGGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240
 CATTITTATA AGTCAAACGC TCACATACGG CTTTCGTTTTT ATTATTTTAA ATGCTCATTT 300
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360
 15 TAAAAAGATT TAAACGCGTT GATTAACTG TGAGTGTCT 400

(2) INFORMATION FOR SEQ ID NO: 3697:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTAA ATAACATTC AAAACTGAAT ACAATATGTC 60
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180
 TTCGACGGCT AGCTCCTAAA AGGTACTTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240
 35 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300
 TTACTAnCGA TTCCAnCTTC ATGTAGTCGA GTTGCACT ACAATCCGAA CTGAGAACAA 360
 CTTTATGGGA TTGCTTGAC CTCGCGGTTT CGTnCCCTT 400

(2) INFORMATION FOR SEQ ID NO: 3698:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

50 AAGGGAATCG AATTTTCTTT CTCTCTCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

CCCCATTTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAAAGCA TATCGTCGTT 180
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240
 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTGGAACAC 300
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAAACTC TTTATTCACT CGGTTGTGCT 360
 TGGnAAAATC TATATTTTAC TTACTTATCT AGGTTTCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

60
 120
 180
 240
 300
 360
 400

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCGT TTGCAAATCC
 AAATTCTTCC GCTCCAAGCG CACATGCGTA CGTACATCT TTACCAGTTA ATAACCTTACC
 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC
 TGTAnCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAGA
 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT
 CGCATTTTTC AAATCATGTA TCAGTTGCGC TAAATCTTCT

(2) INFORMATION FOR SEQ ID NO: 3700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

60
 120
 180
 240
 300

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGT TCGGCATGGG AACAGGTGTG
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG
 TAAGTAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG
 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnG GGGGGGCTTC ATGCTTAGAT

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

(2) INFORMATION FOR SEQ ID NO: 3701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

AACCAAGCCC AATAATGGAC TGGCCGCTA ATAATAAAG CTCTAAAAGT TGTATTTTAA 60

AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT 120

CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180

TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC 240

GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300

TAGATGGTGG AGGGGGGCGAG ATTCGAACTG CCGAACCCGA AGAGCGGnTT TACAGTCCGC 360

CGCGTTTAGC CAnTTCGnTA CCCCTCCAGn TTATTCATAT 400

(2) INFORMATION FOR SEQ ID NO: 3702:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCGCCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60

CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAACACTT 120

CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180

TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240

ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300

CGGCCAGAGG ACTTGGAACC CCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360

GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3703:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

	CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT	60
10	ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAACT	120
	AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGgC GCTCTCCAG CTGAGCTAAG	180
	CCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTG AACCTGCGAC CCCTTGGTCC	240
15	CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG	300
	TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG	360
	CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG	400

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(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

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	CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAATTATT ACGTCAGCTT	60
	ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG	120
35	TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTTCAG	180
	CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA	240
	GCACTGCGCG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT	300
40	AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAAA GGTAACACTA	360
	TCATTTATGC AATACGGCGC ATTACCCAGA GTTGTCATGGT	400

(2) INFORMATION FOR SEQ ID NO: 3705:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

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TGACGGGGAC CCGCACAAAGC GGTGGAGCAT GTGGTTTAAAT TCGAAGCAAC GCGAaGaACC 120
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180
 AAAGTGACAG GTGGTGCATG GTTGTCTCA GCTCGTGTCTG TGAGATGTTG GGTAAAGTCC 240
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300
 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAAA TCATCATGCC CCTTATGATT 360
 TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

(2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

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ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60
 TAACGATCCA AACGAATTGA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTGCGCA 120
 TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCAAAAAGG TCATGCTGAA ACGTTGAAAn 300
 CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360
 AAGCAGTAGA AGATGTTCCA TAACTTTGG TGAGGACCCT 400

(2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

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GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAAATCGAA CCCGCGATCT CCTGCGTGAC 120
 AGGCAGGCGT GTTAACCGCT AACTACGAG ACCTATAAAA TATTGCGGGA GCGGATTG 180

TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCG 300
 GTTTTCAAGA CCGATCCCTT CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC 360
 5 GCTATTAATT ATAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCCAT TAAAGCGGTA CCAGCTGGG TTCAGAACGT CGTGAGCAG TTCGGTCCCT 60
 20 ATCGGGGTG GCGTAGGAA ATTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120
 GACATACCTC TGGTGTACCA GTTGTCGTGC CAACGCATA GCTGGGTAGC TATGTGTGGA 180
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCTC AAGATGAGAT TTCCCAACTT 240
 25 CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360
 30 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAT ACTATTAAGA AGTCCTGAAA 60
 AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120
 45 CAGTGTGTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTTGTCTT 180
 TGCAACGCTA TTAGTATCA GGTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATTr 240
 50 GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360
 CCAAGTTTAC AAAAAGTTGA AATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTTCGAA 420

(2) INFORMATION FOR SEQ ID NO: 3710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

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AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC      60
CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT      120
TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT      180
TTTAAGTCCT GTGCGTCTGC CAGTTCGGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA      240
CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC      300
TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG      360
TGCGTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG      420
ACCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG      480
GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT      540
AACCAATTG AGCTAAGGC                                         559

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(2) INFORMATION FOR SEQ ID NO: 3711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

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AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG      60
GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC      120
TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTTCATT      180
CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCGTATAAGC GTGAGGTCGG      240
TGGTTCGAGT CCACTTAGGC CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC      300
TGGGAGAGCG CCTGCTTTGC ACGCAGGAGG TCAGCGGTTG GATCCCGCTA GTCTCCACCA      360
TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT                                         400

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

10	TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG	60
	CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA	120
15	CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA	180
	AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATCCAA TCGAACCTGG AAATAGCTGG	240
	TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT	300
20	GTTTGGACGA GGGGCCCCCTC TCGGGTTACC GAATTCAGAC AAATCCGAA TGCCAATTTA	360
	ATTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG	400

(2) INFORMATION FOR SEQ ID NO: 3713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

35	TTTTTAAGTC TGATGTGAAA GCCCACGGCT CAACCGTGAA GGGTCATTGG AAATGGAAA	60
	ACTTGAGTGC AGAAGAGGAA AGTGGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT	120
	GGAGGAACAC CAGTGCGGAA GCGCACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC	180
40	GTGGGGATCA nACAGGATTA GATACCCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG	240
	TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGTAAACGCA TTnAAGCACT CCGnCTGGGG	300
45	AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG	360
	AGCATGTGGT TTAATTTCTGA AGCAACGGAG AGGAACCTGA	400

(2) INFORMATION FOR SEQ ID NO: 3714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAANT CGACTACCAT 120
 CGACGCTAAG GAGCTTAACT TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180
 10 AGTCACCAGA CATATGAATG TAATTATATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT 240
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300
 CATGTCACCA TGCTTCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360
 15 CCGAAGTTGG GAAATCTCAT CTTGAGGGGG GCTTCATGTC TTAGCATTTC AGTCACTTAT 420
 GCCCG 425

(2) INFORMATION FOR SEQ ID NO: 3715:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTGTAGG TTTGTCATGC 60
 CCAGTTACAA GTTGCCTTAT CGTAGACACT AACATTAATA TGAAGGTAA TGTGCTGTT 120
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTTC TGCACCTAAC 180
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTGTGTC ACTTTGTAA 240
 ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA GTAATACATC 300
 TCCAACATTT GCCTTTAATT CTTTTCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT AAGTAGTCCT 400

(2) INFORMATION FOR SEQ ID NO: 3716:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACCTCGG TTTTGCTTGG TAAAATCTAT 60

5 GCAATATCAC TTTAACC AAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180
 ATATGTCACA TTATTC CGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240
 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300
 TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGnTTCGGGT GTTACAAACT 360
 10 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60
 25 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120
 GGAATCTGGG AGGACCATCT CTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180
 TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAnGAGTTGA AATAGAACCT GAAACCGTGT 240
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300
 CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAn AAnnTGTTC 360
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 3718:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60
 AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120
 50 AGGCTCATAC AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240
 GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAAATAAGT 300

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TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGTnA

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(2) INFORMATION FOR SEQ ID NO: 3719:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

ATTTAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAANTA AGTnGAGCTA CCATCGACGC 60
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180
 TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT 240
 CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA 300
 GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT 360
 CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAngG 400

(2) INFORMATION FOR SEQ ID NO: 3720:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT 60
 TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC 120
 TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA 180
 AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG 240
 TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT 300
 CACAATTTC TTTTGCCTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA 360
 CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC 400

(2) INFORMATION FOR SEQ ID NO: 3721:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG	60
GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT	120
GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC	180
AGCCGAAAAT GGATGGTGTT AAGAGCGTTA CTTGGTTTGG CCGTATGCTT ATTTTAAATG	240
GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG	300
TGGTGTGTGT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GCGGCCACTG AnAGATCGTG	360
GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCAGCGCA	400

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(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA	60
TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT	120
GGATTCGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT	180
TAATAATAAG GCGGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT	240
GTTAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG	300
GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCCCTA TTAAATGAT AAATGGAGGG	360
GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC	400

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(2) INFORMATION FOR SEQ ID NO: 3723:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

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GGTTCAAGTC CTCTGGCCGG CACCATTtnt GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTTCG 240
 ATTCCTACTG CCCCTGCCAT GCGGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300
 10 CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360
 GGTAAGGCAA CGGACTTTGA CTCCGTCACT CGTTGGTTTCG 400

(2) INFORMATION FOR SEQ ID NO: 3724:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60
 25 ATATGGCGTG CGTCGTTTTC ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120
 AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TTTGTCAATC 180
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240
 TGGGTGCGGG TATTAAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

(2) INFORMATION FOR SEQ ID NO: 3725:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420
 CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGGCG TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60
 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTLAGAC 180
 CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240
 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360
 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

(2) INFORMATION FOR SEQ ID NO: 3727:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCGAA CAGCTCGCG TACCGCTTTA 60
 ATGGGCGAAC AGCAAACCTT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120
 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180
 GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240
 GTCTTTGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCTTATG CCTTTACACT 300
 CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTTAGGAG 360
 GCGAACGGCC CCAGTTCAAA CTGCCCGCCT GAACACTGTC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG 60
 GTGTGTCATT TGAGTGTCCA ATCGGTGCCA CGATTGCGAT TATCGGAGAA AGTGGTAGCG 120
 GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTGTGTGTA 180
 CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT 240
 TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG 300
 TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT 360
 TGGAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3729:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCAGC GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC 60
 TTATATAGTT TGTAATAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 120
 TGCAAAAGC CGCTCTCCA GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA 180
 GACAGGTTTC AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC 240
 TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA 300
 AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC 360
 CGGAATCGAA CCGTAGTGA ATCACTCACC GCAGATTTTA 400

(2) INFORMATION FOR SEQ ID NO: 3730:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

5 ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60
 CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC 120
 ACCATTTTTTA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC 180
 10 GCGTTATTAA TCTTGTGAGT GTTCTTTTGA AACTAGCGA TTATTTCTTA TGAATTCAAG 240
 CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTACTTACTT 300
 ATCTAGTTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360
 15 GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

(2) INFORMATION FOR SEQ ID NO: 3731:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCGG CAATATGTAA GAATAAATGG 60
 30 TGGAGAATGA CGGGTTTGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCAGCT 120
 GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180
 GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT 240
 35 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT 300
 AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAA GTCTTCGATC GATTAGTATT 360
 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

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(2) INFORMATION FOR SEQ ID NO: 3732:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60
 TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

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AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240
 ATATTTATTA ACTGGTGACT TAGCGAGATG GACAACGATG GCGATATATT TATTATTGAC 300
 5 CGCAAAaAAG AaTTAATCAT AACTGGTGgc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

(2) INFORMATION FOR SEQ ID NO: 3733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120
 AAGACGGCAA AGTGGGTCTT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240
 ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300
 TACCAGGTAT TTTTGCAGCA GgGATGTTC GCGACAAAGG TTACGCCAAA TTGTCACTGC 360
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

45 GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60
 CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120
 TTGATAAACA GTCGCTTGGG CCTATTCACCT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180
 CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 240
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTGCGTTT GCGGTACGGG CACCTATTTT 300
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGACT CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCCT CCAAATTAT ATGGACCTTG CAGACTCGAA 60
 CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120
 TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA 180
 TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240
 TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCAGCT 300
 GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGGAAGA CAGGATTCGA ACCTGCGACC 360
 CCTTGGTCCC CAAACCAAGT GGTnTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAAATAA TGGCGGAGGA 60
 AGAGGGATTG GAACCCCCGC GGCCCGTTAA GGCCCTGTCG GTTTTCAAGA CCGATCCCTT 120
 CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAAAT ATAAAATTAA 180
 ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240
 CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 300
 TTAAGCCCCCT GTCGGTTTTT AAGACCGATT CCTTCAGCCG GACTTGGGTA nTcnTCCAAA 360
 ATTATATGGA CTTGCAGGA CTCGAAGTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 60
10 AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC 120
CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT 180
TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA 240
15 TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG 300
ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGT ATTCTACCGC TGAACTACTT 360
CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA 400

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(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60
CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGAnCT 120
35 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 180
GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA 240
GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG 300
40 CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT 360
TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT 400

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(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

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CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA CCGACATCTT 120
 TAATTAATTG CTnTGACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180
 5 TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAA TAACTGATTC 240
 GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300
 CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360
 10 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGTTACTC ATTTAGCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TCGGCTCAT CGCATCCaTT TTTGCCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240
 30 TACCATCGAC GCTAAGAACC TTTCTTGA CTGTGACAATC GCTTGCTTCT TTCCTCTTCT 300
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTG CGCTCTTTTC TCGTTTCGTC 360
 35 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTCTTG TGTTTGCTTT TnA 413

(2) INFORMATION FOR SEQ ID NO: 3741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGGCTCTCT CGTACTAAGG ACAGCTCCTC 120
 50 TCAAATTTCC TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180
 GCTCGGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360
 ACCGGATCAN TAAGTCCGTC TnTCGACCCT GnTGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60
 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120
 CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180
 CATCTGCCTT ACAAGCAGAG GGTGCGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 240
 TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300
 GGTTCAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360
 GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60
 TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120
 TGTATGTAGT ATTGTTACGT TCTGTCCGA AATAACGATA CACTTGCGTT TCTTTACCAA 180
 CACGTAACAA CAATGAACCG GAACCATATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240
 TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300
 CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360
 ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10 CTACTGATT A CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60
 ATGGTGGAGA ATGACGGGTT CGAACCGCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120
 AGCTGAGCTA ATTCTCCGAT TTAAACTGCT CTGGCAACGT TCTACTCTAG CGGAACGTAA 180
 15 GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240
 ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT 300
 AAGTAAAGT GATTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360
 20 TCAGCTCCAC ATGTCACCAT GCTTCCanCT CgnACCTATT 400

(2) INFORMATION FOR SEQ ID NO: 3745:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60
 35 AAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT 120
 CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACTCG GTTTTGCTTG GTAAATCTA 180
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240
 40 CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300
 TTAATGCATT GTCTAACAAC CGCTTGCTTT AAAAAGAATA GATTGnCAAG CGCTCGCATA 360
 AGCAATATCA CTTTAAACCAA AAAATA 386

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(2) INFORMATION FOR SEQ ID NO: 3746:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 677 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTTCGTACCG AnaACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240
 10 TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300
 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420
 15 tTACCAATTc AGACAAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480
 TGATAAGGTC CGTGTTTCGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600
 20 CCATCATTTT AAAGAGTGCG TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCAGG GTATTGCCTT TGAATCGCAT GCACAAAATA 60
 TGATGCTCAT TCATGAAAAT GGTGGCCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120
 GTGTTGTTTT TAAGCGTGAC ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180
 40 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240
 AGTACGCGAC TTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300
 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360
 45 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

5 ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60
 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGTCTTCG 240
 10 ATCGATTAGT ATTGCTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360
 15 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

(2) INFORMATION FOR SEQ ID NO: 3749:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

25 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 30 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120
 GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180
 TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240
 35 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTAATCATTT 300
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360
 40 GCCAAGCCAT TTTTCTTTG TGTTACTTTT TTAATTTTGA 400

(2) INFORMATION FOR SEQ ID NO: 3750:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

50 ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTGCCTGGC 60
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240
 ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 300
 5 GGTCTCAATG CCGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCCTATAA 60
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120
 CCGCTGAACT ACTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTna 180
 25 GnATTTCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
 GGATTGGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300
 30 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAACCCCC AACCTACTGA TTACAAGTCA 360
 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60
 45 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120
 CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180
 50 GCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240
 AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATA 300
 AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360
 55

(2) INFORMATION FOR SEQ ID NO: 3753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTGTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT 120
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 180
 TCTTTTCTCG TTTGCTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 240
 TTACTTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC 300
 TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA 360
 TCGACGCTAA GAACCTTTCT TGA CTGGTGA CAACGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 3754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGA CTCGnACCAC 60
 CGACCTCAGC CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTAATTTGA 120
 ATGAnCAAAC ATTCAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG 180
 ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC 240
 TTGTTACGAC TTCACCCCAA TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA 300
 CTCCACCGGC TTCGGGTGTT ACAAACTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC 360
 GGGAACGTAT TCACCGTAGC A 381

(2) INFORMATION FOR SEQ ID NO: 3755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60
 CCCC GTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120
 CATGAAGTTA CGTTCMTTAA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTCT 180
 10 TTCGAACATA GCGGATTATT TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC 240
 GGTTTTGCTT GTAAAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360
 15 AATATTTGGA ATGTnAAAT AAACATnCAA AACTGAATAC 400

(2) INFORMATION FOR SEQ ID NO: 3756:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180
 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240
 35 ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTTCCGGn GGGGnACACG 300
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG ATTTGTCTGA 360
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

(2) INFORMATION FOR SEQ ID NO: 3757:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC 60

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180
 TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAAGT 240
 5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300
 AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAaRtttGG GAaCTCAtC TTGAGGGGGG 360
 gCTCATGctT AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420
 10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

(2) INFORMATION FOR SEQ ID NO: 3758:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60
 25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTTAAAAAGA ATAGATTGTC 120
 AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA AATAACATT 180
 30 CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240
 ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300
 ACCCCAATCA TTTGTCCAC CTTGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360
 35 GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

(2) INFORMATION FOR SEQ ID NO: 3759:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CTTGCAGGA CTCGAACCTG CGACCGAACG 60
 50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACTA 120
 ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180
 TAGCCAGCTG AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360
 AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

5 (2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60
 ACCAGAGGTA TGTCCATCCC GGTCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120
 20 CGCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTT TGAACCCAGC TCGCGTACCG 180
 CTTTAATGGG CGAACAGCAA ncccttggga cggactacag ccccaggatg cgatgagccg 240
 ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAAGTCTTG GGGGAGATAA GCCTGTTATC 300
 25 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GncCTTnCAT GCGGAACACC GGATCACTAA 360
 GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 623 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

40 TATGTATTTT ATAATGTACA GCTCGTTGAn TChTATTTTT CTTATATTA AGTGCCATTA 60
 ATACAAAACC TAGCTCTCGT TTAACCTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120
 CAAAATAGCC TTCATAAATC CAAAACAGG CTCTACATCA ATTTTTCTTT GACTATAGAT 180
 45 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240
 ATAATTCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300
 AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360
 50 ATCATTACGG TATGCATATC TTTTAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420
 ATCATTAAAGT TCGTCATATT TCCAATTTTA AGTGTGAAA ATGTCACCTT TAACTTTCT 480

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AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600
 AATAACCGAG GGATTGTTGG AAT 623

5 (2) INFORMATION FOR SEQ ID NO: 3762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAA TAGTTCCTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60
 AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCTGA ACCTCTGACC 120
 20 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG
 CTGGATTCTGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240
 CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300
 25 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360
 CAAAATGGTG GaGAATGACG GGTTGGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420
 TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480
 30 CCGTGAAAGG GCGGTGTCTT AACCCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540
 CGAACCTTAC GACCGATCGG TTTAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600
 35 ATTAATATTA TGCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660
 ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

50 TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60
 AAAAATGGAG CAGAAGACGG GATTGGAACC CGCGACCCCA ACCTTGGCAA GGTTGTATTC 120
 TACCGCTGAA CTACTTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

AGGATTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300
 GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360
 5 CAATTGCTCT AnCAATTTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCTGA ATTTGGTTTC 60
 20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120
 CGTTTAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180
 TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240
 25 CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300
 TTATTAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360
 ACAATATACT CTGGTAAATA ACCGAAGGAT TTTGAATCAT TGTAAAAAT GGGATTAATG 420
 30 TTCTAGTATC TGTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTG GAATTTGTCT 480
 CTATTTGgTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540
 35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTTAGGAAA ACCTAATTCC 600
 AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTGGTG CTGCATATCC CCTACAATAA TTAACCTTT TTTCTTATTT AAAATGTGTC 60
 50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120
 ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAATGAA 180

CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGC GCCT ACAnTTCTTA ATTCAGCGGA 360
 5 CGGTCACTTG TTAAACGGT TTAAGGTATT CTACTAATTn 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTrGTA 60
 20 tCTCACGCAA tCTTGTTGGT CATTcAGTTC GTATATGGCA TCCATTAA GA CGCGAAGATC 120
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAATACA GTGTCTCGCT CTGTTTCTGC 240
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTGCGC 300
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360
 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420
 30 TTCTTGSCAT ATTTcATTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60
 45 TGTCCAATTG AAACACCTGA GGGACCAAAC ATTGGATTGA TTAACtCATT ATCAAGTTAT 120
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180
 CATGCTATCA CTGATCAAAT TGA CTATTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240
 50 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTGCTTTCA TGGATGATGA AGTTGTATGT 300
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAA TGGATTATAT GGATGTATCG 360

(2) INFORMATION FOR SEQ ID NO: 3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

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CCTACGACCG ATCGGTTAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT      60
ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG      120
CTTAAC TTCT GTGTTGGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT      180
ATGAATGTAA TTTATACATT CAAAAC TAGTAAGTAA AAGTGATTTT GCTTCGCAAA      240
ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG      300
CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG      360
AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC      400

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(2) INFORMATION FOR SEQ ID NO: 3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

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CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT      60
CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA      120
ATCTTTCTnC TGCACTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA      180
CGTTACCAGC AATAATTTCA TTTTGTGCTT CTTCAAAGG TGCTTTGACA ATGACCGTAC      240
CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAGC      300
CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTCGTATA AACATTAATT      360
GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA      400

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(2) INFORMATION FOR SEQ ID NO: 3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TTAAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300
 AGTGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

(2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60
 30 GGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180
 GCTTGTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300
 TGCGTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTG 400

(2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

50 TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC .GGTCTCAATG CGGCTCATCG 60

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GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240
 5 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTGTGCTTT TTATTTTGAC GTTTTAGACA 300
 TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCCTGGGCA 360
 ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

10

(2) INFORMATION FOR SEQ ID NO: 3773:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTACAC 180
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

35

(2) INFORMATION FOR SEQ ID NO: 3774:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT 120
 CTTTCCTCTC CTTGGGCTCT CACTTACTCA TTTAGCTCTA CTAAACTCGT TCGGTTCTTT 180
 50 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240
 TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAA TCGGCTCAT 300

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GACGCTAAGG AGCTTAAACT TCTGTGTTTC GGCATGGGGA

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(2) INFORMATION FOR SEQ ID NO: 3775:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC 60
 TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT 120
 TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA 180
 TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAAACA CGTGAACGGC TCAAATGGAA 240
 GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC 300
 CAAACATTGG ATTGATTAAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA 360
 TTGAAACACC ATATCGTAAA AGTTGATTG GntACACAGC 400

(2) INFORMATION FOR SEQ ID NO: 3776:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 60
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA 120
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 180
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATT 240
 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAAGCTAG GCGATTATTT CTTATGGAAT 300
 TCAAGCTTAT TTAAACTCT TTATTCATC GGTTTTGCCT GGGTAAAATC TAAATTTTAC 360
 TTACTATCT AGGTTTTCAA TGTACAAATA ATGGTGGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3777:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

	AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TCGTGACAG	60
10	GCAGGCGTGT TAACCTCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA	120
	ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG	180
	GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG	240
15	AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT	300
	AGTGGCGGTG GAGGGGATCG AACCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA	360
	GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG	400

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(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

	CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGTC AGTCATAGTG CCGTCAGCTT	60
	TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT	120
35	CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA	180
	CTTGATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT	240
	GaTGACTTCT GACAGCATAA GCATCTTGaT CTTGCGGTGA TACGTCAAAT TGGGATGCTA	300
40	CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCaA TTGTAAGGTT	360
	GGATTGTTTG TGGGCTTCGT TnGCCACCnn TTGGTACGGC	400

45

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

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CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120
 CTCGGTTGAA ACCTTACTTA TTCATTTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTCGAT GTATCATTG GGTTTAGCAA 300
 ACAGCCATAA CCTTCGTCAT ATAAATGTTT ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

(2) INFORMATION FOR SEQ ID NO: 3780:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGACACn CAGGCGTGTT 60
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTCGAA CCCCCGCGAG 120
 CCGTTAAGCC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180
 AAAATTATAT GGACCTTGCA GGACTCGAAC CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360
 35 CCGCCTTATA TAGTTTGTAA ATAATATGGT GGAGACTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3781:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60
 TCTAGCACGT TCATAAATAG TTAAGTTCTT CAGCAGCAGC 120
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTCA TCTCTACGGC GACTCGGAAC 180
 TTTCGGCGCT ACCCAACCAT TTTCAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

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TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTTCGCTT AAGCGTCATA AGCAGTTTTA 360
 AAATCTTGAT GATACACCAA GTCGTCCanT CAGGATGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60
 CATTGATAAA TCGCTTGAAA TGTTCGCACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120
 TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180
 ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240
 CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300
 AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAAGATGC CATTGCCTAA 360
 ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

AATCGGGTGA TGTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60
 TGGATAACTG TTTTAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120
 TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180
 CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAAT TAAATCGCTG TTGTCCACAT 240
 AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300
 CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGanTT 360
 ACAAATCTT CnaAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTACTAAGA TGTTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCGGA AATCTCTGGA TCAAAGCTTA 120
 CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG AATTTAAACG 360
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnnGA 400

(2) INFORMATION FOR SEQ ID NO: 3785:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60
 35 CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180
 TTTGCAATT TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300
 CTGAAATAGT TGACTAGGCA TTTTGCGGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

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(2) INFORMATION FOR SEQ ID NO: 3786:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTCTACTAG 180
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTAC GACGTGTTAC 240
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCGCC ATAATACCTT TTTCAACCAC 300
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

25 TCTCTTCCCG TTTCGCTCGC CGCTACTAAG GGAATCGAAn TTCTTTTCTC TTCCTCCGGG 60
 TACTAAGATG TTTCAGTTCT CCGGSGTGTC CTTCTGATAT GCTATGTATT CACATATCGA 120
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTCCGAAA TCTCTGGATC AAAGCTTACT 180
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 300
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTAAACG CGTTATTAAT CTTGTGAGTG 360
 35 TTCTTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGACTA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120
 TTTTGGATGA TTCTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTTT 180

TCTTCTGCAA ACAACAACT ATTTTATTAA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300
 CTAGCTGCTA AnACATTATA ATCAGCTGGA TGTTGATGCT TTAACCTCTC TGTTTTAGCT 360
 5 AATGGAGATT TTAAACGATC TACATTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60
 AAAAGATCAG CTGACACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120
 CGGTGTTTTT GCGGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTTG TCCCTATTGT 240
 CACAGCATTG GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTGGC CAAGCATACA 300
 nGCCGGCATT TATCATGTTG GTGGGATTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360
 TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60
 TTAAATTAT ATACCCACCA CATTGGTGA kGAACCTAAA AAAAAGCACT TCCCAAAAT 120
 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAGTCA 180
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300
 AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTgTCTT 540
 AACCGtTGAC CAAGGAGCCA TGGCTCaCcA GGTA_gGACTC GAACCTACGA CCGATCGGTT 600
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660
 CTACTCTAGC GGA_ACTAAAG TTnGA_ACTnA CCATCGACGC TAAAGGAGCT TAACTT 716

(2) INFORMATION FOR SEQ ID NO: 3791:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

20 TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTTA AAGGTAACAC TATCATTTAT 60
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120
 ACGTG_TACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180
 25 AACAGCACAT CAGCTTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240
 AATTAATGAG GATTTGGAAA CATTCTTTGC nTGATTTTCA AACATTAGCT GTGATCGGTA 300
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT G_nAGCATGAA 360
 30 CTTATGTCGT TGT_TAAAACA AATTTTGAAA AAAGGAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3792:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180
 TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAAAT TTGTCATGAT GTGCCTCCTT 300
 ACCGTATGAT GT_tATTCAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA

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(2) INFORMATION FOR SEQ ID NO: 3793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

15 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 60
 AGTGACGGAG NAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG 120
 GAGGGGGGCA GATTGGAAT GCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA 180
 20 GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG 240
 ACGGGTTTGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT 300
 25 CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTGA CCGCCGTGAA AGGGCGGTGT 360
 CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG 400

(2) INFORMATION FOR SEQ ID NO: 3794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

40 ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC 60
 TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA 120
 TGTTTCACAA CGTTACCATT ACGTTTAAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA 180
 45 CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT 240
 GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA 300
 GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC 360
 50 CACATTCGGT TTATTCATAG CGGACCAGTT TGCCTCCATT 400

(2) INFORMATION FOR SEQ ID NO: 3795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA 60
10 TGGTAGGAGA GCGTTCTAAG GCGGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG 120
AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT 180
AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC 240
15 AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT 300
GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTTGATTG CACGTCTAAA GCAGTAAAGC 360
TGAGTATTAG GCnAATCCGG TACTCGTTnA AGGCTGAACT 400

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(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA 60
ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG 120
35 CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA 180
AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTTCATCTAC 240
40 TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC 300
AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC 360
AGTTTChGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT 400

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(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACGTG ACGCTGATGT GCGAAACGTG 120
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180
 5 TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240
 CGACCGCAAG TTGAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300
 GTTTAATTCTG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACACTCTAG 360
 10 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 3798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60
 25 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180
 AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TGCACATAT GGGCCTAGAG 240
 30 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAA CATTACGTAT 300
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 3799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTGCGCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60
 50 CGTTACTTGG TTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTCCGT 180
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

TTTtagTGCg TtactGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTn TTTTCGGTGC 360

CATTAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

5 (2) INFORMATION FOR SEQ ID NO: 3800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAT GTGTTAGGTA AAGGTGTCAT 60

TGTCGTCAAT GATGTGCCTG GCTTTGTCGC AAATAGAGTC GGCACGCAA CAATGAATGA 120

20 TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180

GCAAGCGATT GGTGCTCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240

TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAAGTACC TGAAGAAACA CCTTATTTTC 300

25 ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAnnCGnAA 360

ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GGNAACTTAA 400

30 (2) INFORMATION FOR SEQ ID NO: 3801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

40 TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60

TAAATTGTAA AACGATAGTT CCCGTTGTTT CTAATAGTTG TATTCTATCT GACGCATAAT 120

GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180

45 TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACCTTAA TGTTTCAACT AGTTTTTCTG 240

TCGTTAACAT GGGTTACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300

50 TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360

TTATnATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTTCACTTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGCTCCG GTTCCCCGAA 60
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCAATG ATTAGGCACG CCGCCAGCGT 180
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GCTCATAAAT 240
 ACTAAATAAT GTTTGTAAC TATAGTTACG TTTTTTGGAA TTAACGTTGA CATATTGTCA 300
 TTCAGTTTTT AATGTTCAAT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3803:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 60
 35 TTTTGCTTCG CAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180
 AACC GAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240
 40 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300
 TATGTCCATC CCGTCTCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360
 45 ACGGATAGGG ACCGAACTGT TTTACGACG GTnCTGAACC 400

(2) INFORMATION FOR SEQ ID NO: 3804:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGCCTCTGCC AGTTCGCGCA CCCC GGCACT 60
 ATAAAAATGG AGCAGAAGAC GGGATTGGA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180
 TTAGWATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240
 GAGGATTGGA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCAAC CTACTGATTA CAAGTCAGTT 360
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420
 15 TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

(2) INFORMATION FOR SEQ ID NO: 3805:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTIATT TTGACGTTTT AGACATAAAA AAAGCTCAGG GTCTCAACTT GCCTGGCAAC 60
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240
 35 TTCTTTGTGT TTACTTTTTA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGGGGTC 300
 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGCAACGT TCTACTCTTA GCGGAACGTA 360
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGGACTGTG 400

40 (2) INFORMATION FOR SEQ ID NO: 3806:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60
 TTTACTGAGT CATTGCACTT ATCATACACA TTATATTTAG CATGAGTTAT ATTACTAAAA 120

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TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTACTGCCAA 240
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTGTCTCG AAGTTCAGAT CGCTTTTACA 300
 5 ATTGGGCnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3807:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGAACATA TTCGTCTATT AAAAGCGATG 120
 TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTCTGT CAAGTTATGG 300
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

(2) INFORMATION FOR SEQ ID NO: 3808:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

45 ATGCGCAGAG TATATGGAGG AACACCACTG TCGAAGCGCA CTTTCTGGTC TGTAAC TGAC 60
 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAACTCA AAGGrATTGA CGGGGACCCG 240
 50 CACaAGCGTG GGAGCATGTG GtTTAATTCTG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTGCCA TCATTAA

447

(2) INFORMATION FOR SEQ ID NO: 3809:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

15	CCAACGAGC TACTGAACCA TAATAAAAT GTAATGACTG GCGGTCTCGA CGGGAATCGA	60
	ACCCGCGATC TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACTACTACGA GACCTATAAA	120
	ATATTGCGGG AGGCGGATTT GAACCACCGA CCTTCGGGTT ATGAGCCCGA CGAGCTACCG	180
20	AACTGCTCCA TCCCGCGATA ATAAAAATA ATGGCGGAGG AAGAGGGATT CGAACCCCCG	240
	CGGCCCGTTA AGGCCCTGTC GGTTCCTCAAG ACCGATCCCT TCAGCCGGAC TTGGGTATTC	300
	CTCCATTATT ATAGGTAAAT CGCTATTAAT TATAAAATTA AATGGCGGTC TCGACGGGAA	360
25	TCGAACCCGC GATCTCCTGC GTGACAGGCA GCGGTGTTAA	400

(2) INFORMATION FOR SEQ ID NO: 3810:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

	TGCTTGGTAA AATCTATATT TTAATTACTT ATCTAGTTTT CAATGTACAA ATAATGGTGG	60
40	GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA	120
	GCTATAGGCC CATTTTTTTG AATGTAAAT AACATTCAA AACTGAATAC AATATGTCAC	180
	GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG AGGTGATCCA	240
45	GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTG GTCCACCTT	300
	CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC TCTCGTGGTG	360
50	TGACGGGCGG TGTGTACAAG ACCCGGGAAC GATTTCACCG	400

(2) INFORMATION FOR SEQ ID NO: 3811:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

GCTTCATGCT TAGATGCTTT CAGCATTAT CCCGTCCACA CATAGCTACC CAGCTATGCC 60
10 GTTGGCACGA CAACTGGTAC ACCAGAGGTA TGTCATCCC GGTCTCTCG TACTAAGGAC 120
AGCTCCTCTC AAATTCCTA CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC 180
TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCTTGGG ACCGACTACA 240
15 GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGGAAGTCT 300
TGGGGGAGAT AAGCCTGTTA TnCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC 360
ATGCGGGAAC CACCGGGATT 380

20

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG 60
CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAAGTG 120
35 GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT 180
CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCAGAC GTTCTGAACC CAGCTCGCGT 240
ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 300
40 GCCGACATCG AGGTGCCAAA CCTCCCGTC GntGTGAACT CTTGGGGGAG ATAAGCTGTT 360
ATCCCCGGGT GAGnTTTnTC CGTTGA 386

45

(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

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CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTGGGTAC TTCTGGTGTG 120
GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180
5 TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240
AATTGATAAC TTGGTTTATC TTTATTTGTA TCTTCTTCAA TAATTTTCAGT GTGCTTATTG 300
AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360
10 TACTTAGGTT TGTCTTTTTT TGTAnCTTCC TCGAATGACT 400

(2) INFORMATION FOR SEQ ID NO: 3814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
25 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCnACTA AACTCGTTGC GChCTTTTCT 120
CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180
TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GCTCATCGCA 240
30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300
CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360
TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

TTCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60
GAATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120
50 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180
CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTTAA AGCGATATAT TGATGTCTAG 240

GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360
 TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60
 GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120
 TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TCTTTCTTTG 180
 TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360
 GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300
 TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360
 GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180
 15 CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240
 TTCTGAATAG GGCCTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGCTC 300
 CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCAATCGAA 400

(2) INFORMATION FOR SEQ ID NO: 3819:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAA TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TGCGAGACCT 360
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3820:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TGGCTCGAAC CACCGACCTC ACGCTTATCA GCGCTCGCTC TAACCAGCTG AGCTATAGGC 60
 CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180
 ATACGGCTAC CTGTGTACGA CTCACCCCA ATCATTGTGTC CCACCTTCGA CGGCTAGCTC 240
 10 CTAAAAGGTT ACTCCACCGG CTCGGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300
 GTACAAGACC CGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

15 (2) INFORMATION FOR SEQ ID NO: 3821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

25 TATTAAATTA ATGGTGGGCC TAAnTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120
 30 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180
 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTAC 300
 35 AAActCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360
 GCTGATCTAC GATTACTnAG CnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

50 TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60
 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120
 GCAGATTCTGA ACTGCCGAAC CCGAAGAGCG GATTTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180
 GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300
 TCTCATGTTT TCGAGATCCA CCAAATGThA AATGGGTAT GTGGCATCTA CTAAGCCGGG 360
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180
 ACGCGTTATT AATCTTGTGG AGTGTTCCTT CGAACACTGA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 50 AChTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60
TTACTTACAG CTCCCCAAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120
CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180
GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240
TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA TCTATATnTT ACTTACTTAT 300
CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360
CCAAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60
AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120
ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180
TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300
TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360
CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

5 AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTAG AGAAGACCAA AAGAAGAAAA 60
 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AAACAGAGAA AATATAAAGA 120
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AACTAAAAAC TGGTGAAGCC TTTAGTAAAA 180
 10 TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240
 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGA AAAGCTTGGC CAATCTGTTA 360
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3828:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

TCTCAGTTCC AGTGTGGCCG ATCACCCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60
 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180
 AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240
 TCAGAGAAGC AAGCTTCTCG TCCGTTGCGT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300
 35 GTTCATCCTG AGCCAGGATC AACTCTCCA TAAAAATTAT GATGTTGANT AGCTCATAAA 360
 TACTAAATAA TGTGTAACT TATAGTACGT TTTTnGAAAT 400

40 (2) INFORMATION FOR SEQ ID NO: 3829:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60
 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAAAT 120

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ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTTCGATT 300
 5 CAAGTGGGAR sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCAATT CTGCAAATnC 360
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTT 400

(2) INFORMATION FOR SEQ ID NO: 3830:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

20 GGGTACTAAG ATGTTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 25 GGATCCACCG TGCGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTTA TAAGTCAAAC 240
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT 300
 TTAAAATAAT TTAACCTATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG 60
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGA CTGTGA CAATCGCTTG CTTCTTTCTT 120
 CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTA CTAACT CGTTGCGCTC TTTTCTCGTT 180
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300
 TTTTTGCTT GGGCAACGTT CTA CTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

(2) INFORMATION FOR SEQ ID NO: 3832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

```

AGCTTATTTT AAAACGTCGT TTATTCACCTC TGGTTTTGCT TGGTAAAATC TATATTTTAC      60
TTACTTATCT AGTTTTCAAT GTACAATTTT TTTTGTAGTCA AGCGCTCGCA TAAGCAATAT      120
CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC      180
ACATTATTCG GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC      240
CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC      300
TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG      360
TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA      400

```

(2) INFORMATION FOR SEQ ID NO: 3833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

```

TTTTCTTCTG GTAAATATC TGCAATAACA STATCTATGC CTACTTGTTT TGCAATGGCT      60
TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT      120
TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT      180
AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTATA ATGTGTTAAA      240
TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATnT ACGGGTTACC      300
AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTnAA      360
AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA      400

```

(2) INFORMATION FOR SEQ ID NO: 3834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5 nAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC 60
 TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180
 10 CGCCTTATAT AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240
 TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300
 GGGGAAGACAG GATTCTGAACC TGCGACCCCT TGGTCCCCAA CCAAGTGCTC TACCAAGCTG 360
 15 AGCTACTTCC CGTATAATTA ACGCGCCCCG TAGGAGTCGA 400

(2) INFORMATION FOR SEQ ID NO: 3835:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60
 30 CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120
 AGGCGGAGGA ATCAGATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180
 AAAAAATTAT GGTTCGATTGC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT 240
 35 AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300
 GCAGATGCCT TGTCAGGTGA AGACATCAGC TATCnAGAAG CGTGGGCAGA TGAAGAATAT 360
 40 CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

(2) INFORMATION FOR SEQ ID NO: 3836:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

55 CTAATCGCAT CTTTTTCAAT CTAAGTGCCT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360
 10 CAATTGTGGC AGCTTTTTTnC TTCCGGnGAA AATATCnGGC 400

(2) INFORMATION FOR SEQ ID NO: 3837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGG CCAAGGAGCC ATGGCTCAAC 240
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGGAAGTAAn TCGGACTACC 360
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 60
 GTTGGCGTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT 120
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240
 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

TCAGATCCAA ACGTTTTCAa TCGnCCAAGC CAATTTGCCT

400

(2) INFORMATION FOR SEQ ID NO: 3839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

15 TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrc GACTCCTCTT 60
AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC 120
TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC 180
20 TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT 240
TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC 300
TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT 360
25 CTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTCAG 416

(2) INFORMATION FOR SEQ ID NO: 3840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
40 TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120
CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180
45 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAAACCTG CCTGGCAACG 240
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300
GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 360
50 CTCGTTGGnG CTCTTTTCTT CGGTTTnGTC AGAnTTCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

	CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA	60
10	ATTCTTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA	120
	TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG	180
	ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG	240
15	CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT	300
	AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTTG TAGTGGTGAA	360
20	GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA	400

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

	TCGCGATTCTG CGTGTTTCTG AATCATCGGC ATCGCGTCAT TCAATGATTCT ATATGCATCT	60
	AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA	120
35	TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT	180
	CCTTGTTCTGA CATTTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT	240
40	GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA	300
	CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTT	360
	AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

55

5 GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT 180
 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240
 GGCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300
 10 CTATTTCCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAST 360
 TCATCCGnTC ACTTTCAACG TAATTCGGGT CGGGTCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 3844:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

25 ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60
 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360
 35 AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTTAT TTTCTGCATT 420
 TTTAATAGTA TCGTGTITAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

(2) INFORMATION FOR SEQ ID NO: 3845:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

50 GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60
 GAAGCGGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TCGTAGAGC AATTGCGnAA 120
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

55

TTAACATTCT TACCTTATGT TGTTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60
 20 TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 120
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300
 AATCGCTTGC TTCTTTCTC TCCTTCGGCT CTCGCTACT CATTTAGCTC TACTAAACTC 360
 30 GTTGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAAGG TATTACGATG 60
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120
 45 GCACGTCCAT TAAGACGTAT TGTGTAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240
 50 AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAAA AATGAGCATC AGGTCGCCCT 300
 TGCCTGTGGC TCATTTTTTT GAATTATTC CCTGGGAAAA TGATTCGCTG TGTGCTGTTT 360
 TGTnCCACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

```

TTTAAAACTC TTTATTCACT CGGTTTTGCT TGGTAAATC TATATTTTAC TTACTTATCT   60
AGTTTTCAAT GTACAAATAA TGGTGGGCTT AAGTGGACTC GAACCACCGA CCTCACGCTT   120
ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCATTT TTTTGAATG TTAAATAAAC   180
ATTCAAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA   240
TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTTGGTnACG   300
ACTTCACCCC AAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC   360
GGCTTCGGGn GTTACAAACT CTCGTGGGTG TGACnGGCGG   400
  
```

(2) INFORMATION FOR SEQ ID NO: 3849:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

```

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC   60
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT   120
TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT   180
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTTT ATTTTGACGT TTTAGGCATA   240
AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG   300
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT   360
GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT   400
  
```

(2) INFORMATION FOR SEQ ID NO: 3850:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180
 10 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGAATTTAT TAGGTGTACA AATGACCACC 240
 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360
 15 TCTTTGAGTT TCAGCAATGC TGAATATGA CGGTCTTG TG CAATACCACC AACAACTATG 420
 CACACCAACT TTTAAaTTTG TnCATGATGT GCCnGCTTnA CCG 463

(2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 628 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGAITCG ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120
 AACCCGAAGG AGCGGATTTA CAGTCCGccG CGTTTAGCCA CTTGCTACC CCTCCAGCTT 180
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG CTCTACCACT 420
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAaTAGn 600
 TTAGTAAGTA AAAGTGGATT TTGGnTTn 628

(2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTGGAATT GGCCGTGTAG TAGCCGATAT 60
 ATTTGCCAAT GGTATCAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3853:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

25 TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60
 30 TCATAAGAAA TACTAATTTT TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120
 TGCACATTAT TGTAAGCTGA CTTTCGCCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTGTCACATT 240
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CAACCAACTnC GCATTGCCTG 360
 TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGGCCCA 400

(2) INFORMATION FOR SEQ ID NO: 3854:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300
 TTAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAAnCT 360
 CAGTTGCAAA TgntATTGTC AGCCACGAGT ACGGCTGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60
 AAATCAACAG GTAAAAAATT AACAAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120
 25 TTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180
 GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60
 CTATTTCTTC TATTGTAAa TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTTCGAT TCGTGATTTT 180
 50 GAATACTTTT CTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAGTGA 300

TATAAGAAGG nGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTGA 60
 AGTTGTGAAT GCACATGGTA AACATTTTGT TGCATTACCA CGTGAAGATG AAGATATTGC 120
 AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA 180
 TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT 240
 AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC 300
 TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCCT GCCGAGTAAT 360
 TGTCAAATGT ACTATGCAAT G 381

(2) INFORMATION FOR SEQ ID NO: 3858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

GCATGAAGCC CCCCTCAAGA TGAGATTTC CAACTTCGGT TATAAGATCC CTCAAAGATG 60
 ATGAGGTTAA TAGGTTGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT 120
 CGATCGAAGA CTTAATCAAA ATAAATGTTT TGCGACAATT CACTTTTACT TACTATCTAG 180
 TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT 240
 TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC 300
 GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA 360
 GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA 400

(2) INFORMATION FOR SEQ ID NO: 3859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAT CGTGTCATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTTAAATC TGTTTAAACA TTATTTTGAA TTTTCATTCAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
20	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
	TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGnGC	400

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(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTCGCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3862:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360
 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

(2) INFORMATION FOR SEQ ID NO: 3863:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

50 TCGGCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG 240
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 300
 TGTGCTTTT TTATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG 360
 10 CGGCTCATCG CATnCATtnt TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGTT TATGGGAAAT GAATTAATGT 120
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240
 30 GAAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300
 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360
 TCCAACGCAT GTTAAAGTG CCAGCAGAGC GACTAGCTGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

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TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

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(2) INFORMATION FOR SEQ ID NO: 3866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

AAGTCAATAA CTTTTTTTAT CTGTGCCATT TTATTTTTTA ACCAAAATT GATTAAAAAA 60
 CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA 120
 GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA 180
 TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA 240
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300
 GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT 360
 TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG 400

(2) INFORMATION FOR SEQ ID NO: 3867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGangT GncGATTGGA 60
 TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC 120
 TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTGTTGAT TTCACACTGC CGAGAAAAGC 180
 CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT 240
 CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG 300
 AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT 360
 GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA 400

(2) INFORMATION FOR SEQ ID NO: 3868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTGA TCACTGTTTA 60
10 GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT 120
GTTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT 180
GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAAGT 240
15 ATTAGTACTT ACTTTAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA 300
GGTGCCAACT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA 360
AnTCGATAAA TTTGTGGACG GTG 383

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(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA 60
CGACAACCAC CACCTGTCAC TTTGTCCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA 120
35 GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG 180
nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG 240
GAGTGCTTAA TGCGTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC 300
40 ATCGTTTACG GCGTGGACTA CCAGGTATC TAATCCTGTT TGATCCCCAC GGTTTCGCAC 360
ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT 400

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(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

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GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTTCGAA 300
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360
 10 GCTTGGTAAA AGCnnGn 377

(2) INFORMATION FOR SEQ ID NO: 3871:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCTCCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAAATGG 120
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACCTGCA ACTGGTTTAA CTGTATTACT 240
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360
 35 GCGAGTTACn GGGGTCCAAA CCCnTGGTGT AAAAnCGAAC 400

(2) INFORMATION FOR SEQ ID NO: 3872:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60
 TTAAGCCCCCT GTCGGTTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360
CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 584 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60
CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120
GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180
CAAnngTTTT CatTCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240
GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300
GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360
GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC 420
TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 480
GCCATTTTTC TTTGTGTTTA CTTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540
TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTTGCTTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60
CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 120
TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240
GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

400

(2) INFORMATION FOR SEQ ID NO: 3875:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

15 TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120
 CTTTGCCGCT CACCACCGGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180
 20 CCGACATCTT TAATTAATTG CTTTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240
 GATGGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300
 AACTGATTCG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360
 25 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60
 40 TGGTGATCCT CAATTCGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCCTCA 120
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180
 CGCACGTACA GTGTTTGAAA AAGGTATTAT GCGGGCACTG CACGTnTTGC TGCGAAAAAA 240
 45 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360
 CCGGGGGGTC TACAAAATCT GGTGCTGACT CTAGACCGCA 400

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(2) INFORMATION FOR SEQ ID NO: 3877:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC 60
10 CATCATGTTA TGTGATTGGA ATACTTTTTT AAAATCATAT TTAATACCTG GAGGGAATTT 120
ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT 180
TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT 240
15 ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACTTCTGG GnGTATCAAA ATGnTGCAAT 300
GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC 360
TCAACACCTT AGGGGTTAAC TTCGGCCATA TCCCTTTTGG 400

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(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TGTAGATGCA 60
TACTTAAATG GTGGTGACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA 120
35 GAAGTTGCTG AAACCTCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA 180
AACAAGTGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC 240
TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG 300
40 GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA 360
CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT 400

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(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120
 TGCGGCTCAT CGCATCCATT TTTTGCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180
 5 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 300
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTGCTTTT ATTTGACGTT 360
 10 TAGACATAAA AnAAGAnCCT TCGGnCTCA ATCGGCCAT 400

(2) INFORMATION FOR SEQ ID NO: 3880:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120
 CTTGCTTATA TTGTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180
 GATTACCATT GTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240
 30 ATGGATATTG ATTCAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300
 CTCTCGGTCA TATTCAGGCA TATCCGACA CAACTTGGAT AGCAGTTGTG ATTTCCAGG 360
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

(2) INFORMATION FOR SEQ ID NO: 3881:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180
 TAGGCGAACG TCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360
 ACAGGTAGTC CAAGATGGAG AnTCTnaAGG TGGAGCGAGC 400

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(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

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CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60
 ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTGAAATT CTCTGTGTG GGGCCCCTGA 120
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTC AGTCAACTAC TGCCAATATA 180
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240
 ATATTTAATT TCGTTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300
 TAAGTTTTCA GAAATAAACC TATCTTAAAA TATAAAAAA TCGAGAATTC GTAGTTTAAT 360
 AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACATAA 480
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540
 AGATTCATAA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600
 CGGAGTCAA 609

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(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

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ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120
 TTATTGTTG TTACGTGGAC TTAAACTTT GCATTACGC ATTGAGCGTG CGCAATCAAA 180
 CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

55

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGag GTACKGAAAC ATTAGTGACC 360
 TTCCCTTACA CCCAAACACT GTTGATATGC CAGT 394

5 (2) INFORMATION FOR SEQ ID NO: 3884:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120
 20 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGATTAG CGTAACAAAA TATGGACCTG 180
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240
 ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300
 25 CAATAACGAC GCCAACACTA AAAAnTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360
 AAAGAGGAAT CACAAAAGTT CcNTTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

40 TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180
 45 TATAGGCCCA TTTTTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360
 50 GACGGCTAGC TCCCAAAGG GTACTnCCAn CGGGnTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCAATTGGA AACTGGAATn 120
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300
 20 GTTAGGGGGT TTCCGCCCCCT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360
 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3887:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

ATTTTTTAAT TTTTCATGCAA ATTTTAAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60
 35 CTTTGTGCCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACCTAGT CGAAAATAAA 120
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 300
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAAC 360
 45 TACACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

(2) INFORMATION FOR SEQ ID NO: 3888:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60
 GTCTAGTTTC AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTTCATTCA TAAAATTAAA 180
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTACACA GCTTCATTAA TAAAACGACT 300
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360
 AACGAATCCG CTTTCATCCAA AATCANCCAT TCTAACGCAC 400

15 (2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGChAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aaAGCAAGGC 60
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTaGCTGG TGGCGTTGAA 360
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTTTnAAAT GCTGGAAAAT GTTAGCCTnC 480
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60
 55

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAnTGAAT TCGGACTACC 240
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300
 ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360
 10 GGTITTTGCnT CGCAAAACAT TTATTTTGn 389

(2) INFORMATION FOR SEQ ID NO: 3891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180
 TCTAGTGCCT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTGGAACC 240
 30 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300
 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360
 ATTGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCACTG 180
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACChTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

(2) INFORMATION FOR SEQ ID NO: 3893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT 60
 GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACCTGCT 120
 GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT 180
 TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCCTTATG TGTGTGTAGAT 240
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TATTATCTG AAGCTGAATT CAGAGATTAT 300
 TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAAATGGG TGCCAGAAGG TCATTAAAAG 360
 ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACCTna 400

(2) INFORMATION FOR SEQ ID NO: 3894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCCTG 60
 ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT 120
 TAGTACGTGT ATATATCGTT CAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC 180
 GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTGTA AGAAGATATG CCTTACTTAC 240
 CAGATGGACG TCCGATCGAT ATCATGTTAA ATCCTCTTGG TGTACCATCT CGTATGAACA 300
 TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG 360
 cATCACCAGT ATTTGaCGGT GcAaACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG 420
 GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCChTCCGA 480
 TAACC 485

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT 60
 AGATTGTGGT TTTTLAGTTG GTGCCACTGc TTTAACCTTT TCATTGATTT CAATAACAGG 120
 TGTTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180
 TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCTGGTGTT GCGGGTGTTG GAGTTTCTGG 240
 CTCACTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTCCT GGCTCACTTG GTACTTCTGG 300
 TGTGGTGGGc GTTGGTGTTC CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360
 CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTTGA CCTTCATTTT GGGCCGCTTA 420
 CTTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC 480
 TGGGGTTAAC CTAAATTGG AACCTCC 507

(2) INFORMATION FOR SEQ ID NO: 3896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGGnGACTTG TGACAATCGC 60
 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120
 CTCCTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG 180
 TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT 60
10 CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC 120
ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT 180
CAATACGCAT GTTAAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA 240
15 CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC 300
AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TGCGCACATG CTCCTATCAA 360
ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG 400

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(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT 60
GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA 120
35 TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTTG ATGAGGACTT AGCAACACGG 180
GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA 240
TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG 300
40 ACAAAAATGG TGTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG 360
ATGTCGCGTC ATTTAAngGA AGCGATTAC CATCGnGATC 400

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(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 180
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG 240
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300
 10 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360
 TTCTTGGAAT TGTGGACAAT CGGCTTGGCA nTCTTnCTC 400

(2) INFORMATION FOR SEQ ID NO: 3900:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120
 TAATGTTATT TGTTCAATCA CTTTCATTCC AAACATACCA TCACATCCTC ATTCATTTTT 180
 CATATAATTC TGTAATTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240
 30 TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTTT TTTTCGAAAT TCTCTATGTT 300
 GGGGCCCCGn AACTTGCAAT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360
 CATCCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400

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(2) INFORMATION FOR SEQ ID NO: 3901:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60
 TTTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CACACTCAAT GCGGCTCATC 120
 50 GCATTCAATTT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

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TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTTACCTT TTAATTTGGA CGGTTTAGAC 360
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TCACTTCGC CAAGCCATTT 240
 TTCTTTGTGT TTACTTTTAA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 TCAATGCGGC TCATCGCATC CATTTTGTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360
 AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTGGTGA TTCAAATCA TGAGACTGGG 60
 ACAGAAATGA TGTTCATATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTGTGATG 120
 AACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180
 TTCACACTGA AAATTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240
 ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360
 CTTTTTAGGT GGGTTTAGGG AATTTCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10	CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG	60
	TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG	120
	CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC	180
15	AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC	240
	ATAGCATATC AGAAGGCACA CCCGAGAGnC TGAAACATCT TAGTACCCGG AGGAAGAGAA	300
	AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCCAA CCAnCAAGCT	360
20	TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA	400

(2) INFORMATION FOR SEQ ID NO: 3905:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

	AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA	60
35	TGgTAAATGA ACAATCATT GATATTTTCAG GTCCGTTAAA GGGCGAAATA GAAGTGCCGG	120
	GCGATAAGTC AATGACACAC CGTGCAATCA TGTGGCGTC GCTAGCTGAA GGTGTATCTA	180
	CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTtTTCC gACTGTtTAGG	240
40	TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT	300
	TAACACGCCA CATCAAGTtT TGTtTACAGG TAATTCCGGG TACGACAACA CGATTGATAG	360
	TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG	399

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(2) INFORMATION FOR SEQ ID NO: 3906:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTCAGCAGT AGAAGAGGGGA 60
 ACATTCTAAA CTAAATTTGC TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTG AAAAATGATA AAATCGACTT TATTTGGAGT 180
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAAGTGG GTTCTGTGAC ATTAACGTCT 240
 10 ACAAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300
 AACCATTAAAC AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360
 AAAGGTGGAT TGGCCAC 377

15 (2) INFORMATION FOR SEQ ID NO: 3907:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

25 AATTAGGTAA TTCAAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120
 GGTCTCGTAG TGTAGCGrTT AACACGCCTG CCTGTCACGC AGAGATCGCG GGTTCGATTG 180
 30 CCGTCGAGAC CGCCATTATT ATTACCATTG CGGTTCAGTA GCTCAGTTGG TAGAGCAATG 240
 GATTGAAGCT CCATGTGTCG GCAGTTCGAC TCTGTCTGta ACCATTCTTA ATTCATGGCG 300
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTGAGGG TCGATCCCC 360
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420
 TCCAAGCTGA TGTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTC 480
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

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TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180
 AAAAGATATA GGGATTATAT TGCCTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240
 5 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300
 TATCATCATT TGTTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

(2) INFORMATION FOR SEQ ID NO: 3909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180
 GATATTTTAC ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300
 30 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCGTTCCCT AAAATTAATC CAGGGCTTAA 360
 CATTGCGAGT CCAGGTATTG GntCCAAGCT AATGGGGCCG 400

(2) INFORMATION FOR SEQ ID NO: 3910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180
 50 CTGTAGTTGG TGACGTTATT GTTAAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGAAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 3911:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTACTC AAGTTATGGG TCCTGTAATT GATGTTGAT TTGAACATAA CGAATTCCTA 60
 AAATTAATAA CGCCTTGGTT ATTGATGTGC CTAAAGAAGA AGGTACAATA CAACTAACAT 120
 TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTTCGTAC AATTGCGATG GATTCAACTG 180
 ATGGTGTCCA AAGAGGCATG GATGTAAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240
 GTGACGAAAC ATTAGGTCGT GATTTTAATG TACTAGGTGA AACAAATTGAC CTAAAGAAG 300
 AAATTAGTGA TTCTGTTGCG CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360
 AACTTTTCAA CAGAAGTTCC AAATTTTTAG GACAGGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3912:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAAA TCAACACAAC CAAAAGGTAG AAAATTCAA GATTTCCTA 60
 GTAAATTTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120
 CAAATCCTAA TGGAAATAAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180
 ATGGGAATAT AGTGTGATCG GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240
 TAAATAGTAA ACACGANGCT ATTGGTGTA TCTATGCCGG TAATAAGCCA TCAGGTGAAA 300
 GCACCAGAGG GATTTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360
 TTTAGATAAA TnATTAAGAC CTANGACATT CACCCAATCC 400

(2) INFORMATION FOR SEQ ID NO: 3913:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 60
 10 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA 120
 AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 180
 TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGACTTGTGA 240
 15 CAATCGCTTG CTCTTTTCCT CTCTTCGGC TCTCGCTTAC TCATTTAGCT CTAATAAAT 300
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT 360
 CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA 400

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(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT 60
 CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTTAAT 120
 35 GCCAAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT 180
 CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT 240
 TCGGTCTAGT TGCTAAATAA TCTTTAGCTA ATTGAATTGC TGGTGTGCA GCATAACAAG 300
 40 CTCTTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTG 360
 nACAGCGGCT GCTTTACGAA TTCCAACGTC TGATTCCAGT 400

45

(2) INFORMATION FOR SEQ ID NO: 3915:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

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TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180
 5 TCGAAATTGA ACGAaAATTC AAAAaCATTa TATCGTGACT TAGTTGAAGA AAAAATAATA 240
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300
 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360
 10 ATTAGAAACA G 371

(2) INFORMATION FOR SEQ ID NO: 3916: .

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAAATAGC 60
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180
 GACTAATAGT AAAAaAGTTa ATCACAaAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCCTTGAA 300
 AGAGCTTGAT TTAAaATTGa GAAAACAaCT TATTGAAAAA CAGATCTTTA CGGTAACATG 360
 GGTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400
 35

(2) INFORMATION FOR SEQ ID NO: 3917:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGcCnTGAAG GAATAACAaC CTTTAGACCT 60
 GGAGATTGAG CTAAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120
 50 CCACCAaATG GGCTACGAAT TGTTACAGGT CGAGTTTTAG TACCGCCTGA ACGGAaACGA 180
 GTACGTGCAa TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAaACC TAAGAATTGT 240

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GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTGT TAGTCCTTCA 360
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60
 TCGGGTCAAC GCCTACTGCC TTAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120
 CTTTCACTTT ATCTCCAGAC ATTAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180
 ATGTTCTGTC AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240
 CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300
 GGTCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360
 CCGACCATCA CGGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAACTG 120
 CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180
 GTAAACTGTC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300
 ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnC TTCACAAATG 360
 CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10 CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG 60
 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120
 ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180
 15 ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240
 CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300
 GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360
 20 GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3921:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT 60
 35 TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA 120
 AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT 180
 CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240
 40 ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300
 GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360
 45 TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3922:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180
 CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTIONACC GGCTTCGGGT 240
 10 GTTACAAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTACCCGT 300
 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTGn 400

15 (2) INFORMATION FOR SEQ ID NO: 3923:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120
 30 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGGCACT 180
 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTGATGTTA TCGATATGTG 300
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

40 (2) INFORMATION FOR SEQ ID NO: 3924:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60
 CTTCAAATA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACC G 120
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTCTT ATCATATAAA TGATAGATTC AAATAGATTT 300
 GTAGGGTTGT CATGCCCACT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AantCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTCG AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTCGCTACC CCTCCAGCTT ATTCATATAA 180
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAAG 240
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300
 GTGTTACCGC CGTGaAAGGG CGTGtGCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAantGAAT TCGGACTGAC 480
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

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(2) INFORMATION FOR SEQ ID NO: 3927:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60
 GGTTGCATTT AGCGCAACAT GACCATAGTT TTAATAAAGC ACAGCGCGCA AGTGATTAAA 120
 GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATT TTCAATAGAT 180
 CAGGAAGACT ACCAAGCTTA TGTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240
 ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT 300
 GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGA TGAGTTTAAG TCCATCGCTA 360
 AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC 400

(2) INFORMATION FOR SEQ ID NO: 3928:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTTGTGC 60
 AnTTTGTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA 120
 GTAATACATC TCCAACATTT GCCTTTAATT CTTTTCGAT GACTACCGGT CCTGGATGTG 180
 GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA 240
 CTGAAACATT TCGCGTTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA 300
 CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA 360
 CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3929:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

	CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTTAA CGCTGTTATC TTTATGCCAG	60
10	TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG	120
	TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG	180
	AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA	240
15	CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA	300
	TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT	360
	ATTCACTAC CACGnAAATT ATAGGTGTTG AACCCnAGT	400

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(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

	ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGTTCT AAACATGACG CCCTTATGCT	60
	CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCCAATGA TACATCGAAT	120
35	GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT	180
	GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA	240
	AAAAATAAAT GAATAAGTAA GGTTTCAACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT	300
40	TGTCGTTGTG CCAAATTGA ACGnTTTGA TGGCAATAAG CATGACCATA CAGATTGTGT	360
	ATTATTTCCA TGnA	374

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(2) INFORMATION FOR SEQ ID NO: 3931:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

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TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120
 TTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240
 GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTTAAAATGC 360
 10 CATTnAAATT CTAGGTGTTT CCnTAnC 387

(2) INFORMATION FOR SEQ ID NO: 3932:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTGA GTGGATCCTG AGTACGACGG 60
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120
 TGACCGATAG TGAACAGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

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(2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

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AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60
 CTTTTTGCCCT GGCAACGTTT TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120
 AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180
 ATATGAATGT AAATTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnCTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTAT TTCGTTCGnT 60
 CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCG TGTGGGGCC 120
 CCGCCAACCTT GCCATTGTCT GTAGAAATG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180
 CCCCACCTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240
 AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300
 TTGAAAAGAG CGTGTACAC GGGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10 AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG 60
 TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGGGTGG AGAACCTAAA 120
 AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT 180
 15 GACCCTCTGA TTAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC 240
 TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA 300
 TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT 360
 20 TTACAGTCCG CCGCGTTTAC CACTTCGCTA CCTCCAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3937:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC 60
 35 CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA 120
 TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAGT 180
 40 GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCCTC AGCCGCCCCA 240
 TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAACC TCAGCCTTCC AAGCTGATGT 300
 TGTGGGTTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG 360
 45 GTAGAGCTAT CGGCTGTTAA CCGATCGGTC GTAGGTTTCA GTCCTACCTG TGGAGCCATG 420
 GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC 480
 CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA 540
 50 TkGTTGgAGG aAgTGTcCG AgCyGGGCGG AAGGaGCACG CCTGGAAATG TGTAAGCGTT 600
 CACAAGCTT 609

(2) INFORMATION FOR SEQ ID NO: 3938:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10 TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGAATCGCT 60
 AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT 120
 CACACCACGA GAGTTTGTA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180
 15 CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240
 CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300
 GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360
 20 GnGGTTAnAG CGCACCTGA TnAACGTGAA GTCGGTGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3939:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTCAATG TCTGGTGAAT ATAGCAAGGA GGTCCACCTG 60
 35 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120
 CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180
 40 TCGGCTGTTA ACCGATCGGT CGTAGGTTTC AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240
 CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACAG GGTTCGAGTC CCGTAGAGTT 300
 CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360
 45 GGTTTCGAAC CCTnCATTTT CCACCATTG GTTATTAAAn 400

(2) INFORMATION FOR SEQ ID NO: 3940:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ACACAACAGC TGTTTCAAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300
 10 AAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360
 TAGATAAGGT GCnTGcAGG TATCGTCCAA CTATTATTAG 400

(2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120
 25 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAT GGTGCAGATG AAATTGACAT 180
 30 GGTCAATCAAC ATCGGCGCAT TAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAGTG ATTATTGAGA CGGTATTGTT 300
 35 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360
 AAAAACTTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120
 CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTnAT 300
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360
 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300
 CGCCTTATAT AGTTTGTAAG TnAnnATGGT GGGGAGCTAG CGGGGTTCGA ACCGCTGGAC 360
 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60
 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120
 GCAACCCGTT GACCATTGCC CACACCATTG GATAGGAGCA TGTGCGCAAT GGCATCCACA 180
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGA TAGCGC AACATGATTA 240
 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300
 GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGA 360
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATAtC AATCAn 406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTCGAAT 60
 AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT 120
 TTAAAGGAAA TTCAAGAAGA TGTTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT 180
 GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT 240
 CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA 300
 GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAN GCCAGGACAA 360
 ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGThT TAATAGGnTC TGAAACGATA 60
 CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT 120
 GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC 180
 CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTGCGA GCATCGCCGG 240
 CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC 300
 GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC 360
 CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT 400

(2) INFORMATION FOR SEQ ID NO: 3947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCGGGCCAGA GGACTTGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180
 10 GGCAACGTTT TACTCTAGCG GAANTAAATTC GNACTACCAT CGACGCTAAG GAGCTTAACT 240
 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300
 TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCnTTTCG CAAAACATTT 360
 15 A 361

(2) INFORMATION FOR SEQ ID NO: 3948:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120
 ATAAAGCGGA TTTTCAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACCG CAAGATATAT 180
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGCnGA ATAGGCCACC 360
 GATACATCAC CAACAATTGG na 382

(2) INFORMATION FOR SEQ ID NO: 3949:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG 300
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGn CTCAATGnGG 360
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGGTTTT GCTTGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA 120
 AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360
 30 GTGTACAAGA CCCGGGAACG nATTCACCG 389

(2) INFORMATION FOR SEQ ID NO: 3951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60
 TTACCAATTT TAAATGAATT TAATAAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT 120
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTT TATTACTCTG 180
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240
 GGTTCAACTG GAAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300
 AAACAnTGAT GGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

(2) INFORMATION FOR SEQ ID NO: 3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCAT AAGTTGTTCT CAGTTCGGAT 60
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCGTC ACACCACGAG AGTTTGTAAC 180
 ACCCGAAGCC GGTGGAGTAA CCTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240
 GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360
 GNTTTGGAAT GTTTnTTAA CATTnCAAAA AAATGGGGCC 400

(2) INFORMATION FOR SEQ ID NO: 3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240
 TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA 360
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAATC GGTAAATTAA ATATGGATGA GTTTGCAATG 60
 5 GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTGA CCATAAAGCA 120
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTT 180
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA 300
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360
 15 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 3955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTT 60
 GGTCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180
 CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTCAAT CTACAAAAGG CACGCCATCA 240
 CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300
 35 TCCGGGGGTG CTTTTCACTT TTCTCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360
 TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

5 ATAAAAATGG AGCAGAAGAC GGGATTGGA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240
 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAn 400

(2) INFORMATION FOR SEQ ID NO: 3957:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120
 25 AAGACGCCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240
 TTTTGGGGTG CATATTTTGT ATATGGGTTT TGATGAACAA GGTATTGTTC ACATGGTAGG 300
 30 ACCTGAGACA GGAATTACAC AGCCTGGCnA GACCATCCGT nTGTGGGTGA CTCTCACACA 360
 GCCACACATG GnGCCTTTT 379

35 (2) INFORMATION FOR SEQ ID NO: 3958:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA 60
 ATATATTCAA GGTGAGnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120
 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAACAG CAGTAAGATA 180
 50 ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

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AATAAGACAT TTGnCCAAC TGA CACTACC ATTAAAACT

400

(2) INFORMATION FOR SEQ ID NO: 3959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60
 CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTAA GAGGAGTGGT 120
 TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180
 CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240
 GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300
 CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360
 CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60
 TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180
 ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240
 ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300
 CGCTGGAAC TACTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCA CGCCGTAGGC 360
 TTAAGATTCC TGAAGTCTAG TCGTCTGGC CAATTTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

	TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
10	AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
	GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
	GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC	240
15	AGTAAATGTG GAGCCGTAGC GAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
	GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
	GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

20

(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
35	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
40	ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACTACTT	360
	C	361

45

(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

55

AAGTGTCTTA TTTTTTTAA GTATTTCAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120
 GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180
 5 AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240
 ATTGAAAATT ATCTTACTGC TGTTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300
 ATATTCAC TAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360
 10 TTGGAATATA TTTAT 375

(2) INFORMATION FOR SEQ ID NO: 3964:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACCTTACA 60
 25 ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTGTACAA TTAATGTGAC ATGACTAGGT 120
 CTGACGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTCGTT ATGATTTAAT 180
 30 ACGCCTAATT CTTTCATTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360
 35 ACCATTGCTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

(2) INFORMATION FOR SEQ ID NO: 3965:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAA GTAAATTGCT 60
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAAC TAC CATGCTTGT 120
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180
 55 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA 240

TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAGAA 360
 TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

5 (2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60
 TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120
 20 GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180
 AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240
 AAAGTATTTT AAAGTAAAAT TACATGTTAA TACGTATATA ATGGcGAGAC TCCTGAGGGA 300
 25 GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCTtAGG AAAGCGAcnC ATTcAATACG 360
 AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

30 (2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

40 GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60
 TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120
 45 AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180
 TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGTATCGGCG 240
 AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300
 50 GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360
 TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

10 ACCCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTGCA ACCCGCGACC CCAACCTTGG 60
 CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120
 CACGCCGTAA nCTGAGGATC CTAAGTCTAG TCGTCTGCC AATTCCGCCA CACCCGCAA 180
 15 TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC 240
 AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300
 GGATTACAAG TCAATTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360
 20 GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3969:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60
 35 CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120
 TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180
 40 GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240
 ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300
 CATGTATTCC TATTTTTAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360
 45 ATAAATCATT AGTGGCTCTn TATCATTTTCT GTCCCACTCC 400

(2) INFORMATION FOR SEQ ID NO: 3970:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GATAAGATCA GCCGAAAATG GATGGTGTGA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60
 TTTTAAATGG CATTGTGTAC GACACCATTG CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120
 5 CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTGC GA GTGCAGAGGC GCCACTGAKA 180
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240
 10 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTtnCA ATGTCTAAT 419

15 (2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACITGGGA GACTTCAATA ACAGATTTAG GTTATCTAA AAATCAGGCA TATAATTTCT 60
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120
 30 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300
 35 CACCAACACT AAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360
 GGGTTTCCAn AGTCCGTTAT G 381

40 (2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCG 120
 55 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3973:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACCTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60
 20 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180
 TATGATAATC ATGGTCGCTA ATAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCCTTGA 240
 25 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATACT 300
 TTGTTTCTGC TTCATATTTC GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

(2) INFORMATION FOR SEQ ID NO: 3974:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT 120
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAACT 300
 TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TCGCTGAAA 360
 CACTTGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GGCGACCGCC CCAGTCAAAC TGCCCGCCTG 60
 ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA 120
 TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT 180
 ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC 240
 TGTGCGGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC 300
 AGTGCCCAAA TCGTTAACGC CTTTCGTGCG GGTCGGAACT TACCCGACAA GGAnTTTCGC 360
 TAACTTAGGA CC 372

(2) INFORMATION FOR SEQ ID NO: 3976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 CCCATTGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA 240
 ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT 300
 TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TAACTCATT GTCTGCTAAA 360
 ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn 395

(2) INFORMATION FOR SEQ ID NO: 3977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60
 5 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180
 10 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGGCA CTATAAAAAT 240
 GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300
 TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360
 15 CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG 400

(2) INFORMATION FOR SEQ ID NO: 3978:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120
 CTTTTGGTTA CAGAAATTTT AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240
 35 AGCTCTAAAA GTTGATTTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300
 GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360
 40 GGATTCCGAA CCTCGGACCC TCnGAnT 387

(2) INFORMATION FOR SEQ ID NO: 3979:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60
 55 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120

CGAACCTCTG GACCCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300
 5 ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCAITTTG 60
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTGGGCC AAGCATACAA GCCGGCATTT 120
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGT TATGGCTTCA 180
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG TTTTGGCAGA 240
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACCTAGT TCAAGGTACG CAGAACATCT 300
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360
 30 nGTCAGCCGT TTTAATACGA GGATGTTCCG CTAnGTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

45 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240
 GGATTTCA CA GTTGTGCGAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300
 GGrCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTTATAG ATCCATTCAA 60
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAAGCAAA 120
 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 180
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240
 TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300
 AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA 360
 AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

(2) INFORMATION FOR SEQ ID NO: 3983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60
 AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120
 TCGAAAGACG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG 180
 CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT 240
 AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT 300
 TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360
 GTTACTAACG ACGATATGCC TTGGGGGAGC 390

(2) INFORMATION FOR SEQ ID NO: 3984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120
 10 CGTTTCTTTT ATCCATTTC AATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GCGCTTCTAA 240
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3985:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60
 ATTTCTGATA TTGAAAGTAA AAATACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120
 AAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAATATCT TACTGCTGTT CTCTATTTAT 180
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTGGTCTTC 240
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAAC ATGTnAATTT 300
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCTnCTA 400

(2) INFORMATION FOR SEQ ID NO: 3986:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCATTAT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCCGT GCGGGAACGA 240
 5 TTTTGTATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCCOCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60
 CGGACTTGGG TATTCTCCA AAATTATATG GACCTTCAG GACTCGAACC TGCGACCGAA 120
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180
 TAATAAATAG TGGCGGTGGA GGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240
 30 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTA TAATATGGTG GGGACTAnCG 300
 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60
 ATGTTCCGCCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTTCGAAAGA TCGCGTAAG TCTAAAAATG 180
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGACTCCTAG GCGGTGAACG ACCATCCAAA 300

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

(2) INFORMATION FOR SEQ ID NO: 3989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15	CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA	60
	ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA	120
	GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG	180
20	CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC	240
	ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG	300
	AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT	360
25	CCT	363

(2) INFORMATION FOR SEQ ID NO: 3990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

	TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
40	GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTACTTTCTA GGATCGACCA	120
	ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT	180
45	ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAATGC	240
	CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT	300
	CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT	360
50	CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

(2) INFORMATION FOR SEQ ID NO: 3991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

	AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA	60
10	GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAATTAAT CAAGTGAATT	120
	TCTTTTGGTT ACAGAAATTT CAACAACCTT AAAGCAGTA TAATGATGAT TTTCAGCTTG	180
	TACAAAGGAG AAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
15	GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTGGT	300
	GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
	ATTGGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

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(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

	AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCATTATT ATTACCGTTA TTGTATTAGT	60
	CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGThGACA	120
35	TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
	AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
	CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
40	AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
	TAAAGCCTTh AAATGGATGG TGATATTGAT AATGAATGCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

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TTATCAGAAG AACAAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GGNGCATTAC CCGTTGGATT ATTACCGAAT 180
 5 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGAAGAGCC TTCAGTTGTC 240
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300
 10 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAAnTnT 360
 CCGCCGGCAT TGAGAGCCTT AGA 383

(2) INFORMATION FOR SEQ ID NO: 3994:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60
 25 GCGGGTCGGA ACTTACCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180
 30 GCACCGGCA GGCCTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240
 GATAAACAGT CGCTTGGGCC TATTCACTGC GGCTCTTCTG GCGGTTAACC CTGAAAGAGC 300
 ACCCTTCTC CCGAATTACG GGGTCATTG CCGATTCCTT AACGAGATTC GCTCGCTCAC 360
 35 CTTAGA 366

(2) INFORMATION FOR SEQ ID NO: 3995:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60
 50 TTCATTAAAA GCAACGTTAT GntGAATCGG ATAGAGGCAT CTA CTGGGAA ACGATTACAA 120
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATT TGTGCTGAGC 240

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCantGCG ACAAGCATG

359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA	120
TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTCTT AATTGAAATC ATCTTATGAC	180
TGCTTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTnA GACATAAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTTCCTG GGCAACGTTT TACTCTAGGC	360
GGAAnGTAAG TGGGACTTAC CATCGACGn TAAGGGGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCGGG CAGTTTGACT GGGGCGGTG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGTTTGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAACATTA TTCCTGAAG 60
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG AATTAAATTA TTTTAACAT CCATTACTTT 240
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTTC ATGTCTTACC 300
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCACCAA GGTTAGGGCA 360
 15 TAACACTTTC TATTTCCGAG GTAGCAAAGA CAAATTGCGA 400

(2) INFORMATION FOR SEQ ID NO: 3999:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCCTTAG TGCTGCACtA ACGCATTAAg CACTCCGsCT GGGGAGTACG ACCGCAAGTg 60
 30 AAACtCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120
 AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180
 CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT 240
 35 GGGTTAAGTC CCGCAACGAG CGCAACCCtT AAGCTTAGTT GCCATCATTa AGTTGGGCAC 300
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC 360
 40 CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

(2) INFORMATION FOR SEQ ID NO: 4000:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAAA GGTTAGTTTG 60

55

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240
5 ATTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAAC TG ACAATGsCAA aGtTTATGAT 300
GATTACMaAG CaTTGTTAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360
TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60
CTTAACTTCT TGTTCCTCCG ATGACAGCTT CTATTAGAG AATGTCATGA TTATTTTATA 120
25 TTCACCTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180
AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAT 300
30 CAAGTCTTT CAAGGAAATC TGTTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360
TTGTACCGTA ThATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60
GACGTTTAAA CGTTTAAACG CATGCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120
TTATGCATAC AGATCCAATG AAATCTTAC CTGAAGATGG TAGCTTGCAG TTAAGTCTG 180
50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240
CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

(2) INFORMATION FOR SEQ ID NO: 4003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG 60
 ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA 120
 CGACAGGTGA TGGGGTTGAA AGTGTAAcGn GCTACACTGG TCATGATGCT GCTAAACTAC 180
 GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG 240
 TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT 300
 GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAACAC ATGATTTAAC 360
 AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT 400

(2) INFORMATION FOR SEQ ID NO: 4004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCCTTAAT GGGTGATGGC 60
 GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT 120
 GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC 180
 AGGTGATCTA CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA 240
 CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG 300
 AGGATANTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA 360
 nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG 400

(2) INFORMATION FOR SEQ ID NO: 4005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

	ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
10	GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
	ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTMTA	180
	TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
15	GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
	ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTTAATTT GGTGTTGGAT GACGTTGnAA	360
20	TGTTGCCTAA TTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 444 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

	CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
35	ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
	GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
	AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGTGCTCTTT	240
40	AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
	AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
	TAAAGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
45	CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

50	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

TTTGAAGTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120
 5 TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAT 180
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240
 10 CGTGCCGAAC TGGAACCTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300
 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360
 GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAACATTA GTTTAAACCA ATGCTTAGAG 60
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120
 30 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG 180
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300
 35 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120
 55 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

(2) INFORMATION FOR SEQ ID NO: 4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GSTATGTTACG TGACAATGAA TTACTAAATG GTATTTATTC ATCGAGTTAC 60
 20 ATCTATAGTT TATTAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240
 25 TGGGAGGATG CTTTAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360
 30 ATGGAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

(2) INFORMATION FOR SEQ ID NO: 4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60
 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGCACTGG CACTGCTCCC TCAGGAGTCT 120
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT 240
 50 TCGCGACATG TTAATGAAAT TGTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

(2) INFORMATION FOR SEQ ID NO: 4012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA 60
 AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTT TACTCTAGCG GAAGTAATTG 120
 GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTGTGTGACAA TCGCTTGCTT CTTTCCTCTC 180
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 240
 TCAGATTCAA ACGTTTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG 300
 ACGTTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT 360
 TTTTGGCCTG GGCAACGTTT TnATnCCAGC GGAAnTnAAT 400

(2) INFORMATION FOR SEQ ID NO: 4013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC 60
 TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC 120
 GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT 180
 CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA 240
 AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG 300
 CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG 360
 AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC 400

(2) INFORMATION FOR SEQ ID NO: 4014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

ATTAGGACCT CAAGACGATA TTAATAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
ATTGTTAATT TAACACATAG TAAGAAAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC	300
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTCG ACATAAAAAA	360
nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

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(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAGAGTCA GATGCTCTAC CAACTGAGCT	180
AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GAAAGGTCC	240
GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCGAAC	300
TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GATACCCCTG	360
CCAGnTTATT CATATGA	377

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(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

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5 ATGACGCACC TGACATCCTC TCGGTTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180
 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240
 CTCTGTACAT TTTTTCCTCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATGTA 300
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTACGG 360
 GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA 400

(2) INFORMATION FOR SEQ ID NO: 4017:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

25 CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAAGTG CCCGnCTGAC 60
 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180
 30 AGCTGTGCCG AATTTCATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT 240
 CGCGGTAAC CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAST 300
 GCCCAATCG TTACGTCTTT CGTTGCGGGT CGGAAGTTAC CCGACAAGGA ATTCGTTAC 360
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

50 TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAG ATCGAGCGGC 60
 ATATGAGGCA CGCCAAGCGA TTCCAACAT TAATGAAAC AGTCCGCCAA TATTAATTGT 120
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

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CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360
 TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60
 TTGGGCTGTT CGCCCATTAAG AGCGGTACCA AGCTGGGTTT AGAACGTCGT GAGACAGTTC 120
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCTTAGT ACGAGAGGAC 180
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60
 AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120
 GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180
 ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240
 TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300
 TTTGTTAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360
 TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTTCAGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

(A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

10	CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG	60
	CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG	120
	TTTGCAAGTn TAAAAGATCG TCCATTTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAAG	180
15	GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCCTTT AATGGTTGCA	240
	GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT	300
	TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTTATCANT	360
20	AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT	396

(2) INFORMATION FOR SEQ ID NO: 4022:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

	GATTGGTCTG nAAGAAGAAT TAATGAAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA	60
35	TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT	120
	AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT	180
	ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTTAG	240
40	CAGTAGTTGA CTGTAAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC	300
	CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA	360
45	ACACAGAGGC TGGCGG	376

(2) INFORMATION FOR SEQ ID NO: 4023:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcngGCCAG AGGACTTGAA CCCCCAACCT 120
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180
 GGTGGAGAGT GACGGGTTTC AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240
 10 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATTC 300
 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTT CGGCATGGGA ACAGGTGTGA 360
 CTCCTTGCTA TATCACCAGA C 381

15 (2) INFORMATION FOR SEQ ID NO: 4024:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

25 GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120
 30 TACATGAAGC TGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180
 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300
 35 AACAAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360
 ATTTCCGGnAA CATcTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

50 CTTAGAAGTG AGAATGCCCG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60
 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120
 CGACAnGTAn GCGATGGAT AACAGGTTGA TATTCTGTGA CCACCTATAA TCGTTTTAAT 180

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GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300

GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

5 (2) INFORMATION FOR SEQ ID NO: 4026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

15 TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60

CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120

20 TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180

TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240

AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300

25 AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGTTATTA ATCTTGThG 360

TGTTCTTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

40 TCAIGTTTCG CTGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60

ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTAGTT 120

TCTGCTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180

45 ATGTTACTTG GTTCACAGAA CTTTGTAAGT TATTTTAGA CGTTACTAAT TGGCTATTAT 240

CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300

AGTTAGTGCG TGCAGAACT TGTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360

50 GCCTCCGTTT,TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180
 15 TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT 240
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 4029:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120
 TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180
 TACTCTAGCG GAAnTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTGATA 300
 CATTCAAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGACGCTn 400

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(2) INFORMATION FOR SEQ ID NO: 4030:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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5 GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTGTTTTCT 120
 10 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240
 TTTGAACGCC ATATAAATAA TGATTTTGGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300
 15 CAAATTGTGG TTTGTnTTGG ATTTCACnTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360
 TGAATCTATA CCCTGCATCT TGTAGCnTCC 390

15 (2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

25 TGGTTCGAAT,CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60
 CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT 180
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240
 GAGGTATAGG TGTAATCCT ATCTTCCGCT CCATAATTTA ATATTTGCGG GGAGTAGTTC 300
 35 CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGnC 360
 CATAATGCCT TCCAAAGGGG AATTTTTTTGG TTnACCATT 400

40 (2) INFORMATION FOR SEQ ID NO: 4032:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

50 GTATCGATGA GTTCTTTCGG TCGTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60
 ACATCGGGAT GACCATTAAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120
 55 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300
AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360
5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnaATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTC TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60
20 ACCGACTACA GCCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACt CCCCCTCGAT 120
GTGAACCTCT GGGGGAGATA AGCCTGTTAT CCCCggGGTA GCTTTTATCC GTTGAGCGAT 180
GGCCCTTCCA TGCGGAACCA CCGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240
25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300
AGGGAACTTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCAGTC AAAGTGGCCG 360
30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60
45 TTTCTGGTCT GTAACGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120
CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180
CTGCAGCTAA CGCATTAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA 240
50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG 300
AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360
CAAATGACAG TGGTGCanGT TGTCTCACT CGTGTCGTGA 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTGCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120
 ATGTCAC TTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180
 CATTAACTACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300
 CCTGTTTTTTG GATTATGAA GGCTATTTGG GGTTCACTCG AATGTCAGTT CGAGGAATAA 360
 TAAAGTAAAC GAGAGCCAGG TTGTAATTA TGGCACTAAT 400

(2) INFORMATION FOR SEQ ID NO: 4036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180
 CATTCTTCTA TCGATTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAATG GCTATTGCAC GTACAAAGGC 360
 TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60
 5 TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGGTC TTTTCTCGTT TCGTCAGATT 120
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTCGCCT 240
 10 GGCAACGTTT TACTCTAGCG GAANTAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360
 15 TACnAAACTC GTTTCGCTCT T 381

(2) INFORMATION FOR SEQ ID NO: 4038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60
 TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTTAC TGTATCGTA AAATGCAGCT 120
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180
 AATTGATAAT CTTTAGGAAT AACTTTAAG ACGACATCTT CAATGCGATC AAAATGTTTT 240
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300
 ATGAATGCTT TnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

(2) INFORMATION FOR SEQ ID NO: 4039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60
 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120
 CACCGCAGAT TTAAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

GAACCTCTGC ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 60
TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120
TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAG 180
AGACCTCAGC GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240
CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300
GGCTCTCGCn TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360
AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60
GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT 120
GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180
TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240
CTATCGATTG ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300
CTGTATCACC ATCCATCATA CGATTGAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360
TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AACTGGTAA CACACCAGAC GGACGTAAAG 60
 CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120
 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180
 ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300
 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360
 ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA 60
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120
 AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT 180
 TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCCTACTG GnATAATAGC GAGGCTACCA 60
 TGTGTGTTTCA TCGTAGnCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240
 TCTTTTGTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360
 15 CnTTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120
 CATTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAATGAT TAATTGCACA 180
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGTnG 300
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGnAAGT 360
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGnGn 400

(2) INFORMATION FOR SEQ ID NO: 4046:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

50 CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120
 55

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300
 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACnACn GGATTCTGAG 360
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60
 TTACGTTT CAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120
 GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180
 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TCGGACATTA 240
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300
 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360
 GAATTTGACG GnGGACCAAG ATGcnTGTTT CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGACTCAGAT 120
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180
 GTACTAGTTG CCCC GCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAAGTGT 300
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

(2) INFORMATION FOR SEQ ID NO: 4049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60
 GACACTACCT TCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC AACAATTTGA 180
 ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240
 GCTATATGAT TAAATATTA AAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300
 ATACCTTTTC ATTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360
 CCCATACCGG GGTCAATCGTC CAATACACGT TCCAAnCTnC 400

(2) INFORMATION FOR SEQ ID NO: 4050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCG 60
 GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120
 GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180
 CGCTACCCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCCGTCC TCCATTCACT 240
 GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300
 CTAAACGCCT ATTCAGCTCG ATTTCGTACGG CTCCACATTT ACTGCTAAAnC TTGCATCAAT 360
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAntA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60
 AACAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120
 10 CCATTTCGTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCTTAATC 180
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300
 15 CCAACATGTG GgntCCGGTT CATTGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180
 35 TTCCCCATTC GGAAATCTCT GGATCAAAGC TTACTTACAG CTCCCCAAAG CATATCGTCG 240
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300
 TTAATChATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360
 40 TTCATTAATT TTAAATGGCh CAATTTAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG 360
 10 CGATGATCGT GAAATTGANA CGCANGATTT CCGATATAGA 400

(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCTACAG 180
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240
 30 TACCTGCAAA TGCATATCCG CAAAATATCG TTACTAATAT TTGGGnCATA CTCATCATAC 300
 CACCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

(2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAATCACT TCTACTTGTT 60
 CTGTAATTTT ACTCATAACG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTAC 240
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

(2) INFORMATION FOR SEQ ID NO: 4056:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

15	ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA	60
	TTAAATTAAA TTCTCAGGGA CTTCATGAC GCCACCTGTA TTGCGCTAG TTAGTAGGGC	120
	AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG	180
20	GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTC TTAAATCAAT	240
	AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA	300
	AATATGaCCA ACTGcAATAC CTCTTGTTGGc ACCGGtAAAA ACGCCCATCA GTKaATTaAT	360
25	GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG	420
	nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT	480
30	G	481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

	TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG	60
45	ACCTTTCTTG ACTTGAGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC	120
	ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA	180
	CTTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTC GACATAAAAA	240
50	AAAGAGACCT TCGGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT	300
	ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA	360
55	ATCGGCTGCh TCTGTnCCT	379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120
 TTAAAGGCT AAACACCAA TGTTTTCAAT GGATTTCCTAA AATGAATCAT CTGGGATGAC 180
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTATT AAATGTTGAT ACACCATTG 300
 AATACATTT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360
 GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCTCTCG 400

(2) INFORMATION FOR SEQ ID NO: 4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTG GTATTGCTCA GCTCCACATG 240
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCATTATAAC 300
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360
 ATCCCGT 367

(2) INFORMATION FOR SEQ ID NO: 4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

5 TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTTCAG ACACCGCATT 60
 CAGATTTCAGC ATAGCGATTTC AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120
 GATTTCAGATA GCGATTTCAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA 180
 10 GACAGTGATT CGGATTTCAGC GAGTGATTTCG GATTTCAGATA GTGATTCCGA CTCCGACAGT 240
 GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTTCAGA TAGCGATTTCG 300
 GACTCAGATA GCGATTTCAGA ATCAGACAGC GATTTCAGATT CAGACAGCGA CTCAGACAGT 360
 15 GACTCAGATT CAGA 374

(2) INFORMATION FOR SEQ ID NO: 4061:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

25 AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60
 30 AAATAATTCA CCTTCATCAC ACGTGTACC TACCAATAAT CCCTCAGCAT ATTCATCTAA 120
 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180
 TTTAAATAGA TTTTAAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtKGTtG ATTCGTTAT GATTTAATAC 300
 GCCTAAWTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTtagCCA AGAAATTCAA 420
 40 ACCATGTTTA CC 432

(2) INFORMATION FOR SEQ ID NO: 4062:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

55 TATCTTCGTT CTCAATAGAA TGATTTA AAC CTTCGATTTC TTTATCTAAA TGACTACCAA 60

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTTCGT 180
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGAnTCA 300
 ATTAACGCAT CAGTATTAGG GAnTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360
 nTTGGATTTG GAGCTAACCA CATCCA 386

(2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC ACGTAGGGCG 180
 ATGGATAACA GGTTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240
 CATAGGTATA GCGGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360
 CGAGTTCGTT GgnTTTCACA ATGGCC 386

(2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTT 60
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTAT 180
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240
 AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

(2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

15 AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA 60
 GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA 120
 CGACGCACGC CATATTGACT TGCCATTAAAG TCAAAAATTG TAGCAATACG GACTTTGTCA 180
 20 CCATTGCTA AAGTGAATTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA 240
 CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT 300
 GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTAA AGTTCCACTT CTTACCTTCT 360
 25 TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA 60
 40 GGAACAATCG TTATTAAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA 120
 CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA 180
 45 ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA 240
 GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG 300
 NATATTCATT TGTTTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT 360
 50 GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC 400

(2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

	CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATTG TTATTAAATT	60
10	ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCTAAAA	120
	GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
	TTTGACAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG	240
15	AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAAATA	300
	ATAAGGGCGG CTGAAGGGGA TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTAA	360
	CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

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(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

	TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAAG TGCTGCCAGT TGAGCGCCCA	60
	TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT	120
35	TGAGGATAAG ATAACCATTG AGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA	180
	AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAAATAA	240
	GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
40	ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT	360
	AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

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(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

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AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300
 10 GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCh 356

(2) INFORMATION FOR SEQ ID NO: 4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTtag GGAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60
 GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTG TTAAGGGGCG TTTAAGTAAT 120
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180
 GAAGTTGTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240
 30 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300
 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360
 AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

(2) INFORMATION FOR SEQ ID NO: 4071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTTCG CTA CTACACAC 60
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTTAACAT 300

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361

(2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

15 ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60
 CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120
 GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180
 20 TTTCATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240
 CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300
 AAAC TTGGTA GGAGTATTCT TACTGGATTG CCATTAACCA TCGTACTTAA TTTTAAATAT 360
 25 GCGGTTnCCG TTnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA 60
 40 TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120
 GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180
 TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240
 45 GTAAATGATA CTGAACCACT TGTGAACCGG AACAAGCAAT GGTAGTTACC AnAATTCTTG 300
 AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360
 50 CCGGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

	TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA	60
10	TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG	120
	TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC	180
	CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCTCCCAT ATCGGCGGAG TTATGCATCG	240
15	TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACan CTGTATTTCT ACGGACTGAT	300
	AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTCACT	360
	CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATHAAATG	400

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(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

	GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTGAGAG	60
	GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG	120
35	CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA	180
	GCCCCCTCA AGATGAGATT TCCCAACTTC GGTATAAGA TCCCTCAAAG ATGATGAGGT	240
	TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA	300
40	AGACTTAATC AAAATAAATG TTTTGCGACA AATCCACTTT TACTTACTAT CTAGTTTGAA	360
	TGATAAATTA CATCCATATG	380

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(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

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TTTGCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120
 CTA CTGCGTC CCCCATCGA TTA AACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180
 5 TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300
 10 AnCGGCATTTC TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360
 AAGGTTCTTA CCATGGTCAA 380

(2) INFORMATION FOR SEQ ID NO: 4077:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATT AAATCGAAGA AACCAGCAAC 60
 25 AGATTCTCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGCACCT GCAGCTGGTA 120
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180
 30 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240
 CAAGGCGGGA AAAAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360
 35 ACGGGCTCTT 370

(2) INFORMATION FOR SEQ ID NO: 4078:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60
 50 TGA CTTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

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TAAGAGGGGC CAACCATGTG TAGAATAAC AACGGTTGGC TCTTTAantG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

15	TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
	TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAAC TTGAT TCTTCTGACG	120
	CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
20	TTTGACCAAA TGTTGGGATT TTA CTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC	240
	AGAATGGACC AGGCGCTACA CAGTTCACCT TAATTCCTTT TGGTCCTAAT TCTTCTGAAA	300
	AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATaNG	360
25	GCCAGGGaNT AAAACCCTGG AChAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

	TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
40	AGTAAAATTA AATAAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA	120
	TATATAGATC ACACTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
	GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTTAAATAT	240
45	GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATTA	300
	GGTGCCTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
50	AGATGAATTG GACATGGTCA TCCACATCGG CGCATTA AAAA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTTCGACT CCCAAGTTAA	180
	ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

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(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGT GTTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTTCCT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAACTATTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
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TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360
 TGTnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4084:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120
 25 GTTCTTTTGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAT 240
 TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300
 30 TAAATAAACA TTCAAAACG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360
 ATGTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

(2) INFORMATION FOR SEQ ID NO: 4085:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180
 50 GAACCAGCTG GAGCTATAGG CCCATTAATT TGAATGAAC AAACATTCAA AACTGGAATA 240
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTGTG TCCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAAATCCA TGTGTAGCGG	60
TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAAGTG	120
ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT	180
AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCCTTA GTGCTGCAGC TAACGCATTA	240
AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAAACTC CAAAGGAATT GACGGGCGCA	300
CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4087:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCACCGAA CGTTATGAG CCGTTAGCTC TAACCAACTG	60
AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA	120
CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT	180
AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA	240
GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC	300
AGGATTTCGAA CCTGCGACCC CTTTCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCh	360
GTATAATTTA ACGGGCCCGA TAGGAGTTCCG GAACCCCTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA 60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTAA 120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG 180
GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA 240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA 300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA 360
GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAATAT 400

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(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG 60
GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG 120
CAGAAGCCAT TGTCAATTAT GCAAAGAAA AGCAATTAAT ATTAAGTGA ACAACAACAT 180
TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT 240
TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA 300
TGGATTTAAC ACATTATGAA CGAGATGGTA AAAGTCTAG CTCATTGCTG TTGAATTATT 360
nCATAACGGT ATCA 374

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(2) INFORMATION FOR SEQ ID NO: 4090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

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TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCCGT TGTGACAGTA AGTGACGCGT 180
 5 TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAT GAACAATGTG ACGTATACGA 240
 CGCAAGACGA ACATGGTCAA GTTGTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300
 ACAGTGCACC AGTAACAGTG ACACCACANT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360
 10 TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAATGCGC TTGCAACAAG CTTTTTTCAA 60
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120
 TGGGGTGTGG GCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180
 GGGTGTGGGC CCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360
 35 CGGGGGCCCC ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 4092:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACITCAGC TTGGCAGCCA 180
 CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

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CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360
 CATTTGACCT TCATTGTTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240
 CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300
 AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60
 TGTTCTTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA GCAGGCGCTC 240
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120
 AAGTGAAGGA TGTATAATT TATCCTTCGC TTCTTTTAT TAATTAGTA ATGAATAGTA 180
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300
 TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AntAGGTATG CCAGTGTGCA 360
 15 CTCCTTGAGA GGAAATACTn ATTT 384

(2) INFORMATION FOR SEQ ID NO: 4096:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60
 30 TTACGCCTTT CGTGCGGGTC GGAACCTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCTAG CTTCGCAGAA AGAGCCGACT 180
 CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240
 35 CAGAGACCTG TGTTTTTGAT AACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300
 GTTAACCCTn AAAGAGCACC CTTTCTCCCG AAATnACGG GGTCATTTTG GCCGAGTTCC 360
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

(2) INFORMATION FOR SEQ ID NO: 4097:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180
 AGCGATTTCG ACTCAGACAG TGATTTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC 240
 5 AGCGATTTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300
 TCAGATTTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTTCGGAC 360
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTTCAG 400

(2) INFORMATION FOR SEQ ID NO: 4098:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60
 CTGGATTTCG TGTAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240
 TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGAAT 360
 GGCCAGTTTG CCAAGCACTG GTTTGACCA ATGGnGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4099:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTTCG 120
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT 240
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCCG 300

(2) INFORMATION FOR SEQ ID NO: 4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA 60
 TAAATCAGCA TCATCATTTA CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC 120
 TAGATTTAAG TCGAATAGTA GCGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTTT 180
 CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT AATAGTTTTA CTTTAAGTCC 240
 AGCATTCA CA AAAAGTGCTG CCAGTTGGAG CGCCCATGT GCCTGCGCCA AGAACGGnTA 300
 CTTTATTAAT TGGTCATAGT GANTCCnCCC ATTTAGTTGA GGGATAAGAT AACCATT 357

(2) INFORMATION FOR SEQ ID NO: 4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT 60
 TGA CTGGnCG AAAATGCGCT TGTAACAAGC TTTTTTCAAT TCTAGTCAGG GGCCCCAACA 120
 CAGAGAATTT CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCCACACA 180
 GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA 240
 GAAATTGGAT TCCCAATTTT TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT 300
 TTGCGAAAAT ATCATTCTCTG TCCCACTCCC ATCAAAAGAA TGACAT 346

(2) INFORMATION FOR SEQ ID NO: 4102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60
 GCGATTCACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120
 5 CATGCCAAAG TGGCCGCGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300
 10 ATGAAAATGT ACGTGAGGAA ATtnTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360
 CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGTTcAGGTT TAGCTGTGTG 60
 ATAAATTGCA AGTGCggCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA 180
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300
 GAAGCCATAA rCAAAAGTAC CbGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGk 360
 35 AaTGCCGGTT TGTATGGTTG GcCCAaTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60
 ATTTTTTTAA AGTATTTAAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300
 ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60
 TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120
 TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180
 GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGGAAAGATT TATTCAAAAC 240
 CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300
 CGGTAACACT TCATAAACT GCGSTTTGTn ACCATTACCT AATnGTCAAG GGTACGGCGT 360
 TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn 60
 TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120
 TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180
 TTGAAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAAC TAAGTTACAA 240
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTTCATGGGA GAGTTTGGAT 300
 CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360
 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCh 400

(2) INFORMATION FOR SEQ ID NO: 4107:

(A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120
 TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180
 15 GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AATCACATC AGCCTGCATT 300
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

20

(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180
 AdAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTTGGT 240
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGanTGGTCA AGTAGTAGAA 300
 40 AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

40

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

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CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300
 TTGCCCCTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCG 360
 CACTGTA 367

10

(2) INFORMATION FOR SEQ ID NO: 4110:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

25

GTCGTCCGAT TGAAGGATGG AGTACTGTCT CATTTCGCAA AGACTGGCAA GGACCACCAC 60
 GTTTGCAAAA CGGAACAAGT TGGTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120
 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAACCA AACACCATTG GCCATANGAA 360
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

35

(2) INFORMATION FOR SEQ ID NO: 4111:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

45

TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60
 GTTGCCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTATGCC AGTCACTACA 120
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180
 50 ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240
 ATGAACCTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

55

AATTGGTGGT GCGGTTTTAA TTTCCAGTAT TAGTACTAAC

400

(2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTCACACC ATTTTATAA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAACTCTT 240
 TATTCACCTG GNTTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300
 ACAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360
 GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TGCGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120
 AAGCTGTAGG TGACATTGAA GATTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA 180
 ATCATACGCC GATTGAAGAA AATGTCCTG TTTACCAAGA GATCGTATCC ATTTTATCA 240
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG 300
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360
 TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTGA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGcncAT AATAGATCTA TTTTAAATGG	360
	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

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(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
25	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAAGTGGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT	120
35	ACGATTCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GACTGTAT TTACAACAGA ATATTGGTT CGTACTGCCA GGAAGCTGT	300
40	TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TTnCGCGTnc TTAATGGGAT GGCCATATAC GAACTGGATG	400

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(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
50	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60
 25 TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TCGCCCCCGG 180
 30 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GCGGGGGCCC 240
 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGCCCC 360
 35 CCACCACAGG GAATTCGAA AGAAATnCT 389

(2) INFORMATION FOR SEQ ID NO: 4118:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120
 GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA 180
 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT 240

55

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360
TATnAACCGA A 371

5 (2) INFORMATION FOR SEQ ID NO: 4119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60
 TGAAACAGTG GTGCTAATTG CCGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120
 20 AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180
 TGAAGCTACA CTGCTATTTT CAGCCCATn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240
 TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300
 25 ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60
 40 GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120
 CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTCGCGG GTAACCTGCA TCTTCACAGG 180
 TACTATGATT TCACCGACTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240
 45 GGGTCGGAAC TTACCCGACA AGGAATTTG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300
 CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360
 50 CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

- (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTAACTTT 60
CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATAcataAT 120
AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC 180
ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC 240
ATTGggccAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTc CGCCACCAAA 300
CCCTAACATT ACCAGGCCAT ACCAGCAtAC CCAGggccAC CCGnGGAAGG AAATTAAGTA 360
GCGGTGGTAC TACCAAngAC CAGTGGAAGG TnCCAATTAA 400

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(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT 60
AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAaATTGA GTATATTCAA AAGGATAAGn 120
ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA 180
TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA 240
CGCAaATTAA ATATACTTTT ATAGAAaATT AACTCAGGCT GGGACATAAA TCAATATTCT 300
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT 360
TT 362

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(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

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CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120
 TCTGGGGTGG TGTCTCAGAT ATTGATTAA TGTATGAAGA ACGTGTGAT TTAAGAGGCA 180
 5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240
 GCGATTCCAA ACATTAATGA NAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAAG 300
 10 ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCTTG GTCAGGTGA AGTTCAGGTA AACTGAATG GAGGACCGAA 60
 CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGTA GCGGAGGAAA TTCCAATCGA 120
 25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180
 TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTTAGACA 240
 AACTCCGAA TGCCAATTAA TTTGAACTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300
 30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360
 GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60
 ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA 120
 TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACTAA 180
 50 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240
 GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCATAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

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(2) INFORMATION FOR SEQ ID NO: 4126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

15	AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT	60
	CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAACCT	120
	GAATACAATA TGTACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180
20	GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA	240
	TCAATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT	300
	TACAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGG AACGThATTC	360
25	AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

35	CGAAATTTGT AGTAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
40	GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
	CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	180
	GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	240
45	CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
	CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA	360
50	TGGTTGGnTT CCCCAGTTTG TCGGCAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
AAGTATGCGT TCATTAAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTCG	120
AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

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(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

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AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
ATTGGAAGTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAAATAAT	240
GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT	300
TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCCG	360
TThAACAGCC GGAT	374

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(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

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ATTAAATTC AGTTGTTGCA ATTCCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180
 5 TATATAGTAA TCCGCCTTTT GTTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240
 TCGGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300
 10 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360
 TGGATAAAT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTTCATCATG 420
 TTGGCGGTTT T 431

(2) INFORMATION FOR SEQ ID NO: 4131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GCGCGTGTG TCGCATTGTC TGTTTGTGTC GGTGCTTCTA CTTTAGTTGA 60
 GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120
 25 TGATGTGGTG CTTCCACTTT AGGnAAATGA GTGTTGTGCG GTTTGCTGCT TGCCTTGTCG 180
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTG TTCGATACAT TCATTGAATC 300
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360
 35 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCAGTG TATGCTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120
 TGATCATTAT CAGATTCATC TTTAGTCGCT TTGCTTGAT CCTCTTTTGA TTTATCACTG 180

TCAGCATTAT TTTTATTTGT ATTGCGGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360
 5 ATGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

(2) INFORMATION FOR SEQ ID NO: 4133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCCTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTTGTACC 60
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAAGTG 120
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAC GATTAATAGT 180
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240
 25 TTTCTCTATT CTTGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360
 TAnCGGGTAC CGTCCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTA CTACGTT 60
 CTACAATTTT ATCTTTTTTC GTTTTGTCAT AAACATCTAA CATGTCGATG GCTTTATCAA 120
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180
 CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240
 CTACTTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTTCG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

10 CTGGGATCGC CACCTTTAAG TCTAACCAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60
 CAGTCATTTA TTTTCTTCTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA 120
 ATTTTCAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA 180
 15 ATGACATCCG CTTACGTAT TAAACGCTCA GCCTTTTTCG TCAAATAATT CGGATTACCT 240
 GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300
 20 CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360
 GATTAAACA ATTTTGTATC GTGGGGGGGC AAATACATAT 400

(2) INFORMATION FOR SEQ ID NO: 4136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

35 ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG 60
 TGGGTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120
 ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180
 40 TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240
 ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300
 TTATChTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

(2) INFORMATION FOR SEQ ID NO: 4137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTTCTCA 120
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTAACA CACCGCCCGT CACACCACGA 240
 GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGCGCTGGG 360
 10 AT 362

(2) INFORMATION FOR SEQ ID NO: 4138:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180
 30 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT ACATAAGTAA 240
 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300
 TTAAACGCGT TATTAATCTT GTGAGTGTTC TTTCGAACAC CAGCGATTAn TTCnTGAGGA 360
 35 ATTCAAGCCT AntTAAACC CTTA 384

(2) INFORMATION FOR SEQ ID NO: 4139:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

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TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTG AACCACCCCG GAAGCAATAC 360
 TTAAAAATAA ATTTAATATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGactCG 120
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTA CTGCGTC 240
 CCCCCATCGA TTAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300
 AAGCCTGTGCG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCGGAAGA GCCTTCCTCT 360
 GGAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA 60
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTCCACC ATTTTATAA 180
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300
 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360
 TnCAAGCnTA TTTAAACTC TTAATCACnT GGTTTTCnT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC 60
 TTTGTGTTTA CTTTTTATTT TGACGTTTGA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180
 15 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCTC TTCGGCTCTC GCTTACTCAT 240
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCTG CAGATTCAAA CGTTTCACTC 300
 GCCAAGCCAT TTTCTTGGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCh 400

(2) INFORMATION FOR SEQ ID NO: 4143:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAATG ACATTATTAC TGACCAACA AGTGCACATG ATCCGCTAAA TGGATATGTG 60
 35 CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CAAAAACGT GGCGCTGTAG 180
 40 CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240
 TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300
 GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360
 45 GAGGAAATG 369

(2) INFORMATION FOR SEQ ID NO: 4144:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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5 GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60
 ATGTTTTAGT TGCCTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120
 10 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCCTCGAC ATAGTGCCAC 180
 ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC 240
 AACTAATTTA AGCTGTGCHT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300
 15 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAACAAN 360
 CGGGAGnGGC 370

(2) INFORMATION FOR SEQ ID NO: 4145:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

25 CGAGGTAGCA AAGAACAAAT TCGGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGGT 60
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCGGACG TTGCGGGAGG TCTTGAAACA 120
 30 GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180
 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240
 TTGCTTTGTA GTCAGACCAG AACAAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300
 35 ATCGCACTTC GGCATTGTTT CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360
 TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

50 TGGGGTGTTC TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60
 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTGTATCA TACTAAATTT 180

GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTTnTTTT ATCAGGAGGA 300
 GGATGGCGGT ATCCAATTTA TTTCCATTTG GAAATATATG GnCCCCCGTT TTGGGAACnC 360
 5 ATTTTTTGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA 120
 CATTATTCGG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCACCT 240
 25 TCGACGGCTA GTCCTAAAA GGTACTCCA CCGAATTCGG GTGTTACAAA CTCTCGTGGT 300
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTgn CTGGGTTTAC 360
 nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTTGAA AATGATGAAC GATTCAGTGG 60
 TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCGTGG 180
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240
 50 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300
 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGnCTA 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10 CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTTCACG TTGGAGGATA 60
 CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC 120
 15 AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT 180
 TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAAGGTA TTGTAAGTGG 240
 CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACACTGAAG TAATCTGATT 300
 20 GAATAGTGGG TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA 360
 AACCATCATC ATATTnCAT CTGGTTAGGA CTGAAATGGC 400

(2) INFORMATION FOR SEQ ID NO: 4150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35 AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT 60
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG 120
 GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 180
 40 ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG 240
 TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG 300
 GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG 360
 45 AATAGGCGTT A 371

(2) INFORMATION FOR SEQ ID NO: 4151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60
 5 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180
 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240
 10 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360
 15 TCGTTT 366

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTtagac ATAAAAA 240
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360
 TCGCnTGCCT CCTCCTCCT CCTCGGGCTC TCGGCTTACG 400

(2) INFORMATION FOR SEQ ID NO: 4153:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

50 TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGNATAGGCG 60
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

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CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

(2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60
 nCAGATTGTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120
 CATACCTCCA TCTCACCAA AC GTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360
 30 CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4155:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCAG GTAAACCAGG AATTAAGAAT 60
 45 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTG AGAAAGAACG TAAATTTAAT 180
 50 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240
 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300
 AAAGAAGAAA TCACANAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

(2) INFORMATION FOR SEQ ID NO: 4156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATTAGTTGGGCAC TCTAAGTTGA 120
 CTGCCGGTGA CAAACCGGG GAAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240
 CAAATCCCAT AAAGTTGTTC TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300
 GGAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGATACGT TTCCCGGGGT 360
 CCTTGTTACA CACCGCCCGT 380

(2) INFORMATION FOR SEQ ID NO: 4157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACCTTA 60
 TGGATGATGG ATTCTGCCAA GTTAAATATA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTT TAAAGGGCAA 240
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TCGTCAGGA 300
 GTTTCAGTGG ACCAGCTGGG GTGGATTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360
 ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

(2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

25 AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60
 TCTCTTGtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240
 GGAACCTTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCTGCTCG ATGACCTGGT 300
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTTCTTCT 360
 TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCGT 420

(2) INFORMATION FOR SEQ ID NO: 4160:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

50 ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

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TGCATCTTCA CAGGTACTAT GATTTACCCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240
 TACGCCTTTC GTGCGGGTCC GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300
 5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60
 20 GGCCCGNAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120
 TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180
 CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240
 25 AAGACATTGT GTCTTCGAGT CGTTGATTTT ACGTCCGA GAAAAGCCTC TAGATAGAAA 300
 ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTTAT 60
 TTTTACACG ATGAACATTG AAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120
 GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180
 45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGCCGGC GTGCCTAATA CATGCAAGTC 240
 GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300
 GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360
 50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 4163:

(A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

10 ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT 60
 AAAATAATAC CAATCTCATT TTAAATTCT AACTTGGTT TCGTATAATA CGCTCTTAA 120
 TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180
 15 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACTTTA 240
 GTTGnAAGGC GGTGTTGTG CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG 300
 20 CGGTGTTGTC GCGTTTGGTT TTGnATGCCG TGCTTCTATT TT 342

(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

30 TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCCTTCG GTTGCTTCGA 120
 35 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTTCAACCT 180
 TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240
 40 AACCCCTAA ACACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300
 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGCCCA 360
 nGGGGGTnCC nCCAAAACCTT TGGGGATTTA ACGGTAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

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GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120
 5 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180
 ACTGTCTCAC GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240
 TATTCACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 240
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CnGGTnGTC 360
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60
 50 AGATACACAC CTTTACCGAC TATTTAAAAT AACTTCACC AATTCATTTT AATTTAATGG 120
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180
 ATTTGCACTC CACCGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTGTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT

358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

15	TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
	TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTTTCT AAATATGCAT	120
	ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
20	GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTIONACCA GCATCTTCTT	240
	CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTOGACTTC GATATCGATA	300
	TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAhTTG AGAGCTTnTG GnTTAGCTGG	360
25	ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

	ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
40	TCGTTAAATA AACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA	120
	ATTCAGGTCT CTTCCACGTC ATATTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
	AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACITC TTGTTTTTCC	240
45	GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACTTCA ATGTTATCAA	300
	TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
50	GTGTACnTCC ACGGTTTTCA TTTAAhAACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60
10 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA 120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA 180
AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTACAGGA 240
15 TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGnAGGCGCT GGGTGGGGAT 300
ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT 360
GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG 395

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(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG 60
GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGTGCAA 120
35 GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTGGCTT ATTACCGAGT GGCGGTGGCC 180
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT 240
CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA 300
40 CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT 360
CGAAGTGGCG C 371

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(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

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GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCCA 120
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CCnGAATGAA CCGGTACGTG 300
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA 360
 10 T 361

(2) INFORMATION FOR SEQ ID NO: 4173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360
 35 AGnAATCCCA CCGTTGTAnG 380

(2) INFORMATION FOR SEQ ID NO: 4174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCCG TACTCGTTAG 60
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTGGAAGTC GTTGATTCA CACTGCCGAG 120
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCC TACCGCAAAC CGACACAGGT AGTCAAGATG 180
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTAAC CGTAGGGGAT TGTATAGGGG 360
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGAAGCGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120
 20 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCGGCAT GGGAACAGGT 180
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240
 AGTAAGTAAA AGTGATTTTG CTTGCGAAAA CATTATTTTT GGATTAAGTC TTCGATCGAT 300
 25 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTTAAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60
 GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTGGTA CTGTTTTGT GGTGGCGAT 120
 40 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTGTGGCG TGTGTGTTGA TGGAGGTGTT 180
 GTCACTTTAG TTGAAGGCGG TGTGTGCGCA TTTGCTGTTT GTTGGGTGTC TTCTACTTTA 240
 45 GTTGAGGGCG GTGTTGTCGC GTTTGGTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG AATGAATCG CGATGGAATA TCTCTATCTG AAAACAGATT TCTTTTGTG 60
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTGCG CTTCTTTATC AATGTCATAA 120
 CCTAATGCTT TTAACCTTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA 240
 ATACGCCATC TTGGTGAATA CCGATTTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAATTAAA TCCGAGGTTT TAGTTCCTCG 360
 15 AG 362

(2) INFORMATION FOR SEQ ID NO: 4178:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

25 GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG ATGGAAAGAC GGTCTTGCTG 60
 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGTA AGGTAACGGC TTACCAAGGC 120
 30 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGA, CACGGTCCAG 180
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC 240
 35 GCCGCGTGAG TGATGAAGGT CTTCCGATCG TAAACTCTG TTATTAGGGG AGGACATATG 300
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTAGTAGGGG 360
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

(2) INFORMATION FOR SEQ ID NO: 4179:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

50 GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

55

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180
CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTTCTGTCG TCTAGTTGGA 240
5 AGAGAACGGC GGTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360
10 GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60
GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120
25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180
TAGTAACGTC CTTTCATCGC TTCTAATGCC AANGCATCCA CCGTGCGCCC TTAATAACTT 240
30 AATCTATGTT TCCACCATT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300
nThAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCTG GAACATCTTC 60
TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTTCAGTT TTGAATGTTT GTTCATTCAA 120
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCCGTGG 180
50 TTTCAGTCCA CTTAGGCCCA CCATTAAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTTCGATC CCGCTAGTCT CCACCATTAT 300
TTGTACATTG AAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120
 GTCGATCTGC TAATTTTGCA AGTGTCACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180
 CTTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTC CCTCTTCATA 300
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTTCTTTTCA 360
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

(2) INFORMATION FOR SEQ ID NO: 4183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATT 60
 ACACAGCTGC AGGTGGTTCA TGGATTTTCA TCCATCACGG TGGCGGTGTT GGCATGGGAT 120
 ATTCACTTCA TCGCGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGCCC CGACATGTTG nATGCTGGCT 240
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGGATAGGT AATGGTTT TAG TCGCAACACC 120
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTT TAG CTACAGGATT 180
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240
 10 CAGTATGTTA CAACTAAACT ATGCACCAAG TG TAGCTGCA ACCGTAACAT TTATAGTCAG 300
 CATTGTATTG ATGnTCCTTG GGTnCATTTGT CTGCATACAT GA 342

(2) INFORMATION FOR SEQ ID NO: 4185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTAATTGAAT 60
 25 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTTCAGC GGAACACATG AAACGTTAGC 180
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240
 CGTTATGAAG TACAAGTTGA TGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

(2) INFORMATION FOR SEQ ID NO: 4186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120
 TGTTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360
 GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

5 (2) INFORMATION FOR SEQ ID NO: 4187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120
 20 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180
 TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240
 AGAGCCCGTT AATGGGTGAT GGCCTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTTG 300
 25 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60
 40 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGGAA AGGTGAAAAG 120
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180
 GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240
 45 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300
 TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

50 (2) INFORMATION FOR SEQ ID NO: 4189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTCTTTTGT GTTACAGAAA TTTCAACAAC 120
 TTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACCTCCCC 300
 AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCTCTn nCCCCTCT 358

15 (2) INFORMATION FOR SEQ ID NO: 4190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60
 AAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180
 ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300
 35 AAACCTAAAT ACGGTGGTAA TACCATTTGT GnTATTTGTT GTGAAGTATT GCGGTCATAA 360
 TA 362

40 (2) INFORMATION FOR SEQ ID NO: 4191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

TGATCACCCA TGTTCCTGGAC TCCCAATTGA AATTGAATTG GGCATTCGGA GTTTGTCTGG 60
 nATTCCGTAA .CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

55

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240
 CATTCA GTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300
 5 ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA 360
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTGGGGTGG CAGTGGTATC TGTTC ACTCT 120
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180
 25 TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300
 30 GTTGTCACTA CTAAAGGTGC AGCACTTGGT TACACATCAT TATGGGTCTT GGGTTGAATG 360
 CCAATCGGAA ATTGTAGCAT CnTTAATTTT CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60
 TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATTTTCATA TAATCCGGnA 360

(2) INFORMATION FOR SEQ ID NO: 4194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300
 AGTTtACGAT TTGgATTgCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

(2) INFORMATION FOR SEQ ID NO: 4195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG GCAACGTTCT 60
 ACTCTAGCGG AANTAAGTng GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

(2) INFORMATION FOR SEQ ID NO: 4196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120
 5 GAAGCAGGTG CGACACGTAT TGGTGGCAGC GChGTGTTC AATTATGCAA GGTTTAGAAG 180
 CAGATTCAGA TTACTAATAT ATAThAAThT TGGGAGTGAT AGCTATGACA AGACCATTTA 240
 10 ATCGTGTACA TTTAATCGTA ATGGATTGAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300
 ATTTTTAAAG ATGGAGGTTT ACATACTTTT A 331

(2) INFORMATION FOR SEQ ID NO: 4197:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTGC GCATGGGTGC 60
 25 AGCTGCTATA TTTGAATATG TCGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120
 TGTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240
 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAAThT TATTGCTAAT GChAGTAACT 360
 35 nATCTGATTG T 371

(2) INFORMATION FOR SEQ ID NO: 4198:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGThATTC TACCGCTGAA CTACTTCTGC ATATGCCGGT 60
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGhATCCTA AGTCTAGTGC GTCTGCCAAT 120
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

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TAAGAATAAA TGGTGGAGAA TGACGGGTTG GnACCGTCGA CCCTGTGCTT GTTAAGGCAG 360
 ATGGTTTTTC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGC GCCTT GTGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120
 CCATCCTAGT ACGCCAATAC CATTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCAGGAACA TGTACAACAC TTGCTAAATA 240
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300
 ATGCTTTTCG TTGGCCCAAT TAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC 360
 TAATTTCCnA ATTACGGTTC CnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240
 CACACCATGG TTCAATGCnT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
GCGGTTGGAC	370

20

(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCAATCCA GCTTTGnGG AATGAGtCGG	60
gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTTGT GTTGGCTCGC CGCCTGAATT	240
CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTG GTCTAGTTGC	300
TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTCAGCA TAACAAGCTT CTTTCATTTT	360
AAAGCAGCGT GCAAAAGGTT	380

40

(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

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GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTTGTAGAT 120
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TTTATTATCTG AAGCTGAATT CAGAGATTAT 180
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360
 10 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

(2) INFORMATION FOR SEQ ID NO: 4204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCCTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

(2) INFORMATION FOR SEQ ID NO: 4205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60
 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT 120
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180
 GTTGAAATAC TCCCGCATT TTTATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

(2) INFORMATION FOR SEQ ID NO: 4206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACATAA GTGTGAATAT TACATTCCCA 60
 AATCCAAATC AATATAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60
 CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180
 GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360
 AATGTAACAC GCCGGTGACT TCATCCAGCT GAATAGACGC GT 402

(2) INFORMATION FOR SEQ ID NO: 4208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360
 15 CAGCATCTGG TACnGGTAAG 380

(2) INFORMATION FOR SEQ ID NO: 4209:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

25 AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGTTAAT AAAAAATATC 300
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360
 ATTGGCCCGA TGCCAAAnTT TATATTGAAC CAAGCACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4210:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCCAACC ACAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

AAAAGTGATA AACACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGACTTCA 180
 AACGGCAtnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240
 5 TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTACTGCGAA ATTATTGTnt GATTTGCCAG 300
 TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC 60
 GTTTTCACTT CGCCAAGCCA TCTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120
 AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180
 25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240
 TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300
 ATACATTCAA AACTAGATAG nAAGTAAAG TGATTTTGC 339

(2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AACATTGAC TGATATTAAAGAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
 45 CGTTGAATTG GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
 CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240
 TTTTAGCACA TAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300
 50 GAATTGTAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

(A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAAA TCGTTACGCC TTTCGTGCGG 60
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120
 TGGGGCTTCG ATTTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

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(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

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CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAGACCT 60
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAnTG TGGACAACGn 360
 TGG 363

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(2) INFORMATION FOR SEQ ID NO: 4215:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

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TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCCG GGTCCAACCG ACACTCCACA 180
 5 AGTGAACCG GGATTTTGTAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240
 AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300
 CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGACTACC 338
 10

(2) INFORMATION FOR SEQ ID NO: 4216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120
 25 TGTTTCTGGG AAGTCGCCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTAA CCAGATCCAG AAAGTGCTTT 300
 AATGnTAACA CCTnTTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

(2) INFORMATION FOR SEQ ID NO: 4217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 50 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGTrCT TTCGAACATA 300

(2) INFORMATION FOR SEQ ID NO: 4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA 60
 AGCTATTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA 120
 GTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CanTCAGTGT TACCTGAACT 180
 TCAACCTGGA CCAAGGGTAG ATCACCTGn TTCGGGTCTA CGACCAAATA CTAAACGCCC 240
 TATTCAGACT CGCTTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT 300
 AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA 345

(2) INFORMATION FOR SEQ ID NO: 4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AAACGTTTTT 60
 ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA 120
 AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC 180
 TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTG 240
 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA 300
 CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT 360
 CTCGTC 367

(2) INFORMATION FOR SEQ ID NO: 4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

5 AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60
 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180
 10 nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240
 TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300
 CGGCATGGGA ACAGGTGTGA CCCCnTGGC TATAGTCACC AG 342

(2) INFORMATION FOR SEQ ID NO: 4221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

25 ACCGGATGAC AGCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60
 TGTGAACTCT TGGGGGAGAT AAGctGTTAT CCCCggGGTA GCTTTTATCC gTTGAGCGAT 120
 30 GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180
 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT 240
 GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAAGTGC 300
 35 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

(2) INFORMATION FOR SEQ ID NO: 4222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

45 GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60
 50 TTACCAAGCA AAACCGAGTG AATAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA 120
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

ACATAGATTA AGTTATTAAG GCGGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360
G 361

5 (2) INFORMATION FOR SEQ ID NO: 4223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60
 TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120
 20 ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180
 ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTTCA CTCCTATCGG GCGCGCCATT 240
 TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300
 25 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360
 GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

30 (2) INFORMATION FOR SEQ ID NO: 4224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

40 CATAATATAC TCCTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60
 GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120
 TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180
 45 TAGTGTCAAT TCCAGCAATT TGTTGCGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240
 GnC AAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300
 CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360
 50 TTCGATCCAG TTGGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

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- (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTACCA TTCAACCAA ATTGATCCTG 120
 TGTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180
 TATGCTATTA TTCAATTGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

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(2) INFORMATION FOR SEQ ID NO: 4226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

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TGACGGGTTC GAACCGCOGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60
 TTCTCCGATT TAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAnGTAAG TTCGnACTAC 120
 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300
 TCCACATGTC ACCATGCTTC CACCT 325

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(2) INFORMATION FOR SEQ ID NO: 4227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAA GTGCGGCAAn TnTTCAACA 60

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AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240
 5 AGAAGCTGGT GTTGGTAAAA CTGCCATTGT TGGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60
 TCGAACCCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120
 GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180
 25 AACTATGCCC CTATTAAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

(2) INFORMATION FOR SEQ ID NO: 4229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAAATTAG AGGTGATGTT 240
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TThATGGTAA GGAGTTTCAC 360
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

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CATTAAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTTC      60
CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TCGGTCAC T AGAGAGTATT      120
TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTACTCA      180
GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCA TC      240
TTTcCAGATG ATTCGTCTAA TGTCGTCCTT TGTAAC TCCG TATAGAGTGT CCTAsAACCC      300
CAACAAGCAA GCTTGTGGT TTGGGnTCTT GCCGTTTCG      339

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(2) INFORMATION FOR SEQ ID NO: 4231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

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GAAGTCATAT GCATACACTT GGTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG      60
AATTCGTTA CCTGCGCCTT CTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA      120
TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC      180
AAACTTTTTT ACTTCAGACT GACGTCCGTh TTTAGTTAAT GGGTCAATAA TTCCATAACG      240
ATGAGTATCT GCTTCCGGAA CTCTTGAC ACCTATAACT GAGTGCCCTG ThTCTTCATA      300
AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG      349

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(2) INFORMATION FOR SEQ ID NO: 4232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 5 GAGATAAGCC TGTtATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCC 180
 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAktCA 240
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTtCCAAC CATTCTGAGG GAACTTTGaG 300
 10 CGCCTCCGTT ACCTTTTtAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG AACTGTCTC 360
 CCACCACGAT AAGGTCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTtAACTTGG GAGTCAGAAC 120
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180
 AATATATGTT AAGTGGAaaa GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240
 30 AAGCAGCCGT CATTtAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

35 (2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

45 ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CTGCCTGTC 60
 ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCCGCAG TTCGACTCTG 180
 50 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTtATGG AGGGGTAACG AnTGGGCTAA 300

55

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

400

(2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA 60

GGCGTAATAT CACTCTTTC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120

TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAAT 180

TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCCTAAC CACTATCTGA TACAAGACCA 240

ATTGCATGnT TTGTTGGGAA AATCATTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300

CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

(2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCTTAAAT ATAATTTTAC 60

AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCCGA CCTCACGGGT ATGAACCGTA 120

CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180

GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG 240

CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 300

CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360

TGAACCCATG AACCTnTTGA TCChTAGTnC AAACGGTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5 nAATTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60
 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTGCGACC ATAGAATGAG 180
 10 ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240
 CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300
 CCTTTGCGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAAAT 360
 15 GTATTTTCAG GAAGTC 376

(2) INFORMATION FOR SEQ ID NO: 4238:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

25 CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120
 30 TTTTCTGGGA AAAGTTTGCG CATTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240
 35 GGTACAAAAG CTGGGAAGTC AAAAAAGCATT TTTCACTCCG TATTGAAGGC TACTTGACGA 300
 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

(2) INFORMATION FOR SEQ ID NO: 4239:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

45 CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60
 50 TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

55

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240
 AATGCAAAGG CGCCATCAGC TGATGTGAAA GGTCAAATTT TGCTGTTGGA CGGATGCGAT 300
 5 GAACTACATT ACATTTGTCC ANTACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60
 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120
 TTATGAATGG CATACTGCT GTTGTMTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180
 CAAGTGCACA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240
 TTACGATCAA GATCGTTCAA CGATTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

(2) INFORMATION FOR SEQ ID NO: 4241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120
 CTTTATGTTG GGGCCCCGCC AACTTGCAAT GTTGTAGAA TTTCTTTTCG AAATTCTTTA 180
 TGTGTTGGGCC CCGCCAACTT GCATTGTTTG TAGAATTTCT TTTGAAATT CTTTATGTTG 240
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300
 50 GGACTTTTAT GCGGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10 TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA 60
 TCATCTAAAT GATTTTTAGC TGTGATTAAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC 120
 TCTTGTACTT CTTCACTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG 180
 15 CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA 240
 TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTGAACC ATAATCTTTC 300
 ACAATTnCAG TTGTGTTGAC AGATGAGnGG CGGTGCAGTA AGGACTGGAT ACACTACGAG 360
 20 TGACCGGACT GCTTCGGGnA ATGTGATGA 389

(2) INFORMATION FOR SEQ ID NO: 4243:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT 60
 35 TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT 120
 GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT 180
 40 GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTh TTTTGAAAT GATTGCGGCG 240
 ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT 300
 AAACGACAAG GTGCAATTTT GG 322

45

(2) INFORMATION FOR SEQ ID NO: 4244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

55

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120
 ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180
 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240
 GCCCTTAATA ACTTAATCTA TGTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT 300
 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

(2) INFORMATION FOR SEQ ID NO: 4245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCTATTT CACTCCCCTT 60
 CCGGGGTGCT TTTCACCTTT CCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120
 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTG 240
 ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAAGT CCGTATAGAG TGTCTACAA 300
 CCCCACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGnAA 358

(2) INFORMATION FOR SEQ ID NO: 4246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

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CCCCGGGTAG CTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA      60
AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT      120
ACACTCTATG AATGATTTCC AACCATTCTG AGGGAACCTT GAGCGCCTCC GTTACCTTTT      180
AGGAGGCGAC CGCCAGTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG      240
GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCACCA GCGCTCCACG TAACTAnCGC      300
TCACGTTTCA AAGnTCTACC TATCCTGTAC A                                     331

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(2) INFORMATION FOR SEQ ID NO: 4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

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ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG      60
ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG      120
GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTTG TCATTCTTCA AATAAACCAG      180
AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG      240
GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA      300
ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC      360
TAATGCCCAA T                                     371

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(2) INFORMATION FOR SEQ ID NO: 4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60
 ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120
 5 TGTGGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180
 TCGTTAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240
 10 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300
 GTTTCATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

(2) INFORMATION FOR SEQ ID NO: 4250:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

25 GAGCCCAAAC CAACAAGCTT GCTTGTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60
 AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180
 30 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCGTGCCTT TT 352

(2) INFORMATION FOR SEQ ID NO: 4251:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

45 CATTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC 120
 50 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240
 55 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

(2) INFORMATION FOR SEQ ID NO: 4252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60
 AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120
 CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180
 ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT 240
 ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300
 TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCEAA CCTGTTAAAT 360
 CCGATGGTTA TCCAnATGAT GATCACCATG TCATCANACC 400

(2) INFORMATION FOR SEQ ID NO: 4253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60
 ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120
 GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180
 TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACTT 240
 GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300
 AGnCACGCGAC TCAGACTTCA GACAGCG 327

(2) INFORMATION FOR SEQ ID NO: 4254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120
 TAGGATTGTn CnTTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240
 GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

15 (2) INFORMATION FOR SEQ ID NO: 4255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60
 CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAGAA ATACTTTTTTC 120
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTTAAATACA 180
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTTAAATCAA TATAATTCAA AAAAGGGTCG 300
 35 AAGATATGAn ATCATCTTT CGACCCTTnn TTGTACTAAT TTAA 344

(2) INFORMATION FOR SEQ ID NO: 4256:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTTCGCAT TAATTTCAAT ATTAAATTGC 60
 50 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120
 AAGCTAAATT CTGCGACAAA GCCGCCCAT TGCAGCACCGA CAGCCACACC AATATTTTGC 180
 55 GCTAAGTATA TCGCATTAAG CGTTTGTCTT CCGCCATTTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

(2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

15 GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCC GACTAT TTTTGAAAAG AGCGTGTTAC 60
 ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120
 TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180
 20 AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240
 TTCGGTTTTG AGACAATTCG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300
 25 TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360
 GCGGAGTGA 369

(2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

40 CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60
 TTTTAAATA CTAAATACA TGTTGGAATA CTTGTCCCAT AGAAATATT GGCTGGTAAC 120
 CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180
 45 GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240
 ATGTACCACT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GCGCAACTT GCCGTAACCA 300
 CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT 335

(2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCGTA 60
 GCTTCGCAGC AACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCATATAC 120
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180
 10 CTGCGGhTCT TCTGGGCGTT AACCTTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAhTTCTCA TCTTGACTAC 300
 CTGTGTCGGT TTGCGGTACG GGCA 324

(2) INFORMATION FOR SEQ ID NO: 4260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

25 AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAAATGAG 60
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 180
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAhTT 300
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AAhTATGAAA ACGAGCCCGT 360
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

(2) INFORMATION FOR SEQ ID NO: 4261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGhACACA TTAGCTGTGG 120

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CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240
 TTGTCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTTCGTAAA 300
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60
 20 ATTTTGGACGT TTTAGGCATA AAAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180
 25 AAAGACCTTT CTTGACTTGT GACAATCGCT TGChTCITTC CTCTCCTTCG GCTCTCGCTT 240
 ACTCATThAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACCTTCGC CAAGCCATT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCCTAC GnaATGTCGG AACCACAATC 60
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA AATAATAAAT 180
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

	GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
10	AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
	TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTGCTGT	180
	TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
15	ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
	TTTTTGGAAT ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

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(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

30	ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT	60
	GTAAATACAC CTGTTTCACA GAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
	AGTAACGCAA TCATTCTTTC TAAAAATGCC TCATTGTAAC TTGCCTCTTT AGGTACAGCA	180
35	TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
	ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
40	CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

	TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
55	GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC	120

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240
 5 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TCGTCTGCC AATTCCGCCA 300
 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTTT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60
 20 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCCTGAG 120
 GTnTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180
 25 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240
 ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180
 TGTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240
 GAATCGTTCA TCATTTTCA nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360
 TTTTCCAATG GGGGTCAATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120
 AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

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(2) INFORMATION FOR SEQ ID NO: 4270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30 AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTTGTCCATT 60
 TTATTTTTTA ACCAAAATT GATTAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120
 35 TAAGTCGact ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 180
 TGACCTCctT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240
 40 GTAAGTAAAA GTGGATTTTG CTTGCGAAac ATTTATTTTG ATTAAAGTCTT CGATCGATTA 300
 GTATTTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360
 CGCAGGGAnC 370

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(2) INFORMATION FOR SEQ ID NO: 4271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

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ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTTA CACAATTATG ATTGGCGTAA 120
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACCTG TGGCACAATG 180
 5 GaTTAATTTA CAATATTATG CGTCGACAGT TCGCCGCAT TTTTaCGGtA ATGGGAATAA 240
 AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300
 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CAITCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120
 25 TCAAATTAT CGATGATTTT ACCGTATGA ACTTTCACAG CTGCAATCG ATGATTTTAT 180
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC 300
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTGTCTTT GTCGTTAAGA TGA CTCTAGTA CTCTTATGTT 60
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120
 TATAGAATGG TGCATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT 180
 50 TATTAATAGG ATTTGCAATA ATACCGCCTT GCTTTTTC AA ATCATCTTA AGTGTGTCGA 240
 TnAATTTGTC GACTGCATCA TCTnTGCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA 60
 GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA 120
 GTTGCTTCTG GCGGTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA 180
 ATTAAAGTTG CGCAAGGTGC AAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA 240
 TATCCGTGGA TTGCGAGGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG 300
 CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG 360
 GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCCGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 4275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC 60
 TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT 120
 TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA 180
 TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG 240
 GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT 300
 TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n 341

(2) INFORMATION FOR SEQ ID NO: 4276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCTT 60
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTTC TTTATTTTAA ACATGAACAA 120
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180
 TTAAACAAT GATTAAATTT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240
 CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360
 ACGGTCCG 368

15 (2) INFORMATION FOR SEQ ID NO: 4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTA CTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60
 GAGGGACCAA ACATTGGATT GATTAACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120
 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180
 30 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACCTCTAAA 240
 TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTA CT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60
 50 CAATGGTCGA CATGCCGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120
 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTGTA GTTTGAGGCA CTTTGGCTTG 180
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

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TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTCAC TTGAATGATG TTGAGTCGGA 360
 TTCACTTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

(2) INFORMATION FOR SEQ ID NO: 4279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATTAGACA TAAAATCTAA AAnCAGCACT AAGATGATTT 60
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120
 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTTAC 180
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240
 AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC 300
 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240
 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300
 CCTATAATCG TTTAATCGAT GGGGGG 326

(2) INFORMATION FOR SEQ ID NO: 4281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG 60
 GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGGAAT ATATCCTTAG AAAGGnAGGT 300
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATT 360
 GTGCCCAAnCh 370

(2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60
 30 CTTACAGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300
 GAAACATTAG GnATATCTCT TGTGATTTC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGn 400

(2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

50 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60
 55

TCTGTCCAC TCCCGATTAT CTCGTCGCAA TATTTTTTTC AAAGCGATT AAATCATTAT 180
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240
 5 TGATGGACTC TTGCGCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300
 CTnAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAAC TTCTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC 180
 25 AAGATGCGTT ATAAGCATTG GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240
 AAATCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300
 30 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTAAAGCCA GATTACGTG 360
 ATGTCTAACA AGTTTTnTn GCTAAAATCh GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTTCTT TGTGTTTACT TTTATTTTG ACGTTT TAGA CATAAAAAA GAGACTCAGC 60
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120
 TAAAGACCTT TCTTGACTTG TGACAAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180
 50 TACTCATT TA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTCGTCAG ATTCAAACGT 240
 TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300
 AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480
 ACTCGTTGCG CTCTTTTCTC GTTTCGTGAG ATTCAAACGT TTTCACCTCG CCAAGCCATT 540
 5 TTTCTTTGTG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAGA CGGTCTTGCT GTCACCTTATA 120
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240
 25 GGAGGCAGCA GTAGGAATC TTCCGCAATG GCGGAACTG GACGGAGCAA CGCCGCGTGA 300
 TGnATGGAAG GTCTTCGGAT CGTAAACTC TGTTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60
 CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTAA TTCATCTAAT TCCTTACCCT 120
 45 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180
 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300
 50 GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCACCTG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC 60
 10 GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTCGC TCACCTTAGA ATTCTCATCT 120
 TGACTACCTG TGTCGGTTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTTCTCGG 180
 CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA 240
 15 CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC 300
 GGTTTnGCCT ATCCTA 316

20

(2) INFORMATION FOR SEQ ID NO: 4289:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

TTnTTTATGT CTAAACGTC AAAATAAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT 60
 30 GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAGTAT AATAAAAAGC AGTCATAAGA 120
 TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTCTTAC TATGTGTTAA ATTAACAATG 180
 35 AATATAACAT CTTATTTTCA TTAATATAAA TATTGGAAGG ATCGAATGA TTTACAGTT 240
 GTTTGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG 300
 TATTTTGAGA GATTTTTTAA GT 322

40

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTTAGCT CTAATAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT 60
 CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT AGGCATAAAA 120

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CTCTAGCGGA AATAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACCTCGTTG 300
 5 CGCTCTTnTC TCGTTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AAC TTCACGT 120
 GCTTTTTTAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180
 TTAAGGCGTT ACTTTACCAA CTAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGGAAATGATC 300
 TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360
 TTGCAAGATG GAATGAGAAG TGAACACAGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60
 45 GGCATAAAAA AAAGAGACCT TCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTGCCT 120
 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240
 50 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300
 GCCATTTTTT TTTGTGTnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTCGAT 120
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AACTGAATG ACAATATGTC 180
 15 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240
 TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

20

(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

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TTATCACCCA TGTTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120
 35 GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACITTTT AACGTAATCG GTTCGGTCCT CATTTCAGTG 240
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300
 40 AAACGCCCTA TTCA 314

40

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

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GCAATCTATC TGTGAAGAC ATTGATTGA TCGAATTGAA CGAAGCATT GCTTCTCAA 180
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300
 TAATGAAATG GGGTAAACCG nCCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60
 GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATC TTTCTTTGTG TTGCTTTTAA 120
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180
 ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CnACTACCA TCGACGCTAA 240
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300
 GACATATGAA TGThAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360
 C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTTCACCT CGCCAAGCCA 60
 TTTTCTTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240
 ACTCAITTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCATTTCGC CAAGCCATTT TnCTTTGTGT nTACTnT 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAC 120
 GGAGGAAGAG GGATTGGAAC CCCC GCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240
 TCGGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300
 TTTTACAAC TATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60
 AGTGATGCCA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120
 ATAAATTTT AGCACATAAA ATAAGAGGnG CCAACCATG TTAGACTATA ACAACGGTTG 180
 GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240
 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA 300
 ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA 180
 5 AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240
 GTTnCATTTGA AGTGTtTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTT TTGGACTGTG 300
 CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360
 10 GCTGAATGGC TtGnTGAAT GAATT 385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 180
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300
 CTTCCGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60
 AGGTGTTATG AATGGCATAc ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120
 CAGAAGCAAG TCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

TTTTGAGCGG CAAAACTTT GnCAG

385

(2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTTAAACGCA	60
GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT	120
TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGAC ACGTCATCTT TAACTTAATC	180
GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA	240
GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA	300
TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA	360
CCAAGCCTTG TCCC	374

(2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA	60
ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA	120
ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAT TGGCTATCAC CCTATCGCTG	180
GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGGTA	240
TGCAAGATGC TTTGGTCTAT TCATTACAG AACC GGCAAC ACGTATCGTT TCAGATTCTA	300
TTAAACAAA CGTT	314

(2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60
 CCATTAAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

(2) INFORMATION FOR SEQ ID NO: 4306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CCGTGATTAT 120
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240
 35 TCAACGCCAC CAAGTGACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnC CGGG 360
 GAAAnAGATGG TCAAATTT 378

(2) INFORMATION FOR SEQ ID NO: 4307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGACTTGGGT ATTCCTCCAA AATTATATGG ACCTTGcAGG ACTCGAACCT GCGACCGAAC 60
 GGTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240
 GATCGAACCG CTGGACCTCC TCGGTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300
 5 CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA 60
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTC ACGTAGCTTTT CATTAACTTC 120
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTACG TTAAATACG 240
 25 TGTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360
 30 CAATCCTATT GGATGTCCCA AnaATTGTAC GACCAACACC 400

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60
 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120
 45 GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCATTTG ATGACAATGG 240
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300
 TTCACACTAA TCAATGGTGG CAAAGT 326

(2) INFORMATION FOR SEQ ID NO: 4310:

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(A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG 60
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300
 TCGGATCACT TTT 313

20

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120
 35 TTGGGAAGTG CTTTTTTTTTA GGTCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180
 TATTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240
 TGGTTGTCTT CnTTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300
 40 GTGGTGAATT CTGAACCAA GAATCACTTG ATAATTTATC TATATAATCC TcATAGACC 360
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

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(2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTIT TATAAGTCAA 180
 5 ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240
 CTTTAAATA ATTAACTCAT TGTCTGcNAA ACGTTTTChT TTATAAAAAG ATTAAACGCG 300
 10 TTATTAAncT GTGGAGTG 318

(2) INFORMATION FOR SEQ ID NO: 4313:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCGG CCACCCCGGC 60
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180
 AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240
 30 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCh 300
 AATGGnTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAC 60
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180
 50 TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300
 GGCCATTGTA ACCGGTGGTT TCACATCGGT CATTnCCGT AAAAGnCCAT TCCATG 356

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

10	TATCAGCATT TGTAAGTGGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA	60
	AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT	120
15	CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA	180
	TGTAGCGGAA GGAATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA	240
	TTGGTGTAC AATTATCCTT GGAAGGCTTT GCATATTCnG GGTGTAGGG AATCAGGTCC	300
20	GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT	360
	TGCCTCAGCG GAGGACACGC	380

(2) INFORMATION FOR SEQ ID NO: 4316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

35	GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT	60
	TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT	120
	GTAATTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT	180
40	ATTCTTTGTC CGTTCTGACG TTAAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT	240
	TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT	300
45	TGTTGTCCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AACTTATAA TCCACACCCT	360
	GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn	400

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60
 5 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAAC TATAAGCAAA 120
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360
 15 CCGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4318:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAAC TCTCTTTCT 60
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTATC GTTTCTGGTC 120
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTTCGAT TCACCTGTAC 180
 TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTGGCGT CGTTATTGTC TTCTCACCTn 240
 35 TTTGTCCTTC TCTTGTAAC TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300
 TTCTTGAAGG AATCTCTTC 319

(2) INFORMATION FOR SEQ ID NO: 4319:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

50 AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60
 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTChTTGGn 360
 5 GTTTGCCT 368

(2) INFORMATION FOR SEQ ID NO: 4320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60
 20 TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180
 TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240
 25 TCTACTCTAG CGGAAnTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

(2) INFORMATION FOR SEQ ID NO: 4321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120
 45 ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC 60
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA 120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG 180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAnGG AGCATCGAAA 240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC 300
CACGATCGTT TTGATGCATT TCAGTTCGGC 330

(2) INFORMATION FOR SEQ ID NO: 4323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT 60
TAAATATAAA TTTGGAATGA ATAATAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA 120
CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA 180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTcnGGG ATGGGCCCCA ACATAGAGAA 240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTT 300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG 337

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA 60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG 120

GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAAC TT 60
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120
 TCAGACTCGC TTTGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240
 25 AGCACACGGT TTCAGGTTTC ATTCACTCC CCTCCGGGG TGGCTTTTCA nCTTCCCTC 300
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60
 CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180
 45 AGACATATGA ATGTAAATTA TACATTCAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300
 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAGA CGATATACTA	60
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT	120
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA	180
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA	240
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT	300
TTTGGTTnCA G	311

(2) INFORMATION FOR SEQ ID NO: 4328:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT	60
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT	120
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	180
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA	240
CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG	300
TGGGATACTA CCTAGCTGT TTTGGTnTCT nACCCGACCA	340

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(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

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AATCCATAGC GAAATGTATA CCATCACCCA TCGCTCCTTC TAAAGGTAAA TCTCTACCTT	60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA	120

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TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240
 CGCCTGATTC TCTAGCACGT TCATAAATAG TTAAGTTCTT 300
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CAC TTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120
 GATTGGAAT GCGGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180
 ACCCCTCCAT AAATGGTGCG GCGGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCAGG ACAGAGTCGA 300
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60
 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180
 45 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240
 AGTCATCATA TGCAGGTGGA TTAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300
 GGATAGCCGG ATGGnTTAAA TTGTTAAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360
 50 GTTAAAAACG TCACGGACTT TGTTTAAAAA GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120
 AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTGCA GATAACTGGC TAGCACCGAA 240
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTTATTTTA CAAGGAACAT 300
 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360
 20 CAGGAT 366

(2) INFORMATION FOR SEQ ID NO: 4333:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT 60
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTATT TCGTCGTCCC 120
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180
 40 CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA 240
 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCCTGA 300
 CTGAGAATTG GAAAAAAGCT TGTGACAAG CGnATTTTC GTTCCATGCA ACTGACTGCC 360
 45 AAGAGAAcNT CGTGAGAGCn ATGAAGAAGA TTGGATTGTA 400

(2) INFORMATION FOR SEQ ID NO: 4334:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60
 GTGTTCTTTC GAACnTATGC GATTATTCTT TATGAATTCA AGCTTATTTA AAACCTTTTA 120
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240
 10 TGTTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCGGCCA TCTTCTGnAA 300
 GAAGATGTT 309

(2) INFORMATION FOR SEQ ID NO: 4335:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60
 25 ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAAAACGAT 180
 30 TATAGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTG GnCTCAGCTT 240
 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

35 (2) INFORMATION FOR SEQ ID NO: 4336:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

45 CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT AATTGGGCAC TCTAAGTTGA 120
 50 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180
 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240
 GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

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(2) INFORMATION FOR SEQ ID NO: 4337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT 60
 TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCCATAAG 120
 AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT 180
 CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCATTATTT 240
 TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AntGGCTnCT 300
 CCCATCAGAG CTCAGCCTTA ACGA 324

(2) INFORMATION FOR SEQ ID NO: 4338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG 60
 ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAATT TGATTGGGTT GTTTGCTCAA 120
 TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA 180
 AGATAAGTCT AACAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT 240
 ATTGGTAAAA ACACCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC 300
 TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT 360
 GTGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT 399

(2) INFORMATION FOR SEQ ID NO: 4339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGGCTCTAA CCAGCTGAGC 180
 10 TATAGGCCCA TTTnTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240
 GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300
 AGCCGCACCT TCCGATACG GCT 323

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(2) INFORMATION FOR SEQ ID NO: 4340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

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GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTTCGAT TGGAATTTCT 60
 CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC CTCCATTTCAG 120
 30 TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180
 TACTAAACGC CCTATTCAGA CTCGCTTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTACGGG 300
 35 CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

(2) INFORMATION FOR SEQ ID NO: 4341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

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TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC	60
CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTAA	120
CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAnGA GCTTAACTTC TGTGTTCCGC	240
ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT	300
TCAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA	60
CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC AACTGTTGA	120
AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTTCA GATTGTCACC TTAAAATAC	180
GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAGT	300
TCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

5 ATTCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60
 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120
 GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180
 10 GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240
 CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCTT 300
 TATGGGATTT GCT 313

15 (2) INFORMATION FOR SEQ ID NO: 4345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

25 ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60
 AATAGTTTTA CTTTAAGTCC AGCATTCACA AAAAGTGCTG CCAATTGAGC GCCCATTGTG 120
 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCTCCAAT TTAGTTGAGG 180
 30 ATAAGATAAC CATTAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240
 CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCh TTATGCTTAA nATAAGTCTT 300
 35 TTTTA 305

(2) INFORMATION FOR SEQ ID NO: 4346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

50 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60
 TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120
 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TGTAAGCAAGT TGCTCAAATT 180
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTTCGA TGAnCAACGC CAACCAAAAT 240

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AntACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

5 (2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60
 ATTCCTGTAC CACCTATAAT CGTTTAAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120
 20 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300
 25 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTAAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATT 60
 40 TTTAGGTCTC GTAGTGTAGC GATTAAACAG CCTGCCTGTC ACGCAGAGAT CGsGGGTTTCG 120
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTTT TGCGTTTAAT 180
 ATTATATTAA TAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTTCGTCCA 240
 45 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTh 300
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

5 CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60
 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120
 TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC 180
 10 CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTGG AACCTCTGAC CCTCTGATTA 240
 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300
 CGAACCAACG AGTGACGGA 319

(2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

25 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 60
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180
 30 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300
 35 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

(2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

45 ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120
 50 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTGGAAC ACTAGCGATT ATTTCTTATG 180

ACTTACTTAT CTAGTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300
 TGACC 305

5 (2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTTCATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60
 CTTTAAAACC TGGCTTCTTT GGCTTTTTCG ATATAATGTT GCGATTGTTC TATTGTAAAT 120
 20 ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180
 GCAATCATTT CTTCTAAAAA TGCCTCATTT GAACTGTCCT CTTTAGGTAC AGCATGAGGC 240
 CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACITTC 300
 25 AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60
 TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC CATAGAGGAT 120
 40 TCGAACCTCT GACCCCTCTGA TTAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240
 45 CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300
 GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360
 CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

50 (2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

TGCTTAGATG CTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGga 60
10 CGACAACCTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT 120
CTCAAATTTT CTACGACCAC GACGGATAGG GACCGAACTG TCTCAGCAGC TTCTGAACCC 180
AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA 240
15 GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAac TCTTGGGGGA 300
GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG 360
GAAACCA 367

20

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG 60
TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT 120
35 TATTGAGAGC GGGACGGAAA TGATAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT 180
TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT 240
AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACCTT 300
40 GnCATTGTCT GTT 313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT 60

55

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180
 GCATGAAGCC CCCCTCAAGA TGAGATTTC CAACTTCGGT TATAAGATCC CTCAAAGATG 240
 5 ATGAGGTTAA TAGGTTGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT 300
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

(2) INFORMATION FOR SEQ ID NO: 4357:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGGTGn 60
 nGAACCTAAA AAAAAGCACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120
 TCGAACCTCT GACCTCTGA TAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 300
 AGAG 304

30 (2) INFORMATION FOR SEQ ID NO: 4358:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

40 ATAATGGTGA CGTTGATGAT GCATTAAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120
 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGA GCATTAGCAA 180
 45 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240
 AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTGAT AACATTCAAn TCGACTCAnC 300
 50 AG 302

(2) INFORMATION FOR SEQ ID NO: 4359:

55

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGTTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240
 TCCCAAGGGT TGGGCTGTTT GCCCATTAAA GCGGTACAG GCTGGGTTCA GAACGTCGTn 300
 AGAAAGTTCG GTCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

20

(2) INFORMATION FOR SEQ ID NO: 4360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

30 AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60
 GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA 120
 35 TTCCAGCTTC ATGTAGTCGA GTTCGAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180
 ATTTGCTTGC ACCTCGnGGT TCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240
 40 AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300
 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

(2) INFORMATION FOR SEQ ID NO: 4361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCTTGG CAACGTTCTA CTCTAGCGGA 60

CThTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGGCTCTTTT 180
 TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240
 5 TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300
 GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360
 10 TCGCCAAAGA CCTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTCTCTCT CCTTCGGCTC 420
 TCGC 424

(2) INFORMATION FOR SEQ ID NO: 4362:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

25 CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60
 CGTGTCAGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTTGGTA AAGAAACGCA 120
 ATThAnTCGT TATTTCCGAC AAGAACGTAA CAATACTACA TACAACCTAG CACCATGAAT 180
 30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240
 AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300
 TGGACAGCAG ATTCCA 316

35

(2) INFORMATION FOR SEQ ID NO: 4363:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCCG AAATCTCTGG ATCAAAGCTT 120
 50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180
 AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240
 55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

(2) INFORMATION FOR SEQ ID NO: 4364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

```

ntGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG      60
GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA    120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCAATTACG    180
TGTACCTCAC GCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA      240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAACCAAT TTTAGTACGT GGTATATATC      300
GTTCCAAAAA CGT                                                              313

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(2) INFORMATION FOR SEQ ID NO: 4365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

```

AACCATTGCA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC      60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC      120
TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTh TTAATCACTG      180
CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn      240
CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTh      300
AGTCATTTTC                                                                310

```

(2) INFORMATION FOR SEQ ID NO: 4366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120
 5 AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180
 GTTACAAATT ATTTCAGGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC 240
 10 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300
 ACATTAAaGG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG naATTATAAA 400

15 (2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCT ATTTATCAAC GGTATATGAA 120
 30 GGGGATTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG 180
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240
 CGATGTTACT CGCnATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120
 CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180
 GTGCATCATT TACACCGTCA CCAnCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

55

GTTTTGC

307

(2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

15	TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG	60
	CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT	120
	CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA	180
20	TCGGCTTCTA GTGCCAAGGc ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT	240
	CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACAYTAGC GATTATTTCT	300
25	TATGAATTCA AGCTTATTTA AAACCTCCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA	360
	TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA	396

(2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

35	CAGTAAGATA ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT	60
40	CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
	GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAAACA TGTAATTTTA CTTTACATA	180
45	CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTTAATTC AATAATTGA	240
	ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTA-TGAA	300
	GTGCCTTATG TATAA	315

(2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60
 CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120
 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180
 10 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAATCA CCAGGGnCAC 300
 15 CAAAATTTTT ATCGACGGCn TG 322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CcTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60
 CGAACCTCTG ACCCTCTGAT TAAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120
 30 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTCGnA 240
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

(2) INFORMATION FOR SEQ ID NO: 4373:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120
 AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

TCAATTTTAA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360
 5 GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTCTCTTGT 60
 20 TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTTCT CGAATGGAAT 120
 CTCTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACTT 240
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300
 nCGTTTCTGG GTCCGnAAGT CTGnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTGGGAAA CCGnAGCTAA 120
 45 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180
 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAAct GAGACACGGT CCAGACTCCT 300
 50 ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

	GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
10	AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCGATTCTT GAAGTATTGT	120
	CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTGCTCT	180
	CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
15	GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
	CTTAA	305

20

(2) INFORMATION FOR SEQ ID NO: 4377:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

30	AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
	AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTGCGCTAT CCTACTGCGT	120
	CCCCCATCG ATTAAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
35	CTACGCTGT CGGCCTCAGC TTAGGACCCG ACTAACCAG AGCGGACGAG CCTTCTCTG	240
	GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
40	TCTCACTTCT AAGCGTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

	CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
55	AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300
 5 GGGAAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAntC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAAATATA TCACTTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60
 TTGTGACTGA GATGAAC TTT TATGTCTTAG AACTACAAC ACTATATTGG CAGTAGTTGA 120
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240
 GTGTACTCAT GTTGC GATTA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300
 TCGCTACATA ATCCATCCAT TAGGTCGTTT CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - 35 (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCTT GCTGCTGTTG GTACAAAATT 60
 45 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120
 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180
 CTGTGTTAAC TGGTCGTTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTATGTAAAC 240
 50 AGATATGCTA TTATTCATGG AAGATTAGTG CTTCATCTTT TTTACCCCAA TATTTTATAA 300
 GTGCAATATC GTAGTCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360
 ATn 363

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

```

ACCTGAATGA CTCAAAGTTG ACTTTnCGAC AATTGACTGT nCATTnTTGCA TAGTTGTATG      60
nCTCCATTnG GTAATTATTA GATTnGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT      120
ATAGTTAGCG TATTnGCACC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATT      180
TTAAGTAAAT TAAGGAATCT ATAATGTTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA      240
CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTnGGGAC      300
CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG      360
GCCGTTGTCA CTTAACTTCT GTTTnTCCGA TGACAGCTTC      400

```

(2) INFORMATION FOR SEQ ID NO: 4382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

```

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTnTAC TGACGAATAC TGGCAATGAC      60
ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC      120
CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTTCAG      180
TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT      240
TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT      300
AGGG      304

```

(2) INFORMATION FOR SEQ ID NO: 4383:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60
 GGCGGTTTGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180
 GAATCTGCCC CCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300
 AGTTGGTA 308

(2) INFORMATION FOR SEQ ID NO: 4384:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTCAGAGTG TCATTGGCAT TTATTACACT 60
 25 ATCTCCAAT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGkAGCTA CACCCTTTCC 240
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300
 TTTAGAnAT 309

35 (2) INFORMATION FOR SEQ ID NO: 4385:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

45 AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTGCTAGCC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

55

(2) INFORMATION FOR SEQ ID NO: 4386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA 60
 ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCANG GCAAATATCA 120
 TGGCAAGGTC ATCTTCAAAA TGATTGATT CAAGTGAAG GCATATGACG TCTCATCACT 180
 ATACCCTTTT TCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC 240
 CATTGCGGGC AATCTCGGTn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT 300
 TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG 360
 CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTCnGGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA 60
 TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAA TAATTCACA 120
 GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG 180
 CAACGCTATT TAGTATCAGG TTAAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCnC 240
 GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA 300
 TGGATGACGA 310

(2) INFORMATION FOR SEQ ID NO: 4388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA 60
 5 CTA CTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180
 10 TGA ACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240
 TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300
 TTTGGCGTGG 310

(2) INFORMATION FOR SEQ ID NO: 4389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA 60
 25 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120
 TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180
 30 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGTTAA TACAGTTGGC TCTGGTGATA 240
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300
 35 CA 302

(2) INFORMATION FOR SEQ ID NO: 4390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60
 50 ACATATTACC GAAGCTGTGG ATTGTCTTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

TnCCCTTACCA CCTATAATCG nTTAATCGTG GGG

333

(2) INFORMATION FOR SEQ ID NO: 4391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCGTTTG TGCACAnACT TGACTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG 60
 GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA 120
 TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG 180
 CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT 240
 ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC 300
 AACCAT 306

(2) INFORMATION FOR SEQ ID NO: 4392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTATT AGGACATATA AATTCATCAT 60
 TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT 120
 TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAAATCA TCTATAATAG 180
 CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAATAAAC 240
 CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT 300
 GAATAGGGTC ATGGGATAAA CCAATGnGG AATTTGCCnC AATTnGTAAA TGGAA 355

(2) INFORMATION FOR SEQ ID NO: 4393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTTTCAGG TTTCTTCTTT GCATTTGGTG 60
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTAnTAAC GATAATGGCG 360
 15 nngg 364

(2) INFORMATION FOR SEQ ID NO: 4394:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

25 GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60
 CGGCCTCAGC TTAGGACCCG ACTAACCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120
 30 GTCAATCGGT GGACGGGATT CTCACCGTC TTTGCTACT CACACGGCA TTCTCACTTC 180
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAAGCT CTCCTAnCAT 240
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300
 CATGTnCACT CGACT 315

(2) INFORMATION FOR SEQ ID NO: 4395:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGA CTG AACCACCGAC 60
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120
 ACAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300

ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120

GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAACTTG CCTGGCAACG TTCTACTCTA 180

GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTC ACAATCGCTT 240

GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300

CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTTCTATA AAATTTTTCa 60

ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120

GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180

GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTACATA 240

AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300

TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360

GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TChATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
40	ACGGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
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55

AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTCTACT CTAGCGGAAC GTAAGTTGGC 180
TACCATCGTC GCTAAAGACC TTTCTTGA CTGTGACAATC GCTTGCTTCT TTCCTCTCCT 240
5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAAGTCGTTG CGCTCTTTTC TCGTTTCGTC 300
AaATTCAAAC GtTTTCACTT CGGCCAAGGC ATTTTCTTT GTGGTTACTT TTTAATTGG 360
10 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409

(2) INFORMATION FOR SEQ ID NO: 4401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120
25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180
TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240
30 TGGAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300
TCCATATTT C 311

(2) INFORMATION FOR SEQ ID NO: 4402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60
45 AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120
TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180
AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240
50 TATGGCTAAT TGCTGGGGA AATGACATAC GAATCTCAGG TTAAAACAGA AAATTAAAGC 300
AGGTCCATGT nAAGTGTGGG CGGGnCGCAT 330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC 60
 TTTGGGCCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT 120
 TACTTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC 180
 AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT 240
 TTTGAGGTGG TACTTGATAT AAATTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA 300
 TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTTG 340

(2) INFORMATION FOR SEQ ID NO: 4404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA 60
 CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTGCGAG TTTGTCTGAA 120
 TTCGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCCAA TAATCATCAC 180
 TTGAGGCTAG CCCTGAAAGC TATTTGCGGA GAGAACCAGC TGATTTCCAG GTTCGATTGG 240
 AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC 300
 TGCCATT 307

(2) INFORMATION FOR SEQ ID NO: 4405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

5 AnACTTGAGT GCAGAAGAGG AAAGTGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180
 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGCTAGTCC ACGCCGTAAA CGATGAGTGC 240
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300
 10 CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

 AATTATGGGA TGCAATGGGA TACGAACGTG TTAAACACG TATGGAAGAC GAACTTGGAG 60
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120
 25 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300
 30 ACnChAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

 CACCACCTCC CTACCTACTC GCCCCCATC ATAAATAGG TGGACAGGAA TATCAACCTG 60
 45 TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120
 CTTCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180
 CACCGGCATT CTCATTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240
 50 AGAACGCTCT CCTACCATTG TCCAAAGGAA TChCACAGCT TCGGTAATAT GTTTAGCCCC 300
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG 60
 TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC 120
 ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA 180
 TGTGTTAGAT ATTACAGCAG CACATTTATC TCGCGAAAGT CCCAGCTGTC GATAAAGGTT 240
 GAAACTGAAA AACGGATTTT TGGATTTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG 300
 AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAAATTGG AATCCAAATC nnTTACCAGG 360
 TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC 393

(2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 60
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 120
 GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT 180
 TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTCCTG GCAACGTTCT ACTCTAGCGG 240
 AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCTTG ACTTGTGGAC AATCGCTTGG 300
 CnTCTnTCCT CTCCTTCGG 319

(2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAATACGC CTAAC TTCGT TAACTTTTAA 60
 AATGTATTAA AATTCTAAAG TTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAAGTGACGA CCAGTTTTTC AACTGAGCAC 300
 10 AATTGTGCAC ATCGATTGGT GACAG 325

(2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120
 TGAAATGACG ATAGAGTCAG TATTAAGTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTAA TTGGCCATTC GGGTAAGTTG 300
 TCCGACCATT GCCAAGTGGG TGATGAGTTn AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360
 TCCGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

35

(2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60
 CCCGAGCACA TTATTTATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120
 50 GAATGATAAT CGAACGTCAT ATTTTGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAATTA AACATAACCA TCACCATTTA 240

55

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 120
 20 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180
 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCACTCTA 240
 GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC 300
 25 TTGCGTCCTT nCCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCAGTA CCGTGAGGAA 60
 AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120
 40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT 180
 TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240
 45 TTTAGTATTT GGTCTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTTCA 300
 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60
 TCTTTCCTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT 120
 CTCAAATGCG GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAANTa 180
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn 300

(2) INFORMATION FOR SEQ ID NO: 4416:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTG 120
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180
 30 CATATAAGAT GATTTTAAAC ATCATCTTTG GATGATAGGA TGTTCGCCCA CGATGATGTC 240
 TGAATTCATC GAATTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

(2) INFORMATION FOR SEQ ID NO: 4417:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAATGT TGTTAGAAAT TAAAGATTTA 120
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTCa AAAGCAAATA 240
 TGTAATTTGT TTAGTCCAAC TAGTGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

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GTTTGGTGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 4418:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

15 GTATTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60
 CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120
 GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180
 20 CATGGTCGAA TGCAAAATCC GTTTGGHAAA GGAnCATCGA AATGGTTTATG TAACTCATACT 240
 AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

(2) INFORMATION FOR SEQ ID NO: 4419:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

35 CTCACCTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60
 CCTACCATTG TCCAAAGGnA TGChCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180
 40 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

(2) INFORMATION FOR SEQ ID NO: 4420:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

55

GGTGAGCGGA GCGAACTCnc GTTAAGGAAC TCGGCAAAT GACCCCGTAA CTTGGGGAGA 120
 AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCC 240
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAACT ACGAATCGAA GCCCCAGTAA 300
 10 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

(2) INFORMATION FOR SEQ ID NO: 4421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTGCGATT GGAATTTCTC CGCTACCCCTC 120
 25 AGTTCATCCG CTCACTTTTT AACGTAATCG GTTCGGTCCT CCATTCAGTG TTACCTGAAC 180
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240
 30 TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTACTGCTTA ACCTTGCATC AAATCGT 297

(2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60
 ATTCAACGAT GCGGTTGAAG CGGTTAAGGA ATTGAGGGCG GAAGAATTTT TTCATTTTCGT 120
 45 GCATAATATC TTTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240
 50 CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCAa CAATAGAATG 300
 ACTGAGaGG GATACGGCGA CTTTTAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACAT CAAGCTTTGA 60
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240
 ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGGTAGT T 291

(2) INFORMATION FOR SEQ ID NO: 4424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnG GTTTCAGAA CCTCTATGCA TTTCATCAC AGnCAAATGT 60
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTTTTATn CAGTAATGGG 180
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240
 GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATT AATACTGATT TAGCGTTAGA 360
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

(2) INFORMATION FOR SEQ ID NO: 4425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTTTTGC GA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120
 ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300
 10 CCATTnTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

(2) INFORMATION FOR SEQ ID NO: 4426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAAATTACG GATCATGATG 60
 ATTTACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTCAG 180
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240
 30 ATAGCGACTC AGATTCAGAT ACGGATTCAG ACTCAGACAG CGACTCAGAT TC 292

(2) INFORMATION FOR SEQ ID NO: 4427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60
 AACCAGCTAT TTCCAGGTTT GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120
 45 TTTCACGTA ATCGGTTCCG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180
 TAGATCACCT GGTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240
 50 CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300
 ATTCTAn 307

(2) INFORMATION FOR SEQ ID NO: 4428:

- (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60
 TTTTTCAGCAG CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTAT ACGAGATGGT 120
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180
 15 ATCTTCTTCA GGGAAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAAT GATGATTATT ACACGTACT 300
 AATTGGTTTA CACCAGGTGG AATAATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

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(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30

GTGACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA 60
 CTAATACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCAT 120
 35 TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180
 GTGCACATTA TAAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACCTTCTT 300
 40 GACCTGGTGA CAACCGCTGC GACTTCTCT CTTGGCTCT CGCTTACTCC ATTTAGCTCC 360
 ACTAACTCG TCGGGCCCTT CCGTTTCGGC AGATCCAACG 400

40

(2) INFORMATION FOR SEQ ID NO: 4430:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

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ACCATTACACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180
 ATCGATAGCG TTTTGCGCAA ATTCTTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCTTCCATG CGGAACCACC 120
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180
 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240
 TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGAAGA GCCTTCAGTT 60
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180
 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300
 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

	CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
10	TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
	AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAAG AACTCGGCAA	180
	AATGACCCCG TAACTTCGGG AAAAAAGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC	240
15	AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 336 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

	GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC	60
30	AATCGAACCT GGAGATAGCT GGTCTCTCTn NAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
	GATTATTGGA GGTAGAGCAC TGTGTGGACG AGGGGCCCT CTCGGGTAC CAATTTCAGA	180
	CAAATCCGA ATGCCAATTA AATTTAACTT GGAATTCAG AACATGGGTG ATAAAGTCCG	240
35	TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA	300
	AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

40

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

50	ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG	60
	GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
	GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC	180

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AATCATTGGC TGCCTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300

ACGA 304

5 (2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAAATAAC CGAAGAGTTT TGAATCATTG TAAAAAATGG AATTAnAGTT 60
 CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120
 20 ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCA TATGGTCTTC CTTCAATTCTC 180
 ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATT 240
 TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACCTCT 300
 25 TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTTAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60
 40 TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120
 TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180
 AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTTACA AGGGGGAnAA 240
 45 AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGTT 300
 GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60
 CATAAACCTT GnaAACGGCA ACATTTTTGG GTCCTTCTCC ATCAATTTTAT TTAAGCGC 120
 ATTATGATCA ATATCATGCC CAATTAACCTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180
 10 ATTGTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240
 ATCTTTATTA ACAATTGCTT CATCATTAAT ATGTGAGATT AAATCG 286

(2) INFORMATION FOR SEQ ID NO: 4439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

25 TCGCTTGACT TCTTCTCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60
 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCCAAG CCATTTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 240
 30 GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTCTCTCh 300
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 360
 35 TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT 394

(2) INFORMATION FOR SEQ ID NO: 4440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

45 TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60
 GACTTAATCA AAATAAATGT TTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG 180

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn

295

(2) INFORMATION FOR SEQ ID NO: 4441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60
 CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120
 TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240
 TAAATAACA TTCAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300
 TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

(2) INFORMATION FOR SEQ ID NO: 4442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCCAC 60
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120
 CGTCATTGCT CAAATCATTG ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCA TCGTTAACAT 240
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT 300
 GTATCTTGGA TGC 313

(2) INFORMATION FOR SEQ ID NO: 4443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTC 60
 5 CAGTCTTTAA AAATAGATTG TTTATTTTGA GAATTATTTT TGAATAATTG AATTGCTTTG 120
 TAGCCAAAAT ATGACGTTTC ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240
 10 CTGAAACCCC ATTCCCTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300
 ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTC 336

(2) INFORMATION FOR SEQ ID NO: 4444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60
 25 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGGAAGGG TGAAATTGAA GCGGTACCTG 180
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240
 ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300
 35 TCCGTGTCCA GTTGAACCAT TATGGAGGAA TTA AAAAAGT ATGTTAAGGG ACCTGGGAGT 360
 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

(2) INFORMATION FOR SEQ ID NO: 4445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60
 50 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTTCA CCCTGACTAC GGA CTGTGThA GGTCTGCGGC ATTCAAGCTT 300
 CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTG 339

5 (2) INFORMATION FOR SEQ ID NO: 4446:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCAC TTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60
 CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120
 20 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT 180
 CATTGT TAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240
 ATAAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300
 25 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60
 40 TTTTATTTCA GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120
 ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180
 TTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240
 45 GTAAAAAATG AACGATCAAT GGThTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

5 GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60
 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120
 CCCCAGTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT 240
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300
 GA 302

(2) INFORMATION FOR SEQ ID NO: 4449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

25 CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG 60
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180
 30 TACAAAACAA TGAACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300
 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

(2) INFORMATION FOR SEQ ID NO: 4450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

45 GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAAA CAATACTTTT ATAGGGCAAC 120
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAAGCT 240

GCTATACGGT AGAACGACTT ATTCCC

326

(2) INFORMATION FOR SEQ ID NO: 4451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

5 GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60
 15 TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120
 TCAACAACTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAAAAAAGA 180
 20 AGACAACCAA GCCCAATAAT GGACTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT 240
 TTAAAAATAG GTCTTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAAACCAT 300
 GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA 360
 25 TAAAGCGGGG GGCAATTGGG G 381

(2) INFORMATION FOR SEQ ID NO: 4452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

35 TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT 60
 40 CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC 120
 TCGGTTTTGC TTGGTAAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 180
 CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA 240
 45 AATAAACATT CAAAACTGAA TACAATATGT CACATn 276

(2) INFORMATION FOR SEQ ID NO: 4453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60
 5 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120
 AAATGCGCAG AGATATGGAG GAACACCACT GAGCGAAGCG ACTTTCTGGT CTGTAAGTGA 180
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AGTGGCTGCC AGCTAnACGC 300
 ATTGAAGCAC TCGCCCTGG GGAGTGACGA CCGCAAnTTG A 341

(2) INFORMATION FOR SEQ ID NO: 4454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60
 25 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 120
 CTCACATACG GCTTCGTTTT CATtATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180
 30 TAAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240
 TATTAATCTT GTGAGTGTTT TTTCGAACAC TAGCGATTAT G 281

(2) INFORMATION FOR SEQ ID NO: 4455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60
 45 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTCTACT 120
 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 50 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG 240
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60
 CCATTTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240
 nTCACCTCGC CAAGCCATTT TTCTTGTGTT TACTT 275

(2) INFORMATION FOR SEQ ID NO: 4457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120
 TTCGGTAAGC ACATCAGCGT CATTAAAGTG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCCTCA ACATCACTCA GTGACTCAAC 240
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300
 AntTGAATCC GATTTGTCGT CAACATCTTT AAGTGGATTC AACATCTGCG TcNATGCCAA 360
 AGnnGTGAAT CCGATTCA CAAGCACATCA GCATCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGA CTGGATCTGG CGTTGGTTCT 240
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300
 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

10 (2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTnACAATA 180
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240
 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

30 (2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

50 (2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 274 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG	60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC	120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC	180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAAT CAACAACAT AACTTTCCnG	240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC	274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA	60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA	120
TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTC A GTAGGTGTAA TGTACATGTT	180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT	240
TGnTACACAA CAACCACTTG GCGGTnAAGC G	271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCAATT CTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGTTG CGCTCTTTTC TCGTTTCGTC	180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTA nTTTGAC	240

55

(2) INFORMATION FOR SEQ ID NO: 4464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGTCCTAA GGTAGCGAAA 60
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGCGC ACTGTCTCAA 120
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180
 GAAAGACCCC GTGGGAGCTT TTA CTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360
 G 361

(2) INFORMATION FOR SEQ ID NO: 4465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAG TATAAATTCA 60
 ATCAITCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120
 AAGGTGCTAT TCCTTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGTGTTT TTTTnTTTT TT 292

(2) INFORMATION FOR SEQ ID NO: 4466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300
 10 AATAnTGG 308

(2) INFORMATION FOR SEQ ID NO: 4467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGAAGAC 60
 25 AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAAngCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

(2) INFORMATION FOR SEQ ID NO: 4468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TCGCTCAAAG TCCAGCTGTC GATAAAGTTG 60
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240
 50 AACGATTAAC TGGTATTCCA GTTTCTCAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300
 ATATTT 306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

GGTTTATTAA CAGCATTCTT ATCAGCATT GTAACTGTTA TTGTTTATAA CTTCTGTGTG 60
 AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTT ACAAGTATTT 120
 AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTAGTCATT 180
 CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240
 ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTTAACT TGGGnGCnTT TGCATTAATC 300
 CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

(2) INFORMATION FOR SEQ ID NO: 4470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 60
 AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCAGAC AACTAGGATG TTGGCTTAGA 120
 AGCAGCCATC ATTTAAAGAG TCGTAATAG CTCCTAGTC GAGTGACACT GCGCCGAAAA 180
 TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240
 CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300
 TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360
 GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

(2) INFORMATION FOR SEQ ID NO: 4471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCATTTTATAG AAATATTATC TTTTCCACAA ATCATTTGAT ATAAAGTGCG ATCATTTGCC 60
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC 120
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCCTCC GTTTTnCATG TACCGCGAGG 300
 10 CGTAAnCTTA AAGGGCCCCAA GGnCG 325

(2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

(2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAgaATA GATTGTCAAG CGCTCGCATA 120
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 180
 50 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240
 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCAT 300
 TGTCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCCTGGC GCAGGCACAA TGGGCGCTCA 120
 ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAANA CTATTAGATA TTGTAGTGGA 180
 CAAAAACGAT CCAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTACCAT ATGGTATTTT GATGTGCTTG 300
 GTAAATGTGT GCTGTTTGAT ATCGA 325

(2) INFORMATION FOR SEQ ID NO: 4475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60
 CAATACATCT AGTATTATCT GGTATTTTTG ATCGTTATCC AAAGTTAAAT AATGATTATT 120
 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180
 GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA 240
 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300
 TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120
 GGGTCTTTCC GTTCCTGTGC CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCAACCGA 180
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAAATGG TCCTCCACCT TGAGCTTCTT 120
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240
 GGAnACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

5 GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60
 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120
 ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180
 10 AAGCGCATT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240
 TTTATGTCCC AGCCTGAGTT AATTT 265

(2) INFORMATION FOR SEQ ID NO: 4480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

25 ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60
 ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACTTAA CTTCTTGTTT TTCCGATGAC 120
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180
 30 TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240
 ATATTCCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

(2) INFORMATION FOR SEQ ID NO: 4481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

45 ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

(2) INFORMATION FOR SEQ ID NO: 4482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60
 CATCAAATTA TCGGTGCTAC TGtnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180
 ATGGGGATTG GGACAAATCA TTACATTTAA AGCGTTTCGAA TTAGTCGGCT CATCTCGTGG 240
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

(2) INFORMATION FOR SEQ ID NO: 4483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60
 TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180
 CATTTAGCTC TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240
 ACTTCGCCAA GncATTTTTTC TTG 264

(2) INFORMATION FOR SEQ ID NO: 4484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TCGAGTCGT TGATTTCACA CTGCCGAGAA 180
 NAAGCCTCTA GATAGAAAAA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240
 AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60
 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180
 GATGGANTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAN GTCATGCTTT 240
 CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAACTTG TAGACATACG 60
 TAAATCTGCT TTAATAAGTA ATTAATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGANTTTGAG CGCCTTGCTT 180
 TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240
 TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTCTT CATATTTATT 180
 10 TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACCTC TTAATCTTAG TTCTTTTTTA 240
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTCCCCA ATAGAATGAA TTTAAACCTT 300
 CCGATTTTCCT TTAAnC 316

15 (2) INFORMATION FOR SEQ ID NO: 4488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60
 TCAAAAAGTT ATAGAAGAAG CTAATAAGT TAAAACAGAG ATTGATACTG CCAGAAGATA 120
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180
 ATTAAACCCT TTAATTGTTT GCCAGACACA TCGTATGGA TGAATTTAAA GCGTnAAAT 240
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300
 35 GACTCAA 307

(2) INFORMATION FOR SEQ ID NO: 4489:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60
 50 GTTCCCCAAT CATTAAATTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC 180
 55 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

(2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCGTGTC 60

TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT 120

TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180

TTTACAAATA GCGACAAATT CTCAATTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240

CAGGTACTnA GTAACITTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300

TTCAITTTGAC CGG 313

(2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAGAAAAA ATATCAAACA CCTGAATTAT 60

ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCAAA TGAGCCAGAA CGTGATGAAG 120

TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180

AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240

AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnA A 291

(2) INFORMATION FOR SEQ ID NO: 4492:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

GCCGTCTCAG CCTTGSTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAA ATAAACACT TTGCCCACT 120
 5 TACTACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAAT GATATTTTCGC GATATGTTAA 180
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTTCGATGG AATTCAGACA TCATCGTGGG 240
 10 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300
 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGcNT 400

15 (2) INFORMATION FOR SEQ ID NO: 4493:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120
 30 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180
 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240
 ACGAATCATC TGGAAAGGTG AATCA 265

35 (2) INFORMATION FOR SEQ ID NO: 4494:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60
 TAAGGAAGAG ATTTCCCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120
 50 ACATAATCTT TACGGTAACA TGGGTTGAGG AACATCGTT ATTAAATGA AAAACGGTGG 180
 GAAATATACG TTTGAATTAC ACAAAAACT GCAAnGAGCAT CGTATGGGCA GACGTCATAG 240
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60
 ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180
 GCATTTAACA GCATTtAAAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT 240
 AGGAGCAAGC AGTGCA 256

(2) INFORMATION FOR SEQ ID NO: 4496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTCa CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60
 TTCATCATTa TCTAATTTAa AACAAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTa AnATACCCAA TATACTTTTT 180
 ATATCGTTTCG GATTCTGAGT ATTTcAGACG ATTTTCTGCA TAnAAATAAA CGTGTTTCAA 240
 GGCAATATAT TGCA 254

(2) INFORMATION FOR SEQ ID NO: 4497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CgnTATCTGA ATCCGAGTCG 60
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240
TCACTGTnGG AATCTGAATC GCTATCTGA 269

5

(2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG 60
GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120
CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCCTCT GCCAATTCCG CCACACCCGC 180
AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240
CCAAGTGGC TAAATGGCTC TnAGGTGC CGG 273

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(2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60
TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120
TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180
TCAACGAAGG AGACAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240
AGCAAGTGGG GGAATTCGAA GTTGTTCAnA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300
AGCATCTTAG TCGA 314

45

(2) INFORMATION FOR SEQ ID NO: 4500:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60
 5 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120
 ACTTAACTTT AATGGCGGTC GTCATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180
 CCATTTATGC TGTAAAAAGG CCGTATAGCT GATAAAGTAT GGnCTGATTA CCGTGGCGGT 240
 10 AATTCTATAC AAATTAGGAC CCGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300
 CATT 304

(2) INFORMATION FOR SEQ ID NO: 4501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

25 TTCCTTCATT CTCATAAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60
 TCTTTAAGAA TCGATTTTIG TTCTTCATAT TTATTTTTC TTTCCGnATA ATCATCAAAT 120
 TTCTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTGAGCA 180
 30 CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240
 CAATTAAATC TAT 253

(2) INFORMATION FOR SEQ ID NO: 4502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

45 AGTTCGGTCC CTATCCGTCG TGGCGGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG 60
 AGGACCGGGA TGGACATACC TCTGGGTAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180
 50 TTTCCCAACT TCGTTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240
 AGCATGGTGA CATGTGG 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60
 TATTGATAAC ATTGAAGTGA ATATANAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAATA GTGGCATTTC TATGTCTTAA 240
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAATCATAT 60
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240
 TACCACnGn T 251

(2) INFORMATION FOR SEQ ID NO: 4505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGnCAC TGACTTGTA TCACTAGGTT GGGGGGTCAG TCCTCTGGCC 240
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAAATCGG CTGTGGGTAT 300
TTTGGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120
GCTGTTAATT TACCATCAGC TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180
GGAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

5 CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA 60
 TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180
 10 TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA 240
 ATCGGATTTT GCTCGTGcNt GGTACTnG 268

(2) INFORMATION FOR SEQ ID NO: 4509:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

25 CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60
 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCCACGCTT 120
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180
 30 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGCGGCTT nCACATCACA CTTAnA 296

(2) INFORMATION FOR SEQ ID NO: 4510:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

45 TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60
 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTC CATCTAACGT TACATAGTCA 120
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA 180
 50 TGTGCTGCA CCATTACCCA CTTnTTTCA GTAGCAATA TCCATTGCTT GAGTTGGGAT 240
 TAATTAAATG GTCCTGA 257

(2) INFORMATION FOR SEQ ID NO: 4511:

55

(A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TG TAGTATCT 60
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTAAAT CATCCATAGC AATTCTCGTT 180
 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240
 TGATAAATGC 250

(2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCGA AGAGCGGATT 120
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180
 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240
 CTCTCCCCAG CTG 253

(2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTT ATAAGTCAA CGTTAACATG 60
 nAAGTTACGT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTGC AGTGTCTTT 120
 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

(2) INFORMATION FOR SEQ ID NO: 4514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

GTCAATTGAAT ATGGAAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
TCTTGCAGAA CAGTTAAAAG ACCATTTTAC TGTGTAGCC GTTGATCGTC GTGATTATGG	180
AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCCTGACA GTGATTATCG	240
TGTC	244

(2) INFORMATION FOR SEQ ID NO: 4515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
TCGAGTCGTT GATTTCACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCTAC	120
CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
CCA	243

(2) INFORMATION FOR SEQ ID NO: 4516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180
 5 CCGTCCACCG ATTGACTAAG GTTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240
 CCTTAAACCT GAGGCCGCAA nnGTAGG 267

(2) INFORMATION FOR SEQ ID NO: 4517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTT TAGAGCTAAA TGAGTAAGCG 60
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAT 240
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300
 GAACGAGAAA GAGCGCAGC 319

(2) INFORMATION FOR SEQ ID NO: 4518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

40 GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180
 CATGTCAaNG TACCATTTCG AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240
 ACATGAAAAA CGGGGAACA 259

(2) INFORMATION FOR SEQ ID NO: 4519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

	ATAGGGTGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	60
10	CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
	AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
	TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15	TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 245 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

	AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30	TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
	CTCAACTTGC CTGGCAACGT TCTACTCTAG CCGAACGTAA GTTGGChACC ATCGTCGCTA	180
	AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35	CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 251 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

	GGGCCTAAGT GGA CTGGAAC CACCGACCTC ACGCTTATCA GCGTGCGCT CTAACCAGCT	60
50	GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
	TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
55	CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT	240

(2) INFORMATION FOR SEQ ID NO: 4522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60
 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 120
 GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG 180
 TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240
 ACGTTTGAA 249

(2) INFORMATION FOR SEQ ID NO: 4523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60
 GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAnG CATAGCTGGG TAGCTATGTG 120
 TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180
 CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240
 GACAGTGG 248

(2) INFORMATION FOR SEQ ID NO: 4524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGAnCGGCT GTGGCTCGnA 180
 CCAATACGGG TCGGACCTGC TThAACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

(2) INFORMATION FOR SEQ ID NO: 4525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60
 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180
 25 GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240
 CGCAGTThGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300
 C 301

(2) INFORMATION FOR SEQ ID NO: 4526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60
 TTTCAGTAAC TTGThCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120
 45 CACCCATCCG CTGTAACCTC AGAGTGTCTAT TGGCATTAT TACACTATCT CCAACTCCTA 180
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10 TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
ATCAACAAGT TTAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
TGCACCAT nCAATCATCT GGCCTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15 GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGAATT ATGGACGGGT CTTGGTGGCA	300
ATACCACCCA ACACCT	316

20

(2) INFORMATION FOR SEQ ID NO: 4528:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30 GTCCCAAGGG TTGGGCTGTT CGCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
AAGATGAGAT T	251

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(2) INFORMATION FOR SEQ ID NO: 4529:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50 AGTACGTGAC GTTCACTACT CTCCTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

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ATGGTCGTTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300
 GTGACGCGAC AGTGTChA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60
 GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120
 20 GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180
 CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60
 35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGA CTACCTG 120
 TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180
 40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GCnCAGCCTT AACGAGTACC 240
 GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

55

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTTCATT 60
 40 GAGCAGAAAG AAAATTATGG CACCAAACCTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT CTCGTCCCAC CCCAACTTGG 180
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

5 GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60
 GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240
 10 AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

20 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60
 25 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACtAC 120
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

40 TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCTGAGC TTCGCAGAAG CTAACCACTC 180
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACCTGC 60
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240
 TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60
 TATTGCGTTT GGNCTGTCGT GCCAGTGCAA GATTTCCAAC GATAATTTCT AGGCGTCACT 120
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240
 50 AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60
 TCGTTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 15 GnAGTGTTCCT TTCGAACATA GCGGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GCGGAGGnTG ATGAATGCCT TACGTTTGCG 120
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180
 GANTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239
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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAATA TTATAGAAAA CATCAAAGGA 180
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTC TAnTTTTTCA TGTGCTTCCG 120
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTGACAATG TCACTTACCG 180
 GTTCAACTTG GncGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180
 AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA 60
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCGTTT 300
 GGCACG 306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120
 ATAAAGATTG AATTAAACGCA TCAGTATTAG GATTCACCTCT AATACGATTA ATAGTTTTAT 180
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180
 AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT 240
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA 180
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360
 50 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG 60
CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTA~~CTT~~CTTA AACGATTAGA 120
AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAAACTGGG AATACCATTG 180
AATCGTTGnA ATAGTATCTG GAAATATCAT GGA~~ACT~~GTA~~G~~ CAACAGCAGT GTGTTGCACC 240
ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTGG GATTG~~GC~~ATT TTGGAATGTG 300
CGTGCAGCTT TT 312

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(2) INFORMATION FOR SEQ ID NO: 4553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAA~~ACTA~~ CCAATACCAA ACCATAGAAC 60
AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTT~~CGAT~~ 120
AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA 180
TGCGACAACA AAGnCCGCTA CAAATCTCCA TGA~~ACTA~~AATT GCTAAATGTG GnGAATTCT 240
CCAGTAACAA TGGA 254

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(2) INFORMATION FOR SEQ ID NO: 4554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn 60
AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC 120
TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC 180

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CTGGGGCTTG G

251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60
 ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCCA ATGATTTAAG 120
 AGGGAACATG GATGCGAGTG AATTCGGTAA TTACATTTTA GGCTTGATT CTATCGCTTC 180
 CTATCTGAAA AAGCCChACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240
 AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCAAGAnTT CGCATCGACG GGGAGGTTTG 60
 GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120
 TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180
 TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240
 ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTGCT TTAAAATAAT TTAACCTATT 120
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180
 ACGTGTTTGA TCACCCAATT TAATGATTTT ACGCTTGTGC AATAATnATT TTCGAGACGA 240
 25 GAGGATCGGA TTAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAANTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT 180
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT 180
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240
 CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60
 GCCACAATTA CCATACCAAT TTTCTTTTGT TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120
 TTAGCTCCGA TTGAACGAT GTCTTGTTTT ACAGGACTAA CAGCCATTTT AGTTTGACCA 180
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60
 5 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTAA 120
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180
 10 nGACTCTGCT TTAATAAAT TTAATCATT GTCTGCTAAA CGTTT 225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTcAGCTGC ACCGCAAGCA ACTTCTATTG 60
 ATGGCCTAAC TGCCTTTTAA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180
 AATTATTTCA GGTTCCTTTC TTTTGcATTG GGGTGCTTTA ACCATATCTT nTT 233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120
 TGGAGANTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC 180
 10 TGAGCTAATT CTCCGATTTA AACTGGCCT GGGCAACGTT CTACTCTAGC GGGAACT 237

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAC ACAGCTCATA ATATCAAAAA 180
 GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240
 30 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAGTAG TAATAAGTAT GTCAGTTTAA 300

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTTCA TTCCCATCAC 120
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240
 50 AAACATTCCA 250

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTT AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60
10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120
AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180
TCAGATTCTG ACCCAGGTTT AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

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(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTT TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60
TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTC GATTCGTGAT 120
30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180
CANCAATAAG ATTTTGCTTT AAACATTGAC TATGAACTG GGA 223

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(2) INFORMATION FOR SEQ ID NO: 4571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60
45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120
CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180
GGCAGCAGTA GGGAAATTTT CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240
TGCTGCAGGT TCTTCGGATC GTAAAAT 267

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(2) INFORMATION FOR SEQ ID NO: 4572:

(A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTACTTACTA TCTAGTTTGT AATGTATAAA TTACATTCAT ATGTCTGGTG 60
 ACTATAGCAA GgnGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60
 30 TTCGGTGCA n TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CnAGAGGGG AATTGCTTGA TCAACACAAG 180
 GATGTAGCGC AAGATTGTGA CAAGTTATA AAAAGTCTGG CTTTAAAATG 230

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(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

TCACATATCG ATAACATGAC ATAATCATG CTGGGTTTCC CCATTCCGAA ATCTCTGGAT 60
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CnATGTTTCC ACCATTTTTTA 180
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

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(A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300
 CCTTAAATT 309

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(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

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TGATTCTAGG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60
 ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAA TAATGGTGGG CCTAAGTGGA 120
 35 CTCGAACCAC CGACCTCAG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCC 180
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGRATACC ATATGTCACG GTAATCCGCA 240

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(2) INFORMATION FOR SEQ ID NO: 4577:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60
 TGGGTAAAAA TnTATTAATT GGGTGGTTG TGAAATGCAA TCTTTTAAAC GACTTCAGGG 120
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

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(2) INFORMATION FOR SEQ ID NO: 4578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT 60
 AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCGGCCAC 120
 CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTT TTTTGTAGCA ATGAGTACGC 180
 GCCTTAGCAA TTTTnGTAG CGTAGTCCGC TCCAAAATAA TATTAACTG ACATACTTAT 240
 TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300
 CTTGATTACG CGCGCTCAAC ATTC 324

(2) INFORMATION FOR SEQ ID NO: 4579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAA CTGATTTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT 60
 GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG 120
 GTATGCATAT CGTTTAAAC CTATTCTTTT GTTnTAGGA CATATAAATT CATCATTAAAT 180
 TCGTCATATT TCCAATTTTG AGTGnAAAA ATGTCACTTT TAAACTTTC 229

(2) INFORMATION FOR SEQ ID NO: 4580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA 60

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180
CGTAAGTTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60
CGACTACAGG ATTATTACCT TCTTTGATTTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120
CTTTGTAACT CCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180
CTTCCCCTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60
AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120
TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCanCT 180
TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAG 180
 TAGGTCATAG GGThAAAACh TTTTGTAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCCGG 240
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCTGA GCTTCGCAGA 60
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATT 60
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120
 40 CTATATTTAC TTACTTATCT AGTTTTCAT GTACAATTnG TTTTGTAGTCA AGCGCTCGCA 180
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACC GCCTAC GCGCGCTTGT ACGCCCAATA 180
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCAGC TATTnAGCCG 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60
 TGAAGTGAAT AAGAAATCAA TCATTGCTC TTCTGTAAA TCATGTGTTT TTTCTAATTT 120
 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGTTGCAC AAATAATACC 180
 25 CATCGCAGCA TTGACTTCAT TGTTCGAAGG CACChTTGAC TGCGGCAATC ATTCATATCC 240
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180
 45 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTTAACAGC CGATAGCTCT 60
 5 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180
 10 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60
 ATCnCATTCa TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120
 25 CCTCGGCTAA GAACCTTTCT TGAATTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTTA CCGCGTGTIT AATATTGTTA TACATATATT CTAATTGCAC 60
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120
 45 TTCGTCGTCC CACCCCAACT TgCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180
 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTh TTAGCCGTGG 60
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60
 AGCTTTGATC CAGAGATTTT CGAATGGGGA AACCAGCAT GAGTTATGTC ATGTTATCGA 120
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

(2) INFORMATION FOR SEQ ID NO: 4594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120
 45 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180
 TTATCGGTTT AGGTGCCACA GnaAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240
 TAATTTTTTT Tn 252

(2) INFORMATION FOR SEQ ID NO: 4595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240
 GTTACCCGGG AGnAAAG 258

(2) INFORMATION FOR SEQ ID NO: 4596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCACTAG GATCTGCCGG TGCCGCACGT 60
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180
 TnCATTTGTTT AGTTGGGTAC ATTAATGcng TATTATCGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTCGCCTAT CCTACTGnGG TCCCCCATC 240
 GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

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(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120
 TATTCITATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC 219

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(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAkCCCCAG TAAACGGCGG 60
 CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120
 50 GAAAGGCGTA ACGATTGGG CACTGTCTCA ACGAGAGACT CCGTGAAAAT CATAGTACCT 180
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

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(A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTGCA TTTTTCATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120
 CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACATGCGnAG 180
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGAThAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180
 35 TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAACTAA GTGCGATTAA 120
 55 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180

TATCCn

246

(2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGAAA GGTGTATGGA 120
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180
 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240
 TTTGATGG 248

(2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTGAGCCG GGACTTnTCA CATCAGACTT 60
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTGTTTTn 240
 TGGGTT 246

(2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180
 5 TGCAGTTATT TCAGTTTCTG CTTACAGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60
 20 GACCCCGTAA CTTCTGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCGAGAAG AGCCGCATGA 120
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180
 AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120
 GCTTCAAATG AATCAGCTGC TTTACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTGTG CGATTTTTTA AATCGAATCG 60
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120
 GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAC GCTTTTAAAT 180
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCTnGA ATnGATTAGC 240
 C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180
 TTTCArTTTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTATA AATATGGCGT GCGTTTGGCA 120
 ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180
 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240
 TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360
 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG 240
 ACCGTTAAGG TTnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180
 35 AGCTTTTTTC TACAGCTTTT ACAATATnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAAATTTA 60
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG 180
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60
 TGTGCGAaAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTTCT 60
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120
 ATGTATCAAC ATATCGCGGT ATGTTTAAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

(2) INFORMATION FOR SEQ ID NO: 4618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCAh 60
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTAGTCTGT TCTCTATTTA TACAATACTT 120
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180
 GCTCCCTCAG GGGTCTCGCC ATTAAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60
 GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGTATCTG ACCTAGTCGG TTTAGATATT 120
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

(2) INFORMATION FOR SEQ ID NO: 4620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAATT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120
 CATTTCCTTGGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACC 60
 TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180
 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC 240
 ACAGTCTCGG GCGATTGTCTG AGTCCAC 267

(2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60
 TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180
 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

(2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CChACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCCGGGAA 60

	CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA	180
	CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA	240
5	AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTATTGAA ATCAATGAAA	300
A		301

(2) INFORMATION FOR SEQ ID NO: 4624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20	CGAGGTGCTG CAGAAGGTGT CATTGTCGT TATTTAATTG AAGAAAAGAA CTA	60
	GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA	120
	GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT	180
25	TTTGAAAAAG GGGnAAATCA TAATCATnG GCGATGCCCA AG	222

(2) INFORMATION FOR SEQ ID NO: 4625:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

	TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC	60
40	CTGAGTACGA CGGAGCACGT GAAATTCGGT CGGAATCTGG GAGGACCATC TCCTAAGGCT	120
	AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC	180
45	CCGGAAGGGG AAGTGAAATT AGGAACCCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT	240
	CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA	300
	A	301

50 (2) INFORMATION FOR SEO ID NO: 4626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120
 10 CATTAAATCCC ATTTTtanCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nat 223

(2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

25 TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60
 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

40 ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60
 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120
 45 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180
 TCCACCACAT GTTAAATATG CAGCAGAG 208

(2) INFORMATION FOR SEQ ID NO: 4629:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120
 ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180
 10 ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300
 CACTG 305

15 (2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60
 TGGCGTGCCT TTTGTAGAAT GAACCGGCCA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

55

- (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

70 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAT ATTCTGAACCA TTATTTACAG 60
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCAATTA TTCTGGTTTG 120
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180
 CTAATGTGTT AAGAACTACT ACAT 204

35

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGC GTTACGT TAGCCCGTCT GATGTAGAAG 120
 50 CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180
 AAAAAGCATT CATTAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55

(2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60
 GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTGT 120
 AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTGTGCGC TATTTGTAAA TTGTATCCTG 180
 15 GCTTAAGTTG GCCATTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAAA GTAGACCTTG 60
 30 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

(2) INFORMATION FOR SEQ ID NO: 4637:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA 60
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA 120
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180
 TTCCGCAATT GGCgAAAGCT GTACGGGCAA CG 212

55

(2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60
 TTTTITAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTT GATAATTTTT 120
 CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTGA GATTAACCAA AATTAATATT 180
 15 TACATTTTCCT AACCATTTTT ATGTAAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCCT 60
 GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATCCG TAAAATGCTA 180
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180
 55 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120
 CGCTGAACTA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180
 ATCCTAAGTC TAGTGCCTCT GCCAA 205

(2) INFORMATION FOR SEQ ID NO: 4642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTATGTn CCCAG 235

(2) INFORMATION FOR SEQ ID NO: 4643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

(2) INFORMATION FOR SEQ ID NO: 4644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60
 TTCCTAACAT TTACACCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180
 GTTGGGGGCC CGCGGGCAAG GThACTAGAA TGAAAAAGC CTGTTACAAG CGATTTTCGG 240
 TTCAGTCCAC TACTGGCAAT ATAACCTTGTG GAGCTAGGAC ATTGG 285

(2) INFORMATION FOR SEQ ID NO: 4645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60
 CGCTTGThTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120
 TACGAACGTG TTAACACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180
 ATTTAGATGG TGGCTTTTGA TAAACA 206

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60
 CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTcGnA TA

222

(2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTGCTT AATGAATGCT TTTTCTTCGT 60
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120
 GncGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180
 CCGAAATTAA TGACAGTCCA 200

(2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60
 ACGCAGGAnG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TTATTGTAC ATTGAAAAC 120
 AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTTAAA 180
 TAAGCTTGGA ATTCATTAAG A 201

(2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAA GCTTATAAAC GCTCATCTGn CATTGTAGCA 60
 ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT

218

(2) INFORMATION FOR SEQ ID NO: 4650:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

15

GTGGCGGTGC GACTGTCAGA AGCACGTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60

AGAAGTAAAA GCCATCAGGT GCGGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120

CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180

20

ATTChGATTa CTAATATnTA TG 202

(2) INFORMATION FOR SEQ ID NO: 4651:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG 60

35

AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAGTA AAAGACGGTC 120

TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC 180

CAAGGCAACG ATGCATAGCC GACCTGAGA 209

40

(2) INFORMATION FOR SEQ ID NO: 4652:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60

ATATTGAAAT TCGGCACAGC TTGTACAGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

55

CCACTTATCG TGGTTGGAGA CA

202

(2) INFORMATION FOR SEQ ID NO: 4653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180
 AACCGGTACG TGATCACTCA AcnGn 205

(2) INFORMATION FOR SEQ ID NO: 4654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180
 AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240
 CTATTAATCC ACACGGGTTA GAnG 264

(2) INFORMATION FOR SEQ ID NO: 4655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGtnACGCG 180
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

5 (2) INFORMATION FOR SEQ ID NO: 4656:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60
 GTGTTTGCTT TTATTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120
 20 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

35 TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC 60
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120
 CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC 180
 40 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTGGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

55

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180

AAAAA 185

5 (2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60

GGGAGTACGA CCGCAAGTGT ATAACTCAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120

20 GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180

AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

35 ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTAAAGTCA 60

CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120

GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT 180

40 GATAGAAATC ACTTTTTGAT ATGTATTTnt ATGTACAGCT CGTTGAGCnc TATTTTCCTT 240

ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300

45 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTGAnT GGTTTTCGTT 360

CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT	60
CCAATTCTCC TnATGTTGGG GCCCCGAGT TCAACTACTG CCAATATAGT GTTGTAGTGT	120
CTAAGACATA AAAGTTCATC TCACTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT	180
ACATGAAATT TTTCCAAGTG ATATATTTT	209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA	60
AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC	120
CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA	180
CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG	240
GCCTAA	246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT	60
TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG	120
CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA	180
AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT	226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120
 GTAGCTCAGC TTGGTAGAGC ACTTGTTTTG GGACAAGGGC GCAGGTTTCA ATCCTGTCTC 180
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACCTT 60
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180
 CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60
 TAGATTGTGG TTTTITAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAN 180
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTT 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120
 10 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180
 CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA 120
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180
 30 TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180
 TT 182

50 (2) INFORMATION FOR SEQ ID NO: 4670:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60
 CACCTTTTAA AGTATTACGT AATGTTGTGT TGC GTTTACA TCTTACCCAA AGTGCTAATG 120
 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180
 10 ATTGG 185

(2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

20 CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60
 25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180
 30 CATTGAGACC GCAAGGnTnT 200

(2) INFORMATION FOR SEQ ID NO: 4672:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

40 CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60
 45 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTGCG CATTAAAGCG nACGnTGCTG 120
 GGTTGAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180
 TGTCTTAGT ACAGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTGCG TGCCACGCAT 240
 50 AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

10

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180
CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

30

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180
AAGCTCCACG GGGTTCTTTC CGT 203

35

(2) INFORMATION FOR SEQ ID NO: 4675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

45

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120
GGATTGGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

50

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 178 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTa TTACCTCAAT ATGCTTGTCA 60
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120
TTACAAATTT AGTGTGChGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180
AAATCCCAAT CGAACCTTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAn 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTa TGGAGCGGAA GATAGGTTTA 60
CACCTATACC TCGTTCCGGA AGGAnTGTTT TAAAAGTGAA CTACTCCCGC AATATTAAAT 120
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180
AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACh 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACCTT 60
10 CGCCAAGCCA TCTTTCCTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG 120
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60
25 TTAAGTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180
30 CCC 183

(2) INFORMATION FOR SEQ ID NO: 4681:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60
45 AGATGGTCCT CCCAGATTCC GACGAATTTT ACGTGTTCCTG TCGTACTCAG GATCCACTCA 120
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180
TTCGTCTAAT GTCGTCCTTT GTA 203

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(2) INFORMATION FOR SEQ ID NO: 4682:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60
 5 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCCAAA AAGTGGGATG CGATGGAGCC 120
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180
 10 ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180
 TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60
 AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120
 45 AGCTTATTTA AAACTCTTTA TTCACTCGGT TTTGTAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA 60
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120
 AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

(2) INFORMATION FOR SEQ ID NO: 4686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120
 nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

(2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

(2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180

GTGACAAAC 189

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(2) INFORMATION FOR SEQ ID NO: 4689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60

GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT 120

20

CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180

CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCGG 227

25

(2) INFORMATION FOR SEQ ID NO: 4690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60

GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120

40

TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAn AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60

TTAAAGGGGG CCAATTTTTT CCCAAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAAA 120

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GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240
 TTAAGGGAAT TTAAAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300
 5 AAAATTAATT AAAAACCCTA TTTTTTTTTT TTAATTTTAA AACCCAAAGG GGGTAATTG 360
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60
 HTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGG AATGATAAAA 120
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTACTTAA 180
 25 AAATAGGAAT ACATGAGTAA AACTCANTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120
 TATAACCAAT TGGAAATCTC ATCTTGAGGn NGCTTCATCT TAGATGCTTT CACACTTATC 180
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

(2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

35 AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120
 40 TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

50 CCAAACCTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60
 TTGGGCGTAA ACGCGCGTAG GnGTTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120
 GGGTCATTGG AAAGTGGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60
 TGACATACCA TATCGACTAG GTACCTTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120
 GGGCAAGGTC ATCTTGCAAA ATGGATTCCA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180
 TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG 240
 CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 120
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTTC TGTTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60
 ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120
 GGCAACGTTT TACTCTAGCG GAACGTAAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60
 AATGCCAATT AATTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA 120
 nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAAATATA TGT 163

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60
 CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTG ATTGGCTGCA GTCGCGATGG 120
 TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTITGACn GTACCCGTCA GATATCCGCA 180
 GCAATGCAAT GTGTGCAAG TTT 203

45

(2) INFORMATION FOR SEQ ID NO: 4707:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCACAGA GGAGGCTCGT CCGCTCTGGG 60
 5 TTAGTCGGGT CCTAAGCTGA GGCACAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCOGATTG TTCGATGCTT TAATTCAGTT 60
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

25 (2) INFORMATION FOR SEQ ID NO: 4709:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60
 TTGTCACCTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

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TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

(2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60

TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTTCAG AATCTTTTTC 120

AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

(2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60

CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120

TAGAAATGAAC CGGCGAGTTA CGATTTGATG C 151

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60

CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120

CCTGGGAGAT AGCTGGTTCT CTCCG 145

(2) INFORMATION FOR SEQ ID NO: 4714:

(A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120
 AAACCGACAG GCCTTAACGG GCCGCGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

40 GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA 120
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGANT AAATCTTTTA AGGCTTATAA 60
 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAGAC GATATACTAC GAACTCCTA 120
 CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60
 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120
 CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAAGTGA ATGGTGTCGT 120
 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

15. CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60
 TTAATTAGCT TAAACGCGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120
 TTACAGCTAT CTTAGCTAGT TTAGCC 146

20

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

30

CCACACCAAT ATTTTGCCT AAGTAAATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60
 CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120
 35 TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACCTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60
 50 GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120
 AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

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(A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTGCG GGGTAACCTG CATCTTCACA GGTACTATGA 60
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCCAA 60
 CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120
 30 GCATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAATA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60
 45 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120
 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180
 CAGCATGCCG GTGTTCTTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

10

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60
AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

25

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT 120
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

40

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120
GCCCTCCCAT ACCTCGGG 138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCCG ATTGTCTGA ATTCGTAACC 60
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
 AAAGTATTTT GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60
 AGCTGGGTTT AGAACGTCGT GAGACAGTTC GGTTCCTAT CCGTCGTGGG CGTAGGAAAT 120
 TTnAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAATA TAGCTATTAC TATAAAAAC AGCAGTAAGC ATATTTCCAA 60
 ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG AACAGCAAAT GATATTTTCG 120
 ACAAATTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAATTGC ACATnATTGC 60
 AAGCTGACTT TTCGTCACCT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120
 TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT 60
 TTTTGTAACT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

(A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCTTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60
 AGTTCAGGTA AACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAANT GAGCGGATGA 120
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15

(2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25

GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTGAGGTG 120
 30 GAACATGGTG ACATGThATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40

GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAATGGC TTGGCGAAGT 60
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

5 TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60
 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120
 TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180
 10 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

20 GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA 60
 TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA 120
 25 TCATGATACT GTCAn 135

(2) INFORMATION FOR SEQ ID NO: 4742:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

35 ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

(2) INFORMATION FOR SEQ ID NO: 4743:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

55

TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120
TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60
AGGCGATAAA ATCANAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120
TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAATTTG AATGAACAAA CATTCAAAAC 60
TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120
AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60
GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120
GACAnTGACT CCGATTCA 138

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCAC TT GCTGGTGT GGGGACCCCA CCAACTTGGC 60
 ACATTATTGG TAAGCTGACT TTTCGTCAC TACTGTGTG GGGCCCCGCC AACTTGCATT 120
 GTCGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGCG CCACACCCCA ACTCGACATT 180
 GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60
 CTAACACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCT ATTTTCATGG TGTCAAAAAT 180
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTAAATAAG CTTGAATTCA 60
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTAAATCTT 120
 TTTATAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

25

AATCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180
 TCCG 184

(2) INFORMATION FOR SEQ ID NO: 4752:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AAAGTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTC TGTTCGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60
 ACGCTATGGC TGGAGCACTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120
 TGGCGCAAAA TATTGGTGTG GCTGTCCGGT CTGCAATGGG CG 162

(2) INFORMATION FOR SEQ ID NO: 4754:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTCT CCTTAGTAGC GCGGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120
 25 CTTGGGAAAG ATGA 134

(2) INFORMATION FOR SEQ ID NO: 4755:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCCTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60
 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120
 40 TGAAGCATGn ATCGTAAGG 139

(2) INFORMATION FOR SEQ ID NO: 4756:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

55

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120

ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

5

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60

TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAGAT 120

20

TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60

35

GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120

ACTGCTGTTC TCTATTTATA CCAATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

50

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60

ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA AChTTATGGG 120

ATTTGCT 127

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCCTCG TCGGGTTACC GAATTCAGAC AAATCCGnA ATGCCAATTA ATTAACTTG 60
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120
 AGTCCCAAAT ATATGTTAAT GAAAG 145

(2) INFORMATION FOR SEQ ID NO: 4761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCCTGCG GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180
 TTAACACACC AAAACAGCTC CCACCACCAC TANATCGAnC AACACTAG 228

(2) INFORMATION FOR SEQ ID NO: 4762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCCG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC 120
 AGCAGGGTTG 130

(2) INFORMATION FOR SEQ ID NO: 4763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60
10 GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60
25 CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTACAAG CGCATTTTCG TTCAGTCAAC 120
TACTGCCA 128

30 (2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

40 AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120
45 TTTCCATGTG GnAAC 135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

GATTCTCACC CGTCTTTGCG TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120
 5 CACAGC 126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
 GATTTTAAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60
 35 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
 TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60
 50 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

(2) INFORMATION FOR SEQ ID NO: 4770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
 ACCGTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120
 TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120
 ATGTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 4772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTGGCTA 60
 ATGCCTCCAT CGTGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTGGTGT 120
 GTACTT 126

(2) INFORMATION FOR SEQ ID NO: 4773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60
10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAn ACCTTGCGGT CTCATGCGG 120
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60
TGCACTCTTA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40 ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120
45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

CCCCCTAGTC TCCACCATTT ATTTTTTACA CGATGAACAT TGAAAACtNa ATACAATATG 60
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC TG GACGCTGGAT GTGCGAAACG 120
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCAC TGCTC 120
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAACTATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60
 AACAAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

(2) INFORMATION FOR SEQ ID NO: 4780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCantGTC CTCGACTAGT GAGCTATTAC 60
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120
 TCCTTTT 127

(2) INFORMATION FOR SEQ ID NO: 4781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60
 GTCTTATTTT TTAAAGTAT TTAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120
 CGAGACTCC 129

(2) INFORMATION FOR SEQ ID NO: 4782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG 120
 GTCAGATTTA GGACCA 136

(2) INFORMATION FOR SEQ ID NO: 4783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60
10 AGTGTTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60
25 nATCCCATG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60
40 ATGACAATTT TATCTGCAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCAACAC TTTATCGTGG TGGGGAGACA GTGTTcAGGC GGGCCAGTTT 60
55

AATCATTTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTAAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AATACCTTT 60
 TTCATCTTGG TCTTGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCACT 60
 TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120
 GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTTCAAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120
 GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

10

CATTATTTAG TATTTATGAG CTAATCAAAC AncATAATTT TTATGGAGAG TTTGATCCTG 60
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

25

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60
TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

40

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60
AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120
nCTGATAAC 130

5 (2) INFORMATION FOR SEQ ID NO: 4794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

20 (2) INFORMATION FOR SEQ ID NO: 4795:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAA ATTCCCAATT TTTTnTGGGG GGTnGGGAAT TTAAAAATTT GGTnTTTAAC 60
CCAAAGGCC TTTTCCCAA AATTAAATT CCCTTAAAAA TTAAAAATTT GGAATTTTTT 120
35 TTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCA ATTTTnAATT TAACCCTTAA 180
AACCCCCAAA CCTTTTTTCC TTTTnTAAAA TTTTnTAAAA TGGA 224

40 (2) INFORMATION FOR SEQ ID NO: 4796:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

50 TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCnTCGAT GTGAACTCTT GGGGGCAGAT 120

55 (2) INFORMATION FOR SEQ ID NO: 4797:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120
 ATCTG 125

15

(2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

25

CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30

(2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

40

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45

(2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

55

TCAGTGGGAT GATTCGTGAA ATTGAAACGC AAGATTTTGA TATCGAnCAC CT

112

(2) INFORMATION FOR SEQ ID NO: 4801:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

15 ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60
 ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

30 GAACCAAGTT GTTATTGAAA AntCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60
 TTA CTCTAT ATCAGCACCT ACTGTATCTT TCATTAAATT AACGTCTTCT GCAGTCGCAC 120
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180
 35 CATCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60
 50 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60
GTTAGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

10

(2) INFORMATION FOR SEQ ID NO: 4805:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60
CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

25

(2) INFORMATION FOR SEQ ID NO: 4806:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60
GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

40

(2) INFORMATION FOR SEQ ID NO: 4807:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60
TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

55

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60
 ATCATTGCTA GCTTTTCTTG TATTAAGTGA TATTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTTGA TTGGAATTTTC 60
 TCCATACCT CAGTTCATCC GTCACCTTTC AACGTAAGTC GGTTCCGGTCC TCATCAGTGG 120
 TACCTGACTT CAACTGACCA GGGTAGACAC 150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60
 AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCTG AGGAAGACAC 60
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120
 ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60
 35 TAGCCCTAAA GCTATTTTCG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGCGGTT GAACCCGTCA TTCTGCACCA 60
 TTTATTCTTA CATATTGCCG GACTAGCTCA ATTGGTAGAG CAACTGACCT TGTATCAGT 120
 AGGTT 125

15

(2) INFORMATION FOR SEQ ID NO: 4816:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

25

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60
 CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

30

(2) INFORMATION FOR SEQ ID NO: 4817:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40

GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45

(2) INFORMATION FOR SEQ ID NO: 4818:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

55

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTG 120

A 121

5 (2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

20 (2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

30 CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGAG 60

AGAACCAGCT ATCTnAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

35 (2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

45 TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

50 (2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60
AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60
TTTGAnTTGT GACAAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCTTGTGTC GGGTAAGTTC 60
CGACCCGCAC GAAAGGCGTA ACGATTGCGG CACTGTCTCA ACTAGAGn 108

40

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60
nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGTA ATGGGT 116

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120
 ATCCTTGTAT TCGGTGTCAT AAAGTCTTTG CTCCTTGAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAATAAAA AAGTAAACAC 60
 AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTTATAATC CAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60
 TCAGAAAGCT TTTGATTAACT TTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCAGAC GTTCThAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60
 GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCC GCCGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
 TTTGTTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60
 AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACCGGCGAG TTACGATTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60
 TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120
 TTTTCAGCAT CAATTTGATC AATC 144

10 (2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

25 (2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GgGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60
 CTTAGAAGTG AGAATGCCCG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTnGnCTT GACCTCGCGG 60
 TTTGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60
CGGAATTTC AATTGCAAGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60
GAATGTAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120
A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60
ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAN AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60
TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTA CT ACCCTAGCTG TGTGGCCTT 120
CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCCCCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTGGTTACA ACGTTATTTT 60
CATTCACTCA ACTACTGCCA ATATAATATT GnaAACTATA GGACATTTAT TAGTGTTC 120
GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60
CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTGGGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60
TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATThTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTG TGCTCTGTAA CGTGCTTTCC AATTGGGAAC GCACGTGnCC CTGCCCATAC 60
 CTACGGGACT TGAATTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCCATG 120
 CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTAATTACCG 60
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60
 TTATAGTTAC GGTCCGCCGT TTAAGGGGGC TTCGATTCTG ATCTTCGCAG CTATATCTCA 120
 CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTTGG TGGGAGAACC 60
 TAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60
 GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

30 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTnTA 60
 35 ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

45 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60
 50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

55

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120
CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60
TGGATGGCGC TATTGCTTTA GGTCAATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCAC TG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

15

GTAACGCGCC GGTTCACTTCT ACAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60

CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCTTT CCGGGGTnGC 120

TTTTTCAACC TTTTTCCTCC TCCACGGTTA CT 152

20

(2) INFORMATION FOR SEQ ID NO: 4860:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

30

GCCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAGGAA TTCTAAGGTG AGCGAGCGAA 60

CTCTCGTTAA GGAACGCGC AAACGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

45

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60

AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTANTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120
 GCANTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
 TCGACTACTT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
CGGTTTAGCA GAGACCTGTG TTTTGTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCST GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACTACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120

AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

5 (2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTThAACC 60

AAAATTTGAT TAAAAAAGTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

20 (2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT 60

GGGCGTTAAC CCTAAAGAGC ACCC 84

35 (2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60

ATGATTTTAC CGATCTCTCh ATGAACAGTG CCAAATCGTA C 101

50 (2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60
 GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTG ATCCCGCTAG TCTCCACCAT 60
 TATTTGTACA TTGAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAATCCAA GAAAAATAAG 60
 35 CGAACTGAAT AAATAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60
 50 TGGACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

55

(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60
CGGGGAGGTT TgncCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AACAGCTCG CTAGGTGTCT 60
CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60
AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60
 CTTACAGCTT CTTCGCATT 80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAACTGGA AAAGTTGAGT 60
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120
 CGGTAA 127

(2) INFORMATION FOR SEQ ID NO: 4884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60
CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 60
ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGTCCGA 60

25

GTTCCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGGCCCC AAACCAAGGA GCTGGCTTTC TGTCACCTTA CCATTAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60
 AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG GCAGTTCGAA 60
 TCTGCCCCC TCCATTTATT ATTTTAAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
 GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120
TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTCGGATTT AATTTGATTC ATTTGTTGCG TAATTTTACA AGCCATTTTA TGAAAAGAGT 60
GATTTAATTC ATAAATTTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
AAACCAATTA GTA 73

35 (2) INFORMATION FOR SEQ ID NO: 4898:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
TGGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60
TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60
CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60
AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60
CAAAACTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCGGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60
AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60
TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

30 (2) INFORMATION FOR SEQ ID NO: 4905:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGAATTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60
TTATCGTGGT GGGGA 75

45 (2) INFORMATION FOR SEQ ID NO: 4906:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGA CTCAGAT CAGATAGTg CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

15

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGACAC GTGCTACTAA
AGGTTTACCA

60

70

(2) INFORMATION FOR SEQ ID NO: 4908:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

30

AGAAGATACA AATAAGnTA AACCCAAATT ATTCAATTTT GGTGGGACAC AATAGTGTG
ACTTTGAAGA AGATACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC
C

60

120

121

35

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

45

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCTGA GATGTTGGGG
TTAAGTCCCG

60

70

50

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCCGG AGAACTGAAA CATTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
 TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

15 ntCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60
 20 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTGAT 120
 GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

30 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60
 AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

45 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

10

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA
ATACTTCAT

60

69

15

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

25

TATTTTCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT
CATCCGCTCA

60

70

30

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

40

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTCACTCC
CCTTCCG

60

67

45

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

55

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
GGCGCACGTA GGCGATGATA CAGGTTATAT CCTACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60
ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
AGTGACAATA CTTCAGGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTTCGATTTCG 60
TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60
20 GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60
35 TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

45 GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60
50 TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTTG GGCAGTGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
GTGGGTCCCG ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGTTTT GGGACCAAGG GGTGCGAGTT CGAATCCTGT CTTCCCGATT 60
ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60
CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60
GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60
GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

15 ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60
20 TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

30 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
35 GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

45 TAGAAATCAG CTTTTTGGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60
CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60
TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60
CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTAGAACAAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60
TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

55

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
 GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60
 CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60
 TCCCTATAGC GGCgncGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
 TACAGCGCTG AACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTITGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTCC TTTCTCTTCC 60
T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTAAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60
TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60
CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60
TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGGGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

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CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

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AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

35

TTTCAATGTA CAATTTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG

60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG

59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG

59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG

59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTGGCGCT ATGTATATCG CATTAAACGT

60

(2) INFORMATION FOR SEQ ID NO: 4968:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTT TAGAGG CGACGCCAG TCAA ACTGCC CGCTGACACT GTCTCCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTCACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60
TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGA CTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60
AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATGTC ATAAGAAATA CTAATTTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTCGA CCCTGACTCG ACTTG TAGGT CTCGCAGTCA AGCTCCCTT

59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT

58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG

58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC

60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTGA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

25 AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAACGC TATCGATACT GAAGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

10

(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

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TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

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G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCG TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTC 60

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ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT

57

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(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

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CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG

57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTTCAG ACTCGCTTTC GCTACGG

57

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(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

45

CAAACCTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC

60

ATGCCGGTCT ACG

73

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(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTAAAT TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTGCGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG

(2) INFORMATION FOR SEQ ID NO: 5006:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG

(2) INFORMATION FOR SEQ ID NO: 5007:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA
AACCAAAGA

(2) INFORMATION FOR SEQ ID NO: 5008:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

10

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

56

- (2) INFORMATION FOR SEQ ID NO: 5010:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

25

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC

60

TTGGG

65

- (2) INFORMATION FOR SEQ ID NO: 5011:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

40

TTTACTTGTA TTGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

56

- (2) INFORMATION FOR SEQ ID NO: 5012:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTIGATAA ACAGTCGCTT

60

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- (2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAA TTGTGCAAGT TGGCGGGTCC 60
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCACT GGCCTCCACG TAAGCTAGCG CTTCACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTGAA 60
40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGACAT 60
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

40

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50

TACGGCGTTT AGTATTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA 55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGT TTGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

35

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGAATT 60
CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60
AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAAGTTCTG TGTTCCGGCAT GGGAACAGGT GTGA

54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG

56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10

GACCGGGATG GACATACCTC TGGTGTACCA GTTGTGCGTG CCAACGCATA AGCT

54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG

54

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(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG

60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG

105

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(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC

54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

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(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

35

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

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TTTCGTGCTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

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TT

62

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(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTCGTCAC CGGCAGTCAA CTTAGAGTGC CCA

53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG

53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60
TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

30

(2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

55

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG

53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA
CAA

60

63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTCATTGT CTGTAGAATT CCTTTTCGAA ATTC

54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG

53

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

(2) INFORMATION FOR SEQ ID NO: 5062:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT, CA

(2) INFORMATION FOR SEQ ID NO: 5063:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTGAC GTTTAGACA TA

52

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(2) INFORMATION FOR SEQ ID NO: 5064:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

(2) INFORMATION FOR SEQ ID NO: 5081:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

(2) INFORMATION FOR SEQ ID NO: 5082:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA

CG

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

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GTGTACCACT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG

52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC

60

CCGAGGAGCG GATTAACA

78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT

52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50

AAGTTGTTCT CAGTTCGGAT TGTAAGTCTGC AACTCGACTA CATGAAGCTG G

51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T

51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTAAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC C

51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

15 GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

40 CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60
CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA

50

(2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT TTAGACATAA

50

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGATTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTAATTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

(2) INFORMATION FOR SEQ ID NO: 5119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

(2) INFORMATION FOR SEQ ID NO: 5120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCAAT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

(2) INFORMATION FOR SEQ ID NO: 5121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

T

(2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTGAGATA

50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT

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(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35

CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCGAGAAG GTCTCTATCT

60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT

60

50

AGAA

64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

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(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAAGTTG

50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCACTTGTTG CTTGCTTCAA TTTTATGGGG CCATTTATGG

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35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGTTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

(2) INFORMATION FOR SEQ ID NO: 5135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

(2) INFORMATION FOR SEQ ID NO: 5136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

(2) INFORMATION FOR SEQ ID NO: 5138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

(2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10

GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC

52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT

56

(2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT

56

(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTACATC CAAACCTTCA TCACTCACGC GGC GTTGCTC CGTCAGCTTT 60
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA.

50

5

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGA CTCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GAAAGAGAAA

50

30

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTGCG ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

55

(2) INFORMATION FOR SEQ ID NO: 5152:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAAC TT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCCTACAA CCCCAACAAG CAAGCTTGTT G

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T

(2) INFORMATION FOR SEQ ID NO: 5160:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCTTTGTAT 60
T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

40

(2) INFORMATION FOR SEQ ID NO: 5163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50

CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAAACG TCTATGACGT 60

CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

55

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60
 AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60
 40 AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAAACTAG ATAAGTAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA

55

25 (2) INFORMATION FOR SEQ ID NO: 5170:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAAGCT GATTCTATT

50

50 (2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTGGAAG

60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn

50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAATAC CCCGTAAGTT CGGAGTAGGT CTCTTTA

57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA

60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACCTT ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAAGTGT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

15

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC
GCAATAT

60

67

(2) INFORMATION FOR SEQ ID NO: 5182:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

30

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAAGTAG CGAAGGCAAC TTTCT

55

(2) INFORMATION FOR SEQ ID NO: 5183:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

50

(2) INFORMATION FOR SEQ ID NO: 5184:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

55

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
 1 5 10 15

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	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
40	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
45	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55

(2) INFORMATION FOR SEQ ID NO:5193:

- (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

```

Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu
1           5           10           15
Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn
20           25           30
Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu
35           40           45
Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr
50           55           60
Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser
65           70           75           80
Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp
85           90           95
Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser
100          105          110
Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys
115          120          125
Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr
130          135          140
Val Phe Lys Phe Lys Asp Thr Thr Lys Leu Met Gly Lys Ala Leu Gly
145          150          155          160
Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val
165          170          175
Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro
180          185          190
Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr
195          200          205
Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg
210          215          220
Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln
225          230          235          240
Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe
245          250          255

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Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
 260 265 270
 Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
 275 280 285
 Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
 290 295 300
 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
 305 310 315 320
 Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
 1 5 10 15
 Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
 20 25 30
 Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
 35 40 45
 Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
 50 55 60
 Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
 65 70 75 80
 Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
 85 90 95
 Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
 100 105 110
 Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
 115 120 125
 Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
 130 135 140
 Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
 145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
 165 170 175
 5 Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
 180 185 190
 Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
 195 200 205
 10 Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
 210 215 220
 Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
 225 230 235 240
 15 Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
 245 250 255
 Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
 260 265 270
 20 Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
 275 280 285
 Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
 290 295 300
 25 Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
 305 310

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
 1 5 10 15
 45 Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
 20 25 30
 Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
 35 40 45
 50 Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
 50 55 60
 55 Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
 65 70 75 80

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Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
20 25 30

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
 35 40 45
 5 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
 50 55 60
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
 65 70 75 80
 10 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
 85 90 95
 Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
 100 105 110
 15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
 115 120 125
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
 130 135 140
 20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
 145 150 155 160
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
 165 170 175
 25 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
 180 185 190
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
 195 200 205
 30 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
 210 215 220
 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
 225 230 235 240
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
 245 250 255
 40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
 260 265 270
 Lys

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
30	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
25 35 40 45
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60
Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
30 65 70 75 80
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
35 100 105 110
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
40 130 135 140
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
45 145 150 155 160
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
50 180 185 190
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
55 210 215 220

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Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
 180 185 190
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
 5 195 200 205
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
 210 215 220
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 10 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 15 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 275 280

(2) INFORMATION FOR SEQ ID NO:5200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
 35 1 5 10 15
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
 20 25 30
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
 40 35 40 45
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
 50 55 60
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
 45 65 70 75 80
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
 85 90 95
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
 100 105 110
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
 55 115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
130 135 140

Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
165 170 175

Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
1 5 10 15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
20 25 30

Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
35 40 45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
50 55 60

Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
65 70 75 80

Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
85 90 95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
100 105 110

Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
115 120 125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
130 135 140

Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 165 170 175

Arg Ala Cys Glu Pro Asp Lys Tyr
 180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
 1           5           10           15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
 20           25           30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
 35           40           45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
 50           55           60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65           70           75           80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85           90           95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
100          105          110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
115          120          125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
130          135          140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145          150          155          160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
165          170          175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180          185          190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
195          200          205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210          215          220

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225 230 235 240
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
 245 250 255
 Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
 260 265 270
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile
 275 280

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly
 1 5 10 15
 Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu
 20 25 30
 Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln
 35 40 45
 Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys
 50 55 60
 His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn
 65 70 75 80
 Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly
 85 90 95
 Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala
 100 105 110
 Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg
 115 120 125
 Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu
 130 135 140
 Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr
 145 150 155 160
 Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr
 165 170 175

180 185 190
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
 195 200 205
 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
 210 215 220
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
 225 230 235 240
 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
 245 250 255
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
 260 265 270
 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
 275 280 285
 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val
 290 295 300
 His Ser Lys Asp Glu
 305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
 1 5 10 15
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
 20 25 30
 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
 35 40 45
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
 50 55 60
 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
 65 70 75 80
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
 85 90 95

100 105 110
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His
 115 120 125
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp
 130 135 140
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His
 10 145 150 155 160
 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln
 165 170 175
 15 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys
 180 185 190
 Ser

(2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala
 1 5 10 15
 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser
 20 25 30
 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe
 35 35 40 45
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys
 50 55 60
 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser
 45 65 70 75 80
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile
 85 90 95
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe
 100 105 110
 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn
 115 120 125
 55

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130 135 140

Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala
145 150 155 160

Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu
165 170 175

Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp
180 185 190

Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn
195 200 205

Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp
210 215 220

Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn
225 230 235 240

Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser
245 250 255

Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile
1 5 10 15

Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn
20 25 30

Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln
35 40 45

Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser
50 55 60

Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly
65 70 75 80

Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp
85 90 95

100 105 110
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
 115 120 125
 5
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
 130 135 140
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys
 10 145 150 155 160
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
 165 170 175
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
 15 180 185 190
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
 195 200

20 (2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
 35 1 5 10 15
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
 20 25 30
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
 40 35 40 45
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
 50 55 60
 45 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
 65 70 75 80
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
 85 90 95
 50 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
 100 105 110
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
 115 120 125
 55

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130 135 140

Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile
145 150 155 160

Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu
165 170 175

Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp
180 185 190

Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly
195 200 205

Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu
210 215 220

Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys
225 230 235 240

Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr
245 250 255

Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile
260 265 270

Lys Phe Val Leu Glu Asp Lys Gly Lys Ala Ala Glu Glu Ala Gly Tyr
275 280 285

Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys
290 295 300

Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp
305 310 315 320

Lys Lys Ser Glu Asp Lys Lys
325

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr
1 5 10 15

Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
20 25 30

	35	40	45
5	Asn Leu Met Met Thr Lys 50	Lys Leu Leu Ser Gln Tyr 55	Asn His Pro Lys 60
	Tyr Lys Leu Glu Leu Val 65	Lys Phe Asn Asn Trp 70	Pro Asp Leu Met Asp 75 80
10	Ala Leu Asn Ser Gly Arg Ile Asp Gly 85	Ala Ser Thr Leu Ile Glu Leu 90	
	Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu 100		110
15	Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu 115	120	125
	Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His 130	135	140
20	Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu 145	150	155 160
	Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu 165	170	175
25	Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala 180	185	190
	Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu 195	200	205
30	Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val 210	215	220
	Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe 225	230	235 240
35	Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln 245	250	255
	Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu 260	265	270
40	Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro 275	280	285
	Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe 290	295	300
45	Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu 305	310	315 320
50	Ala Ser Arg Ser		

(2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
 1 5 10 15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
 15 20 25 30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 20 50 55 60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
 65 70 75 80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
 25 85 90 95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
 100 105 110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
 30 115 120 125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
 35 130 135 140

Val Asp Tyr Trp
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
 1 5 10 15

55

20

25

30

His

5

(2) INFORMATION FOR SEQ ID NO:5212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 amino acids

10

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160

45

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
165 170 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180 185 190

50

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
195 200 205

55

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	210	215	220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu		
	225	230	235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln		
	245	250	255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
10	260	265	270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
	275	280	285
	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
15	290	295	300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
	305	310	315 320
	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
20	325	330	335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
	340	345	350
	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
25	355	360	365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
	370	375	380
	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
30	385	390	395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
	405	410	415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
	420	425	430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
40	435	440	445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
	450	455	460
	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
45	465	470	475 480
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
	485	490	

50 (2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
 1 5 10 15
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
 20 25 30
 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
 35 40 45
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
 50 55 60
 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
 65 70 75 80
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
 85 90 95
 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
 100 105 110
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
 115 120 125
 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
 130 135 140
 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
 145 150 155 160
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
 165 170 175
 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
 180 185 190
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
 195 200 205
 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
 210 215 220
 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
 225 230 235 240
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
 245 250 255
 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
 290 295

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
 1 5 10 15
 Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
 20 25 30
 Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
 35 40 45
 Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
 50 55 60
 Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
 65 70 75 80
 Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
 85 90 95
 Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
 100 105 110
 Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
 115 120 125
 Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
 130 135 140
 Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
 145 150 155 160
 Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
 165 170 175
 Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys	Glu	Arg	Val	Leu	Met	Lys	Lys	Leu	Leu	Thr	Ala	Ser	Ile	Ile	Ala	1	5	10	15
Cys	Ser	Val	Val	Met	Gly	Val	Gly	Leu	Val	Asn	Thr	Ser	Ala	Glu	Ala	20	25	30	
Ala	Ser	Gly	Asn	Ser	Ile	Asp	Thr	Val	Lys	Gln	Leu	Ile	Lys	Gly	Asp	35	40	45	
Gln	Ser	Leu	Glu	Asn	Val	Lys	Ile	Gly	Glu	Ser	Ile	Lys	Asp	Val	Leu	50	55	60	
Thr	Lys	Tyr	Lys	Asn	Pro	Met	Tyr	Ser	Tyr	Asn	Glu	Asp	Gly	Thr	Glu	65	70	75	80
His	Tyr	Tyr	Glu	Phe	His	Thr	Lys	Lys	Gly	Met	Leu	Leu	Val	Thr	Thr	85	90	95	
Asp	Gly	Lys	Lys	Asn	Asn	Gly	Lys	Val	Thr	His	Ile	Ser	Met	Met	Tyr	100	105	110	
Asn	Asp	Ala	Asn	Gly	Pro	Thr	Tyr	Gln	Ala	Val	Lys	Asn	Tyr	Val	Gly	115	120	125	
Lys	Ala	Val	Thr	His	Thr	Glu	Tyr	Ser	Lys	Val	Ala	Gly	Asn	Phe	Gly	130	135	140	
Tyr	Ile	Glu	Lys	Gly	Lys	Thr	Thr	Tyr	Gln	Phe	Ala	Ser	Ala	Pro	Lys	145	150	155	160
Asp	Lys	Asn	Ile	Lys	Leu	Tyr	Arg	Ile	Asp	Leu	Glu	Lys	165	170					

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

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1 5 10 15
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val
 20 25 30
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile
 35 40 45
 10 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn
 50 55 60
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu
 65 70 75 80
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu
 85 90 95
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr
 100 105 110
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala
 115 120 125
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys
 130 135 140
 25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr
 145 150 155 160
 30 Asp Asp Asn Lys Gln Pro Ala
 165

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
 1 5 10 15
 Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
 20 25 30
 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
 35 40 45
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
 50 55 60

65 70 75 80

Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
 85 90 95

Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
 100 105 110

Thr Ile Ser
 115

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

	Asn	Phe	Lys	Met	Gln	Glu	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys
	1							5								15
30	Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe
				20					25					30		
	Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu
			35					40					45			
35	Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile
		50					55					60				
	Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala
	65					70					75					80
40	Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe
					85					90					95	
	Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr
				100					105					110		
45	Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val
			115					120					125			
	Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala
50		130					135					140				
	Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe
	145					150					155					160
55	Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile			
					165					170						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

```

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
1           5           10           15

Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
          20           25           30

Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
          35           40           45

Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
          50           55           60

Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
65           70           75           80

Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
          85           90           95

Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
          100          105          110

Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
          115          120          125

Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
          130          135

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(2) INFORMATION FOR SEQ ID NO:5220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

```

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
1           5           10           15

```


20 25 30
 Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp
 35 40 45
 5 Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile
 50 55 60
 10 Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn
 65 70 75 80
 Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu
 85 90 95
 15 Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys
 100 105 110
 Val Thr Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu
 115 120 125
 20 Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu
 130 135 140
 Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile
 145 150 155 160
 25 Met Gln

(2) INFORMATION FOR SEQ ID NO:5221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu
 1 5 10 15
 45 Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn
 20 25 30
 Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu
 35 40 45
 50 Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys
 50 55 60
 55 Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg
 65 70 75 80

	85	90	95
5	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp 100 105 110		
	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn 115 120 125		
10	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His 130 135 140		
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn 145 150 155 160		
15	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr 165 170 175		
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala 180 185 190		
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn 195 200 205		
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu 210 215 220		
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile 225 230 235 240		
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys 245 250 255		
30	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp 260 265 270		
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys 275 280 285		
35	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys 290 295 300		
40	Tyr Gln Asn Lys Leu Ala Ser 305 310		

(2) INFORMATION FOR SEQ ID NO:5222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

1	5	10	15
Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr Arg Ile Lys	20	25	30
Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Thr Asn Glu Glu	35	40	45
Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala Asn Ala Gln	50	55	60
Tyr Tyr Tyr Lys Gln Tyr Xaa Arg Met Lys Thr Arg Xaa Arg Glu Leu	65	70	75
Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr Phe Ser Thr	85	90	95
Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile Asp Glu Ile	100	105	110
Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg Lys Asn Gln	115	120	125
Thr Lys Lys Lys Lys Ala Gln Ile Gln Leu Gln His Tyr Val Ser Thr	130	135	140
Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln Asn Asp Tyr	145	150	155
Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu His Thr Lys	165	170	175
Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala Pro Ser Asp	180	185	190
Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe Ser Lys Ala	195	200	205
Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile Lys Asn Val	210	215	220
His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr Asp Asn Gln	225	230	235
Lys Thr Leu Tyr Ala	245		

(2) INFORMATION FOR SEQ ID NO:5223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 35 40 45
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 65 70 75 80
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95
 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
 1 5 10 15
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
 20 25 30
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
 35 40 45
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
 50 55 60
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
 65 70 75 80
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
 85 90 95
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
 100 105 110

115

120

125

His Ser Ile
130

5

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

20

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

25

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

30

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

35

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

40

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

45

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

50

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

55

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

	210	215	220
	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly		
	225	230	235 240
5	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn		
		245	250 255
	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val		
10		260	265 270
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys		
		275	280 285
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr		
		290	295 300
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp		
		305	310 315 320
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly		
		325	330 335
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu		
		340	345 350
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr		
		355	360 365
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly		
30		370	375 380
	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro		
		385	390 395 400
35	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn		
		405	410 415
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu		
		420	425 430
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr		
		435	440 445
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr		
		450	455 460
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly		
		465	470 475 480
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp		
50		485	490 495
	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr		
		500	505 510
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser		
		515	520 525

530

535

540

(2) INFORMATION FOR SEQ ID NO:5226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
 1 5 10 15
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
 20 25 30
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
 35 40 45
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
 50 55 60
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
 65 70 75 80
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
 85 90 95
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
 100 105 110
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
 115 120 125
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
 130 135 140
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
 145 150 155 160
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
 165 170 175
 Lys

(2) INFORMATION FOR SEQ ID NO:5227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
 1 5 10 15
 Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
 20 25 30
 His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
 35 40 45
 Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
 50 55 60
 Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
 65 70 75 80
 Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
 85 90 95
 Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
 100 105 110
 Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
 115 120 125
 Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
 130 135 140
 Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
 145 150 155 160
 Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
 165 170 175
 Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
 180 185 190
 Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
 195 200 205
 Cys

(2) INFORMATION FOR SEQ ID NO:5228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
 1 5 10 15
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
 20 25 30
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp
 35 40 45
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
 50 55 60
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
 65 70 75 80
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
 85 90 95
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
 100 105 110
 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
 115 120 125
 25 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
 130 135 140
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
 145 150 155 160
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
 165 170 175
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
 180 185 190
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
 195 200 205
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
 210 215 220
 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
 225 230 235 240
 45 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
 245 250 255
 50

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10

Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15

Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30

15

Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45

Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60

20

Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80

Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95

25

Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110

Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125

30

Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140

Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160

Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175

40

Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190

Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
 195 200 205

45

Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
 210 215 220

Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
 225 230 235 240

50

Leu Gly Ala Trp Gly Phe
 245

55

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser	1	5	10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala	20	25	30	
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe	35	40	45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp	50	55	60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp	65	70	75	80
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys	85	90	95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu	100	105	110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val	115	120	125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile	130	135	140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp	145	150	155	160
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln	165	170	175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe	180	185	190	
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser	195	200	205	
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His	210	215	220	
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile	225	230	235	240
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala	245	250	255	

EP 0 786 519 A2

Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
260 265 270

Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
275 280 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
290 295 300

Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
305 310 315 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
325 330 335

Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
340 345 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
355 360 365

Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
370 375 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
385 390 395 400

Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
405 410 415

Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
420 425 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
435 440 445

Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
450 455 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
465 470 475 480

Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
485 490 495

Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
500 505 510

Leu Ile Thr Thr Asp Phe Lys
515

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
30	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
40	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
55	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
 290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
 1 5 10 15
 Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
 20 25 30
 Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
 35 40 45
 Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
 50 55 60
 Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
 65 70 75 80
 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
 85 90 95
 Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
 100 105 110
 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
 115 120 125
 Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
 130 135 140
 Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
 145 150 155 160
 Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
 165 170 175
 His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
 180 185 190
 Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
 195 200 205

Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile
 210 215 220
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr
 225 230 235 240
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly
 245 250 255
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His
 260 265 270
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met
 275 280 285
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met
 290 295 300
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val
 305 310 315 320
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr
 325 330 335
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys
 340 345 350
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro
 355 360 365
 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His
 370 375 380
 30 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu
 385 390 395 400
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly
 405 410 415
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg
 420 425 430
 40 Lys

(2) INFORMATION FOR SEQ ID NO:5233:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

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Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
1 5 10 15

Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
5 20 25 30

Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
35 40 45

Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
10 50 55 60

Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
65 70 75 80

Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
15 85 90 95

Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
20 100 105 110

Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
115 120 125

Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
25 130 135 140

Asp Ile Asn Val Lys Thr Lys
145 150

(2) INFORMATION FOR SEQ ID NO:5234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
1 5 10 15

Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
20 25 30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
35 40 45

Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
50 55 60

Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
55 65 70 75 80

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	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala	
					85					90					95		
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser	
				100					105					110			
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr	
			115					120					125				
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile	
		130					135					140					
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr	
	145					150					155					160	
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln	
					165					170					175		
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys	
				180					185						190		
20	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys	
			195					200					205				
	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	
25		210					215					220					
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys	
	225					230					235					240	
	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn	
30					245					250					255		
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn	
				260					265					270			
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly	
		275					280						285				
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser	
		290					295					300					
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp	
	305					310					315					320	
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile	
					325					330					335		
45	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala	
				340					345					350			
	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr	
50			355					360					365				
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp	
		370					375					380					
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu	
	385					390					395					400	

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn
405 410 415

Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln
420 425 430

Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln
435 440 445

Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln
450 455 460

Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala
465 470 475 480

Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile
485 490 495

Pro

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn
1 5 10 15

Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr
20 25 30

Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser
35 40 45

Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile
50 55 60

Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp
65 70 75 80

Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn
85 90 95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
100 105 110

Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
115 120 125

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	Gln	Leu	Leu	Asp	Lys	Asn	Asn	Glu	Thr	Gln	Tyr	Tyr	His	Phe	Phe	Ser
	130						135					140				
5	Ile	Lys	Asp	Pro	Ala	Asp	Val	Tyr	Tyr	Thr	Lys	Lys	Lys	Ala	Glu	Val
	145					150					155					160
	Glu	Leu	Asp	Ile	Asn	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
					165					170					175	
10	Glu	Asn	Asn	Gln	Lys	Leu	Pro	Val	Arg	Leu	Val	Ser	Tyr	Ser	Pro	Val
				180					185					190		
	Pro	Glu	Asp	His	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asp	Gly	Thr	Gln
			195					200					205			
15	Glu	Leu	Lys	Ile	Val	Ser	Ser	Thr	Gln	Ile	Asp	Asp	Gly	Glu	Glu	Thr
	210						215					220				
	Asn	Tyr	Asp	Tyr	Thr	Lys	Leu	Val	Phe	Ala	Lys	Pro	Ile	Tyr	Asn	Asp
	225					230					235					240
20	Pro	Ser	Leu	Val	Lys	Ser	Asp	Thr	Asn	Asp	Ala	Val	Val	Thr	Asn	Asp
					245					250						255
	Gln	Ser	Ser	Ser	Val	Ala	Ser	Asn	Gln	Thr	Asn	Thr	Asn	Thr	Ser	Asn
25					260				265					270		
	Gln	Asn	Ile	Ser	Thr	Ile	Asn	Asn	Ala	Asn	Asn	Gln	Pro	Gln	Ala	Thr
					275			280					285			
30	Thr	Asn	Met	Ser	Gln	Pro	Ala	Gln	Pro	Lys	Ser	Ser	Thr	Asn	Ala	Asp
	290						295					300				
	Gln	Ala	Ser	Ser	Gln	Pro	Ala	His	Glu	Thr	Asn	Ser	Asn	Gly	Asn	Thr
	305					310					315					320
35	Asn	Asp	Lys	Thr	Asn	Glu	Ser	Ser	Asn	Gln	Ser	Asp	Val	Asn	Gln	Gln
					325					330					335	
	Tyr	Pro	Pro	Ala	Asp	Glu	Ser	Leu	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Ala
				340					345					350		
40	Ile	Ile	Asp	Lys	Glu	His	Thr	Ala	Asp	Asn	Trp	Arg	Pro	Ile	Asp	Phe
			355					360					365			
	Gln	Met	Lys	Asn	Asp	Lys	Gly	Glu	Arg	Gln	Phe	Tyr	His	Tyr	Ala	Ser
45		370					375					380				
	Thr	Val	Glu	Pro	Ala	Thr	Val	Ile	Phe	Thr	Lys	Thr	Gly	Pro	Ile	Ile
	385					390					395					400
	Glu	Leu	Gly	Leu	Lys	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
50					405					410					415	
	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Val	Glu	Leu	Val	Ser	Tyr	Asp	Ser	Asp
				420					425					430		
55	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	Arg	Glu
				435				440					445			

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	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490						495	
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
			530				535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570						575	
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
	610						615					620					
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
	625					630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
					645					650					655		
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680					685				
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
	690						695					700					
45	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
	705					710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
			755					760					765				

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met
 770 775 780
 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys
 5 785 790 795 800
 Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys
 805 810 815
 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys
 10 820 825 830
 Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys
 835 840 845
 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser
 15 850 855 860
 Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg
 865 870 875 880
 20 Asn Asn Xaa Gln Ala Asn
 885

(2) INFORMATION FOR SEQ ID NO:5236:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: protein
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:
 Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile
 1 5 10 15
 40 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser
 20 25 30
 Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys
 35 40 45
 45 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val
 50 55 60
 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn
 50 65 70 75 80
 Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys
 85 90 95
 55 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
 100 105 110

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Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
115 120 125

Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
130 135 140

Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
145 150 155 160

Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
165 170 175

Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
180 185 190

Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
195 200 205

Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
210 215 220

Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
1 5 10 15

Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
20 25 30

Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
35 40 45

Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
50 55 60

Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
65 70 75 80

Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
85 90 95

Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
 115 120 125
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
 130 135 140
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
 145 150 155 160
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
 165 170 175
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
 180 185 190
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
 195 200 205
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
 210 215 220
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val
 225 230 235 240
 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
 245 250 255
 25 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
 260 265 270
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
 275 280 285
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
 290 295 300
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
 305 310 315 320
 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
 325 330 335
 40 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
 340 345 350
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
 1 5 10 15
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
 20 25 30
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
 35 40 45
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
 50 55 60
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
 65 70 75 80
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
 85 90 95
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
 100 105 110
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
 115 120 125
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
 130 135 140
 Val Asp Thr Lys Lys Gln
 145 150
 30

(2) INFORMATION FOR SEQ ID NO:5239:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
 1 5 10 15
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
 20 25 30
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
 35 40 45
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly
 50 55 60
 55

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	Arg	Asp	Gly	Met	Glu	Val	Cys	Arg	Glu	Val	Arg	Lys	Lys	Tyr	Glu	Met	65	70	75	80
5	Pro	Ile	Ile	Met	Leu	Thr	Ala	Lys	Asp	Ser	Glu	Ile	Asp	Lys	Val	Leu	85	90	95	
	Gly	Leu	Glu	Leu	Gly	Ala	Asp	Asp	Tyr	Val	Thr	Lys	Pro	Phe	Ser	Thr	100	105	110	
10	Arg	Glu	Leu	Ile	Ala	Arg	Val	Lys	Ala	Asn	Leu	Arg	Arg	His	Tyr	Ser	115	120	125	
	Gln	Pro	Ala	Gln	Asp	Thr	Gly	Asn	Val	Thr	Asn	Glu	Ile	Thr	Ile	Lys	130	135	140	
15	Asp	Ile	Val	Ile	Tyr	Pro	Asp	Ala	Tyr	Ser	Ile	Lys	Lys	Arg	Gly	Glu	145	150	155	160
	Asp	Ile	Glu	Leu	Thr	His	Arg	Glu	Phe	Glu	Leu	Phe	His	Tyr	Leu	Ser	165	170	175	
20	Lys	His	Met	Gly	Gln	Val	Met	Thr	Arg	Glu	His	Leu	Leu	Gln	Thr	Val	180	185	190	
	Trp	Gly	Tyr	Asp	Tyr	Phe	Gly	Asp	Val	Arg	Thr	Val	Asp	Val	Thr	Ile	195	200	205	
25	Arg	Arg	Leu	Arg	Glu	Lys	Ile	Glu	Asp	Asp	Pro	Ser	His	Pro	Glu	Tyr	210	215	220	
	Ile	Val	Thr	Arg	Arg	Gly	Val	Gly	Tyr	Phe	Leu	Gln	Gln	His	Glu		225	230	235	

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

45	Xaa	Leu	Ser	Thr	Val	Ile	Gly	Ala	Xaa	Leu	Phe	Phe	Lys	Ser	Ser	Val	1	5	10	15
	Ser	Leu	Val	Phe	Lys	Met	Val	Lys	Lys	Phe	Arg	Xaa	Gly	Val	Ile	Ser	20	25	30	
50	Val	Asn	Asp	Val	Met	Phe	Ser	Ser	Ser	Ile	Met	Tyr	Arg	Ile	Lys	Lys	35	40	45	
55	Asn	Ala	Phe	Ser	Leu	Thr	Val	Met	Ala	Ile	Ile	Ser	Ala	Ile	Thr	Val	50	55	60	

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Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
65 70 75 80

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe
100 105 110

Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
115 120 125

Phe Asp Val Lys Ala
130

(2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly
20 25 30

Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
50 55 60

Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
85 90 95

Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
100 105 110

Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
130 135 140

Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
145 150 155 160

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	Pro	Ile	Gly	Val	Val	Gly	Ala	Val	Val	Ala	Trp	Asn	Phe	Pro	Met	Leu
					165					170					175	
5	Leu	Ala	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Asn	Thr	Ile
				180					185					190		
	Val	Ile	Gln	Pro	Ser	Ser	Ser	Thr	Pro	Leu	Ser	Leu	Leu	Glu	Val	Ala
			195					200					205			
10	Lys	Ile	Phe	Gln	Glu	Val	Leu	Pro	Lys	Gly	Val	Val	Asn	Ile	Leu	Thr
		210					215					220				
	Gly	Lys	Gly	Ser	Glu	Ser	Gly	Asn	Ala	Ile	Phe	Asn	His	Asp	Gly	Val
	225					230					235				240	
15	Asp	Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Asp	Val	Gly	Tyr	Gln	Val	Ala
					245					250					255	
	Glu	Ala	Ala	Ala	Lys	His	Leu	Val	Pro	Ala	Thr	Leu	Glu	Leu	Gly	Gly
					260				265					270		
20	Lys	Ser	Ala	Asn	Ile	Ile	Leu	Asp	Asp	Ala	Asn	Leu	Asp	Leu	Ala	Val
			275					280					285			
	Glu	Gly	Ile	Gln	Leu	Gly	Ile	Leu	Phe	Asn	Gln	Gly	Glu	Val	Cys	Ser
25		290					295					300				
	Ala	Gly	Ser	Arg	Leu	Leu	Val	His	Glu	Lys	Ile	Tyr	Asp	Gln	Leu	Val
	305					310					315					320
	Pro	Arg	Leu	Gln	Glu	Ala	Phe	Ser	Asn	Ile	Lys	Val	Gly	Asn	Pro	Gln
30					325					330					335	
	Asp	Glu	Ala	Thr	Gln	Met	Gly	Ser	Gln	Thr	Gly	Lys	Asp	Gln	Leu	Asp
					340				345					350		
35	Lys	Ile	Gln	Ser	Tyr	Ile	Asp	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Gln	Ile
			355				360						365			
	Leu	Ala	Gly	Gly	His	Arg	Leu	Thr	Glu	Asn	Gly	Leu	Asp	Lys	Gly	Phe
		370					375					380				
40	Phe	Phe	Glu	Pro	Thr	Leu	Ile	Ala	Val	Pro	Asp	Asn	His	His	Lys	Leu
	385					390					395					400
	Ala	Gln	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Thr	Val	Ile	Lys	Val	Lys
					405					410					415	
45	Asp	Asp	Gln	Glu	Ala	Ile	Asp	Ile	Ala	Asn	Asp	Ser	Glu	Tyr	Gly	Leu
					420				425					430		
	Ala	Gly	Gly	Val	Phe	Ser	Gln	Asn	Ile	Thr	Arg	Ala	Leu	Asn	Ile	Ala
			435					440					445			
50	Lys	Ala	Val	Arg	Thr	Gly	Arg	Ile	Trp	Ile	Asn	Thr	Tyr	Asn	Gln	Val
		450					455					460				
	Pro	Glu	Gly	Ala	Pro	Phe	Gly	Gly	Tyr	Lys	Lys	Ser	Gly	Ile	Gly	Arg
55		465				470					475					480

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
 1 5 10 15
 Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
 20 25 30
 Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
 35 40 45
 Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
 50 55 60
 Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
 65 70 75 80
 Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
 85 90 95
 Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
 100 105 110
 Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
 115 120 125
 Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
 130 135 140
 Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
 145 150 155 160
 Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
 165 170 175
 Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
 180 185 190
 Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
 195 200 205

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Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
210 215 220

5 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
225 230 235 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
245 250 255

10 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
260 265 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
275 280 285

15 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
290 295 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
305 310 315 320

20 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
325 330 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
340 345 350

25 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
355 360 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
370 375 380

30 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
385 390 395 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
405 410 415

35 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
420 425 430

40 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
435 440 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
450 455 460

45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
465 470 475 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
485 490 495

50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
500 505 510

Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
515 520 525

55

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
 1 5 10 15
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
 20 25 30
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
 25 35 40 45
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
 50 55 60
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe
 30 65 70 75 80
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
 85 90 95
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
 35 100 105 110
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
 115 120 125
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
 40 130 135 140
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
 145 150 155 160
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
 45 165 170 175
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
 180 185 190
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
 50 195 200 205
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
 55 210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr
245 250 255

15 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile
260 265 270

Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn
275 280 285

20 Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly
290 295 300

Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser
305 310 315 320

25 Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln
355 360 365

35 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp
370 375 380

Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp
385 390 395 400

40 Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr
420 425 430

(2) INFORMATION FOR SEQ ID NO:5245:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe	100	105	110	
	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
25	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
30	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
35	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
45	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
50	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

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Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr
 305 310 315 320

5 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp
 325 330 335

Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr
 340 345 350

10 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
 355 360 365

Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
 370 375 380

15 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
 385 390 395 400

Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
 405 410 415

20 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
 420 425 430

Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
 435 440 445

25 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
 450 455 460

30 Gly Gly Asp Ile Ile
 465

(2) INFORMATION FOR SEQ ID NO:5246:

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 414 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
 1 5 10 15

Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
 20 25 30

Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
 35 40 45

55 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
 50 55 60

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	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	65	70	75	80
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser	85	90	95	
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser	100	105	110	
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe	115	120	125	
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu	130	135	140	
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His	145	150	155	160
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His	165	170	175	
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile	180	185	190	
	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe	195	200	205	
25	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys	210	215	220	
	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu	225	230	235	240
30	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val	245	250	255	
	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala	260	265	270	
35	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala	275	280	285	
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp	290	295	300	
	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val	305	310	315	320
45	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp	325	330	335	
	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser	340	345	350	
50	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn	355	360	365	
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	Leu	Ala	Met	His	Leu	370	375	380	

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
 385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
 1 5 10 15

Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
 20 25 30

Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
 35 40 45

Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
 50 55 60

Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val
 65 70 75 80

Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
 85 90 95

His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
 100 105 110

Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
 115 120 125

Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
 130 135 140

Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
 145 150 155 160

Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
 165 170 175

Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
 180 185 190

Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
 195 200 205

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Lys Leu Phe Asn Arg Thr Glu Gln Thr Glu Lys His Ile Tyr Asp Asp
 210 215 220
 5 Ser Thr Gln Phe Arg Thr Leu Thr Met Arg Ile Leu Arg Ser Ala Phe
 225 230 235 240
 Leu Ser Gly Leu Met Leu Glu Phe Ile Ser Met Leu Gly Ile Gly Leu
 245 250 255
 10 Val Ala Leu Glu Ala Thr Leu Ser Leu Val Val Phe His Asn Ile Asp
 260 265 270
 Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn
 275 280 285
 15 Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr Gly Lys Gln Ser Glu
 290 295 300
 Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn
 305 310 315 320
 20 Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln
 325 330 335
 Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu
 340 345 350
 25 Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val
 355 360 365
 Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly
 370 375 380
 30 Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu
 385 390 395 400
 Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile
 405 410 415
 35 Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu
 420 425 430
 Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr
 435 440 445
 40 Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly
 450 455 460
 45 Gly Gln Met Arg Arg Ile Glu Leu Cys Arg Leu Leu Val Met Lys Pro
 465 470 475 480
 Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr
 485 490 495
 50 Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr
 500 505 510
 Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg
 515 520 525
 55

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
 530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
 545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
 1 5 10 15
 Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
 20 25 30
 Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
 35 40 45
 Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr
 50 55 60
 Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
 65 70 75 80
 Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
 85 90 95
 Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
 100 105 110
 Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
 115 120 125
 Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
 130 135 140
 Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
 145 150 155 160
 Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
 165 170 175
 Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
 180 185 190
 Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp
 195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
 210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
 225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
 245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
 260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala
 275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
 290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
 305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
 325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn
 340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
 355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn
 370 375 380

30 Gln Ile Asn Gln Ile Met Gln Tyr Lys
 385 390

(2) INFORMATION FOR SEQ ID NO:5249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
 1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
 20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala
 35 40 45

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	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	Ser	Ala	Ser	Asn	Glu	Ser	Lys	
	50						55					60					
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr	
	65						70				75					80	
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr	
						85				90					95		
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser	
				100					105					110			
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr	
				115				120					125				
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn	
		130					135					140					
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser	
	145					150					155					160	
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr	
						165				170					175		
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr	
25				180				185						190			
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys	
			195					200					205				
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala	
		210					215					220					
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp	
	225					230					235					240	
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr	
					245					250					255		
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe	
				260					265					270			
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val	
			275					280					285				
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro	
		290					295					300					
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser	
	305					310					315					320	
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp	
					325					330					335		
50	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn	
				340					345					350			
	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr	
55			355					360					365				

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	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe	
	370						375					380					
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn	
	385					390					395					400	
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val	
					405					410					415		
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn	
					420				425					430			
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp	
				435				440					445				
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe	
	450						455					460					
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln	
	465					470					475					480	
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr	
					485					490					495		
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu	
25					500				505					510			
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg	
			515					520						525			
	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser	
30		530					535					540					
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro	
	545					550					555					560	
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser	
					565					570					575		
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser	
				580					585					590			
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	
			595					600					605				
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	
			610				615					620					
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser	
	625					630					635					640	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
					645					650					655		
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
					660					665				670			
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
55					675					680				685			

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	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	690						695						700			
5	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	705					710					715					720
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					725					730					735	
10	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					740					745					750	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					755					760					765	
15	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	770						775						780			
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
20	785					790					795					800
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					805					810					815	
25	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					820					825					830	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Gly	Ser
					835					840					845	
30	Asp	Ser	Asp	Ser	Ser	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asn	Ser
	850						855						860			
	Asp	Ser	Glu	Ser	Val	Ser	Asn	Asn	Asn	Val	Val	Pro	Pro	Asn	Ser	Pro
35	865						870					875				880
	Lys	Asn	Gly	Thr	Asn	Ala	Ser	Asn	Lys	Asn	Glu	Ala	Lys	Asp	Ser	Lys
					885						890				895	
40	Glu	Pro	Leu	Pro	Asp	Thr	Gly	Ser	Glu	Asp	Glu	Ala	Asn	Thr	Ser	Leu
					900					905					910	
	Ile	Trp	Gly	Leu	Leu	Ala	Ser	Ile	Gly	Ser	Leu	Leu	Leu	Phe	Arg	Arg
			915					920						925		
45	Lys	Lys	Glu	Asn	Lys	Asp	Lys	Lys								
	930						935									

(2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala
 1 5 10 15
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro
 20 25 30
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu
 35 40 45
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys
 50 55 60
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys
 65 70 75 80
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
 85 90 95
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
 100 105 110
 Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
 115 120 125
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
 130 135 140
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
 145 150 155 160
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
 165 170 175
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
 180 185 190
 Ile Leu

40

(2) INFORMATION FOR SEQ ID NO:5251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55

Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
 1 5 10 15

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Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser
20 25 30

5 Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr
35 40 45

Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His
50 55 60

10 Leu Phe Gly Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys
65 70 75 80

Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp
85 90 95

15 Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu
100 105 110

Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile
115 120 125

20 Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala
130 135 140

25 Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu
145 150 155 160

Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys
165 170 175

30 His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly
180 185 190

Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser
195 200 205

35 Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu
210 215 220

Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp
225 230 235 240

40 Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile
245 250 255

Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn
260 265 270

45 Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His
275 280 285

50 Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly
290 295 300

Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu
305 310 315 320

55 Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile
325 330 335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
 340 345 350
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
 355 360 365
 Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile
 370 375 380
 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
 385 390 395 400
 Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
 405 410 415
 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
 420 425 430
 Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro
 435 440 445
 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro
 450 455 460
 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala
 465 470 475 480
 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val
 485 490 495
 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro
 500 505 510
 Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly
 515 520 525
 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile
 530 535 540
 Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala
 545 550 555

(2) INFORMATION FOR SEQ ID NO:5252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu
 1 5 10 15

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Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
130 135 140

25 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
145 150 155 160

Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
165 170 175

30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
180 185 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
195 200 205

35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
210 215 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 5 20 25 30
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 10 50 55 60
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 65 70 75 80
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 15 85 90 95
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 100 105 110
 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
 115 120 125
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
 130 135 140
 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
 145 150 155 160
 Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 20 25 30
 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Lys Thr Thr Thr Val Glu Asn Gly Asn Ser Ala Thr Asp Asn
 50 55 60

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	Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu	65	70	75	80
5	Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala	85	90	95	
	Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln	100	105	110	
10	Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys	115	120	125	
	Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn	130	135	140	
15	Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln	145	150	155	160
	Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala	165	170	175	
20	Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala	180	185	190	
	Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser	195	200	205	
25	Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn	210	215	220	
	Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu	225	230	235	240
30	Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu	245	250	255	
	Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro	260	265	270	
35	Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu	275	280	285	
40	Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val	290	295	300	
	Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr	305	310	315	320
45	Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu	325	330	335	
	Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn	340	345	350	
50	Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn	355	360	365	
	Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr	370	375	380	

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	Thr Ser Val Thr Val Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn	385	390	395	400
5	Gly Asn Gln Pro Lys Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu	405	410	415	
	Asp Ile Ala Lys Ser Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe	420	425	430	
10	Lys Glu Val Thr Ser Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn	435	440	445	
	Gly Ser Tyr Ser Leu Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val	450	455	460	
15	His Tyr Asp Gly Glu Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg	465	470	475	480
	Thr Gln Met Val Gly His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp	485	490	495	
20	Arg Gly Tyr Thr Leu Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn	500	505	510	
	Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys	515	520	525	
25	Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr	530	535	540	
	Asp Lys Asn Leu Val Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr	545	550	555	560
30	Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Tyr Val	565	570	575	
	Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp	580	585	590	
35	Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly	595	600	605	
	Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser	610	615	620	
40	Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu	625	630	635	640
45	Asp Thr Asn Pro Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val	645	650	655	
	Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser	660	665	670	
50	Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn	675	680	685	
	Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln Ala Gln	690	695	700	
55					

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Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser
 705 710 715 720
 5 Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu
 725 730 735
 Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu
 740 745 750
 10 Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu
 755 760 765
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe
 770 775 780
 15 Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe
 785 790 795 800
 Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn
 805 810 815
 20 Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn
 820 825 830
 Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser
 835 840 845
 25 Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu
 850 855 860
 Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp
 865 870 875 880
 30 Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro
 885 890 895
 35 Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu
 900 905 910
 Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu
 915 920 925
 40 Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro
 930 935 940
 Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu
 945 950 955 960
 45 Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys
 965 970 975
 Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro
 980 985 990
 50 Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly
 995 1000 1005
 55 Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn
 1010 1015 1020

His Lys Ala
1025

5 (2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
(B) TYPE: amino acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

20 Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
1 5 10 15
Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
20 25 30
25 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys
35 40 45
Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp
50 55 60
30 Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu
65 70 75 80
Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val
35 85 90 95
Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
100 105 110
40 Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys
115 120 125
Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys
130 135 140
45 Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg
145 150 155

50 Claims

- 55 1. Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
 - (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;
 - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - (c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
11. A vector comprising a fragment of claim 8.
12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
13. A vector comprising a fragment of claim 12.
14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
15. A method for producing a polypeptide in a host cell comprising the steps of:
 - (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
 - (b) isolating said protein.
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
 - (b) identifying members of said library which contain sequences that hybridize to said target sequence;
 - (c) isolating the nucleic acid molecules from said members identified in step (b).
19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) isolating mRNA, DNA, or cDNA produced from an organism;
 - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
 - (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8.
21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
 - (a) an isolated polypeptide antigen of claim 24, and
 - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

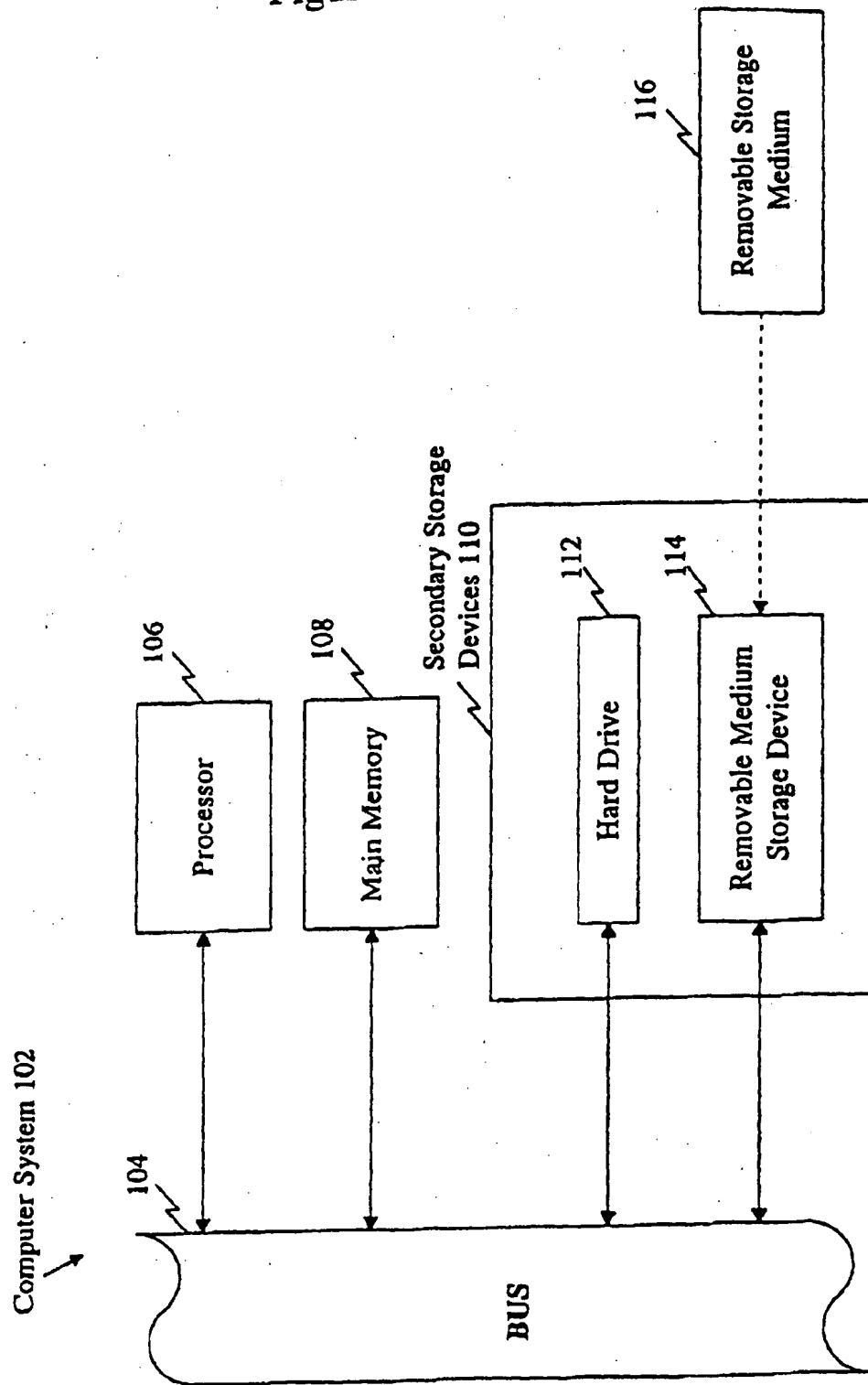


Figure 2

